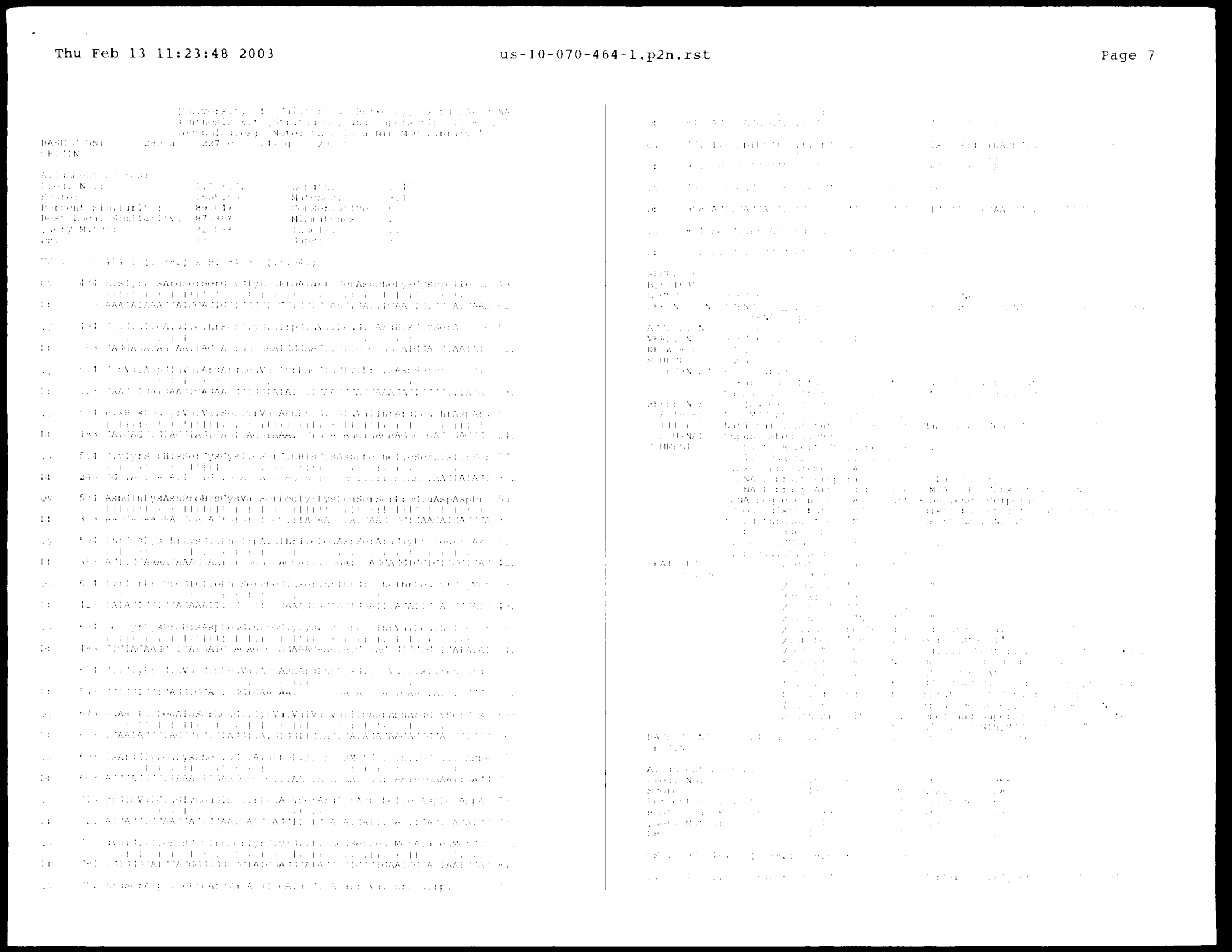
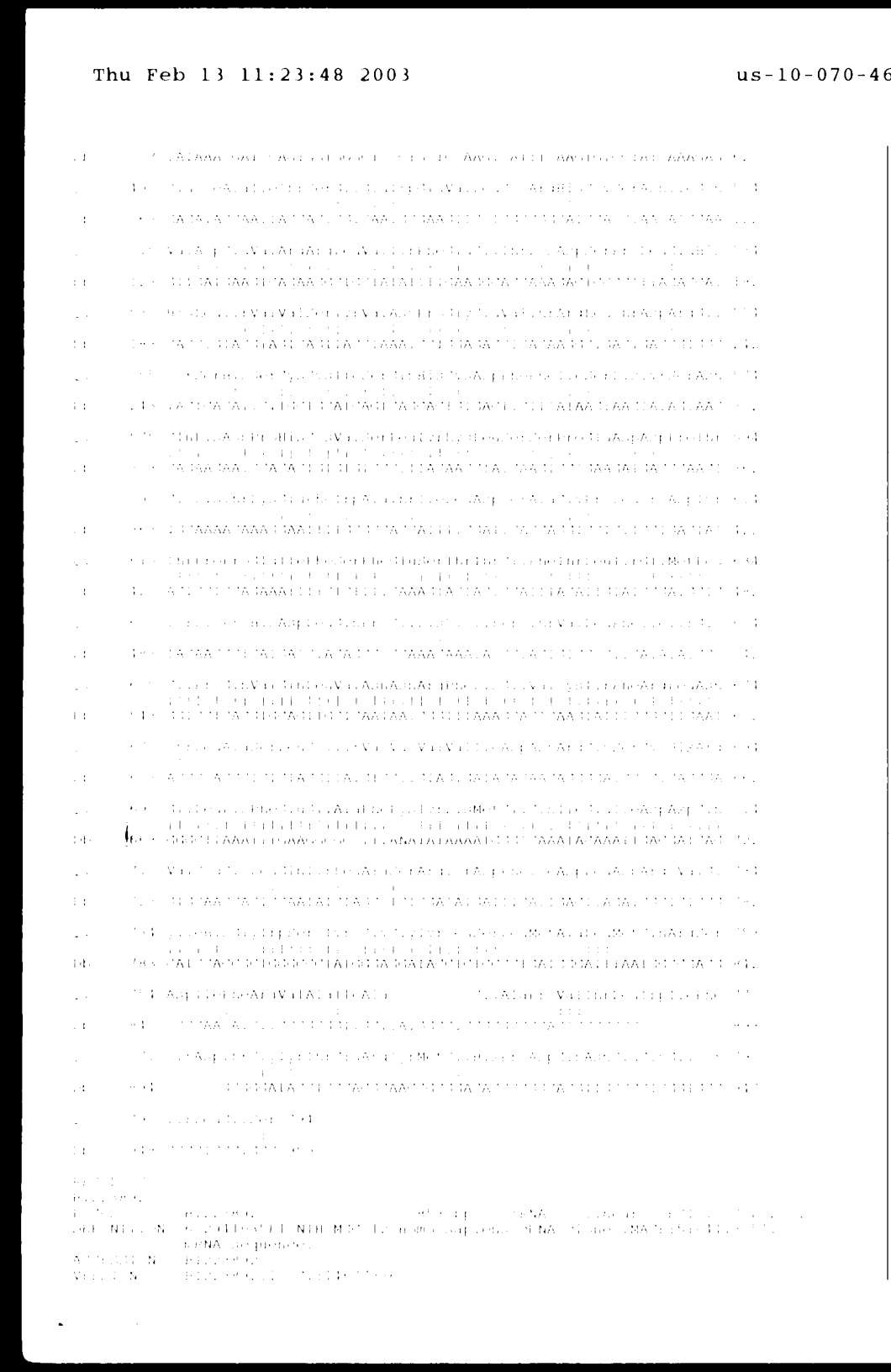
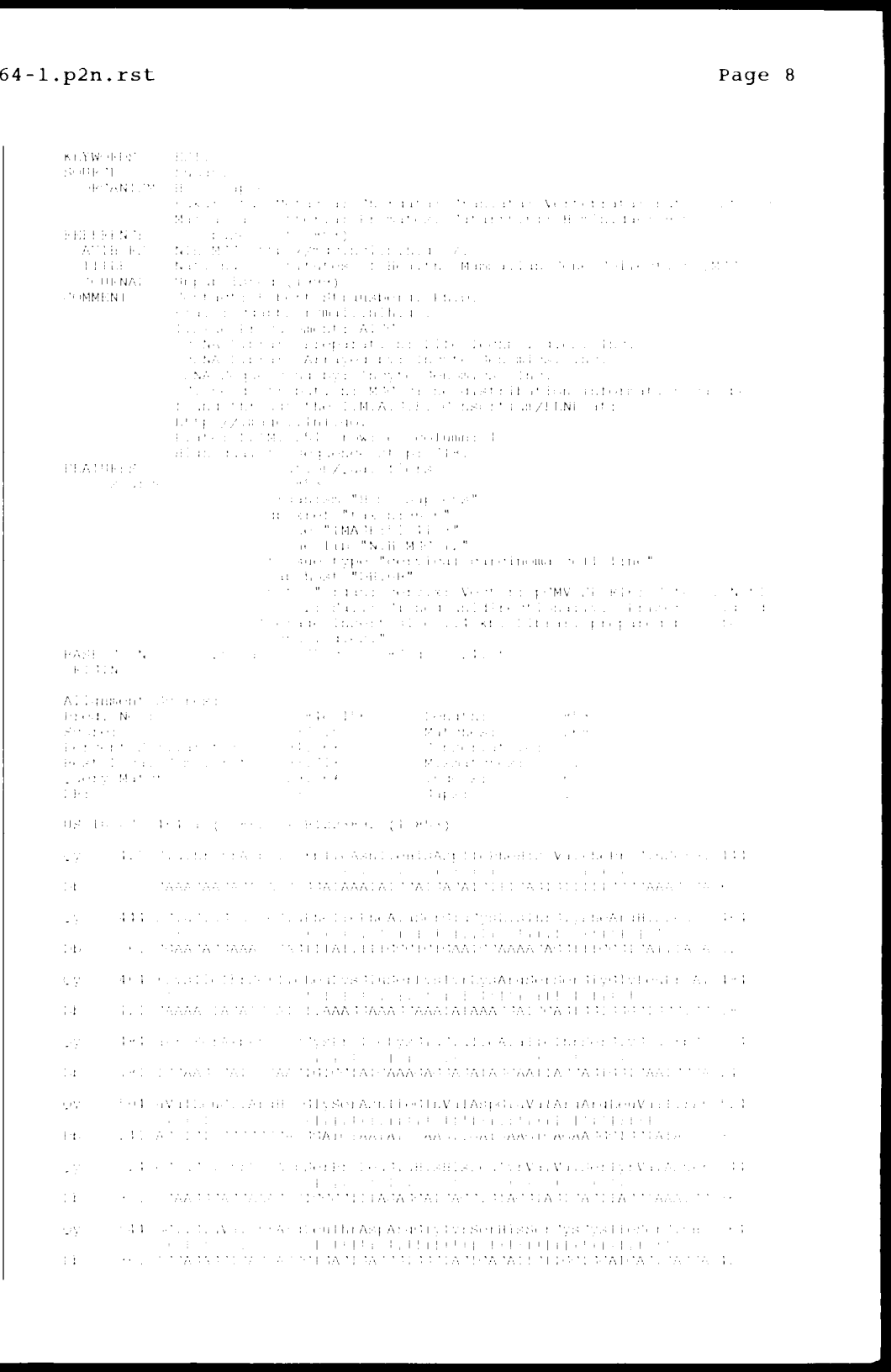
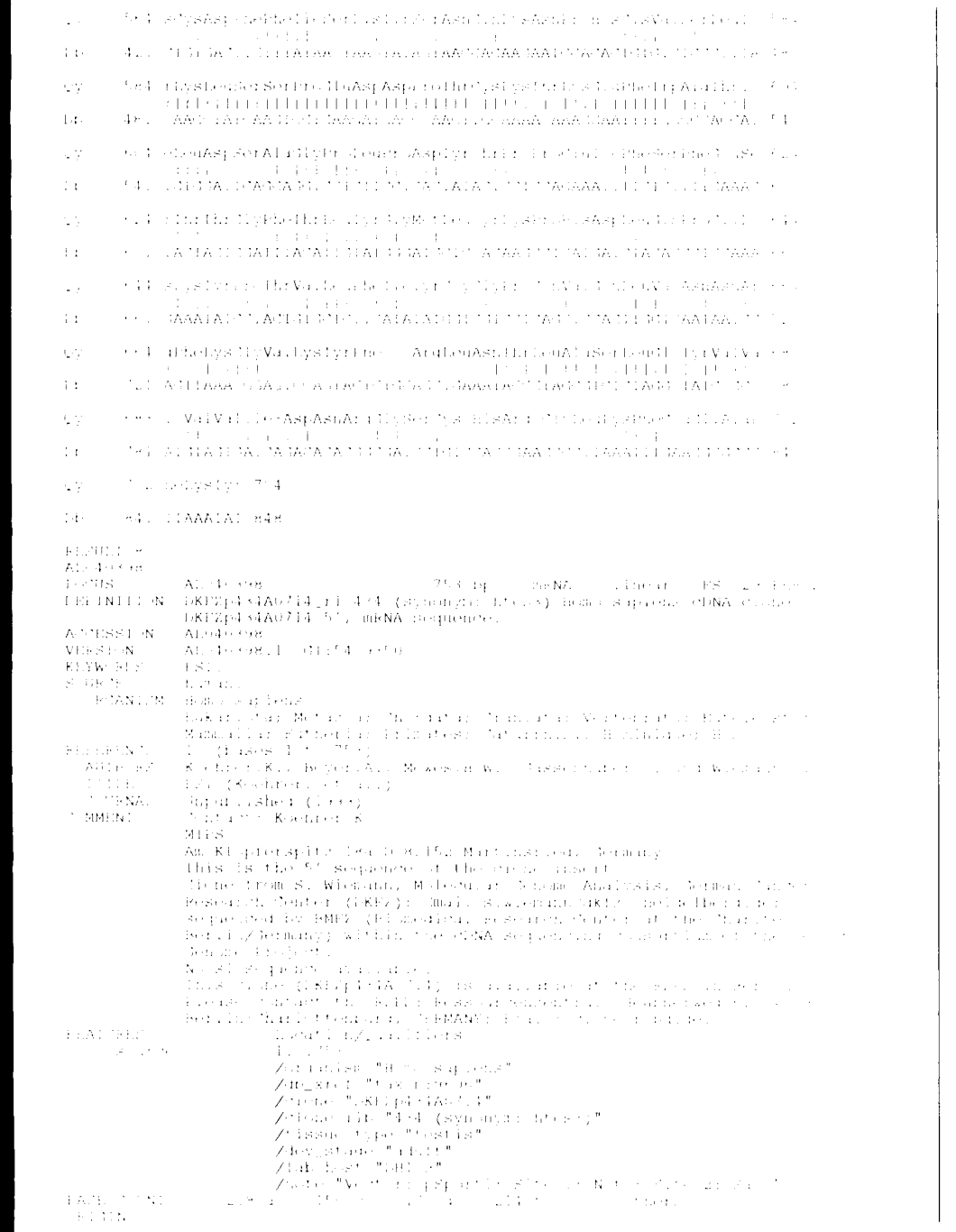
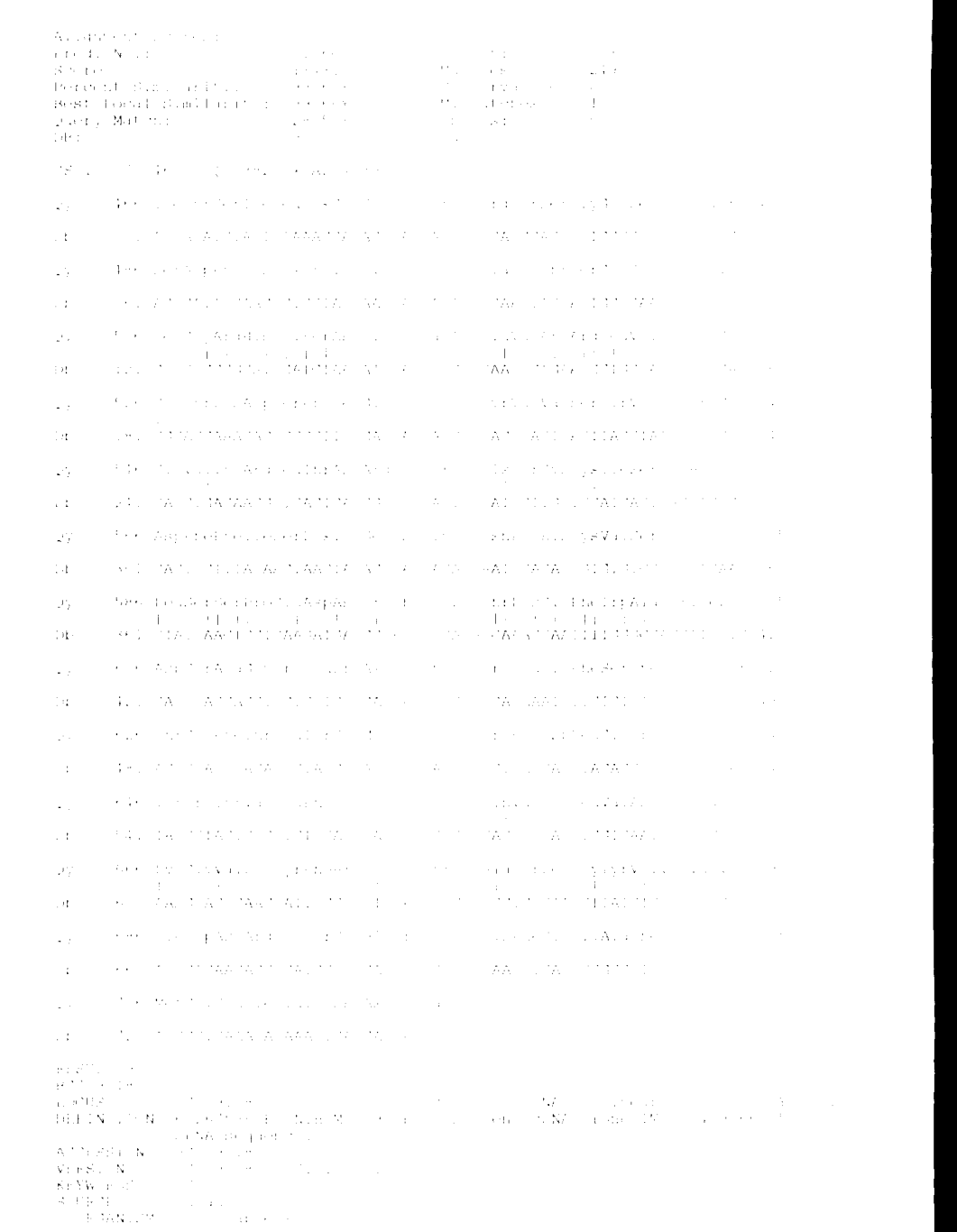
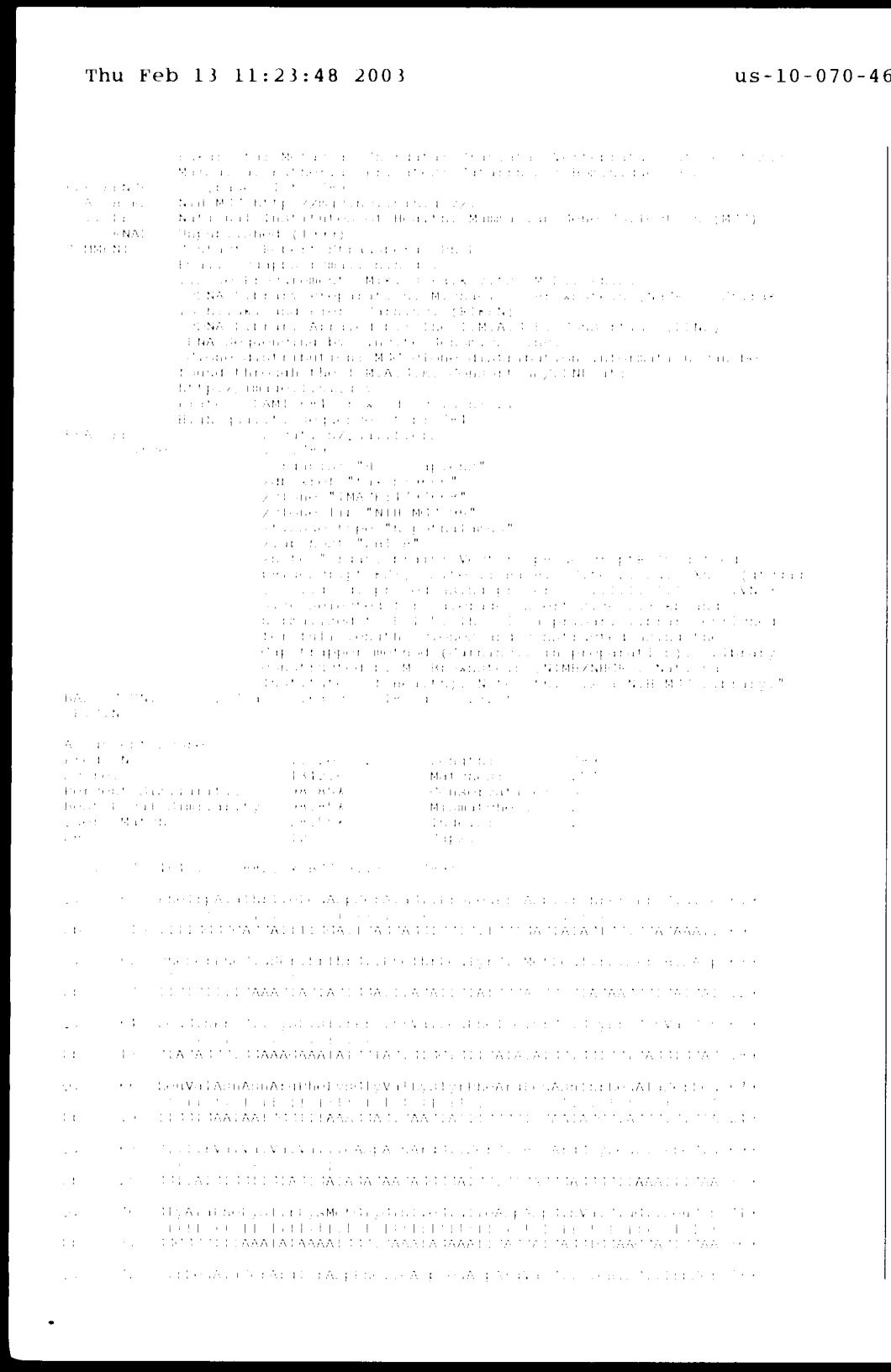


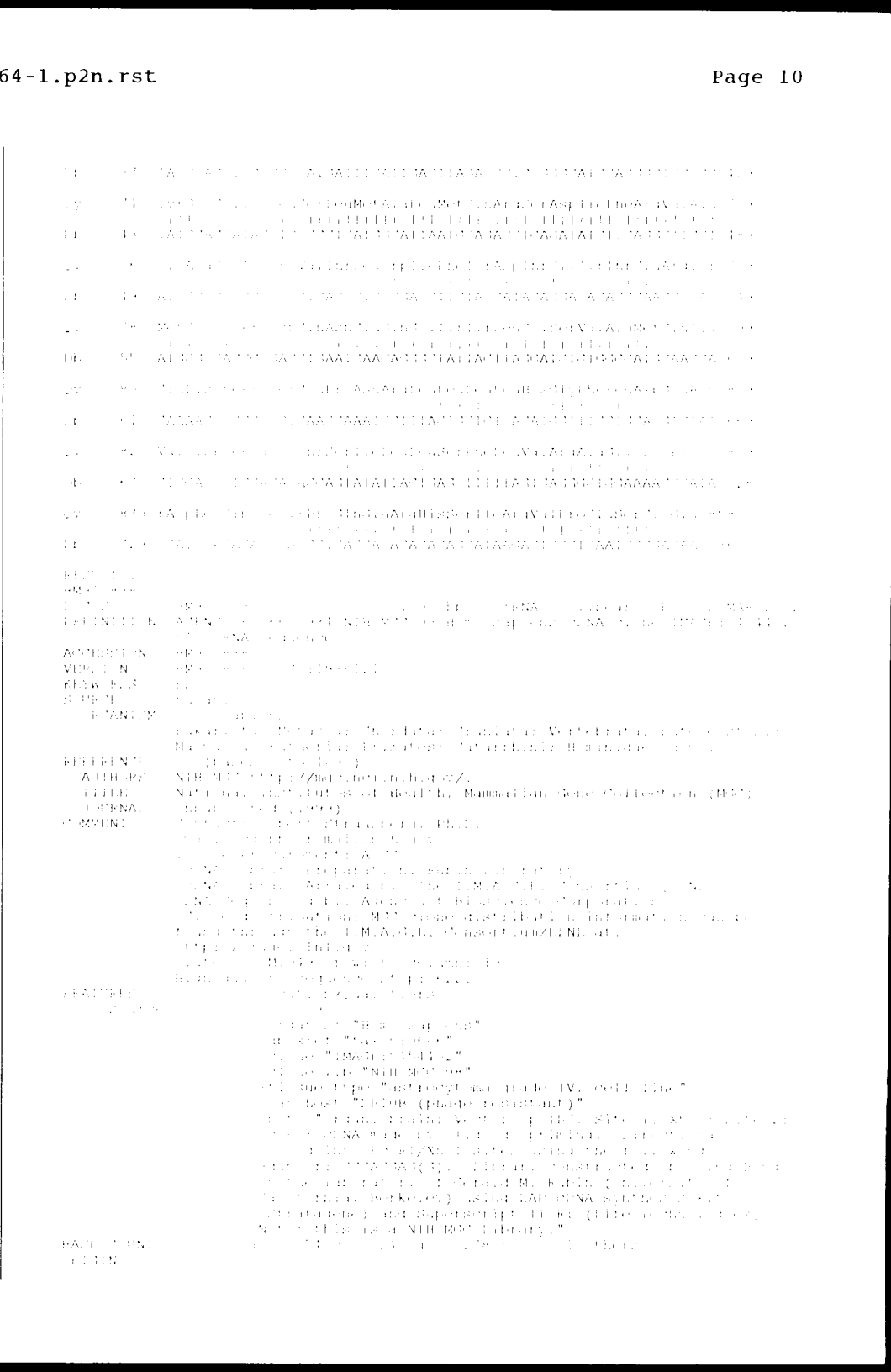


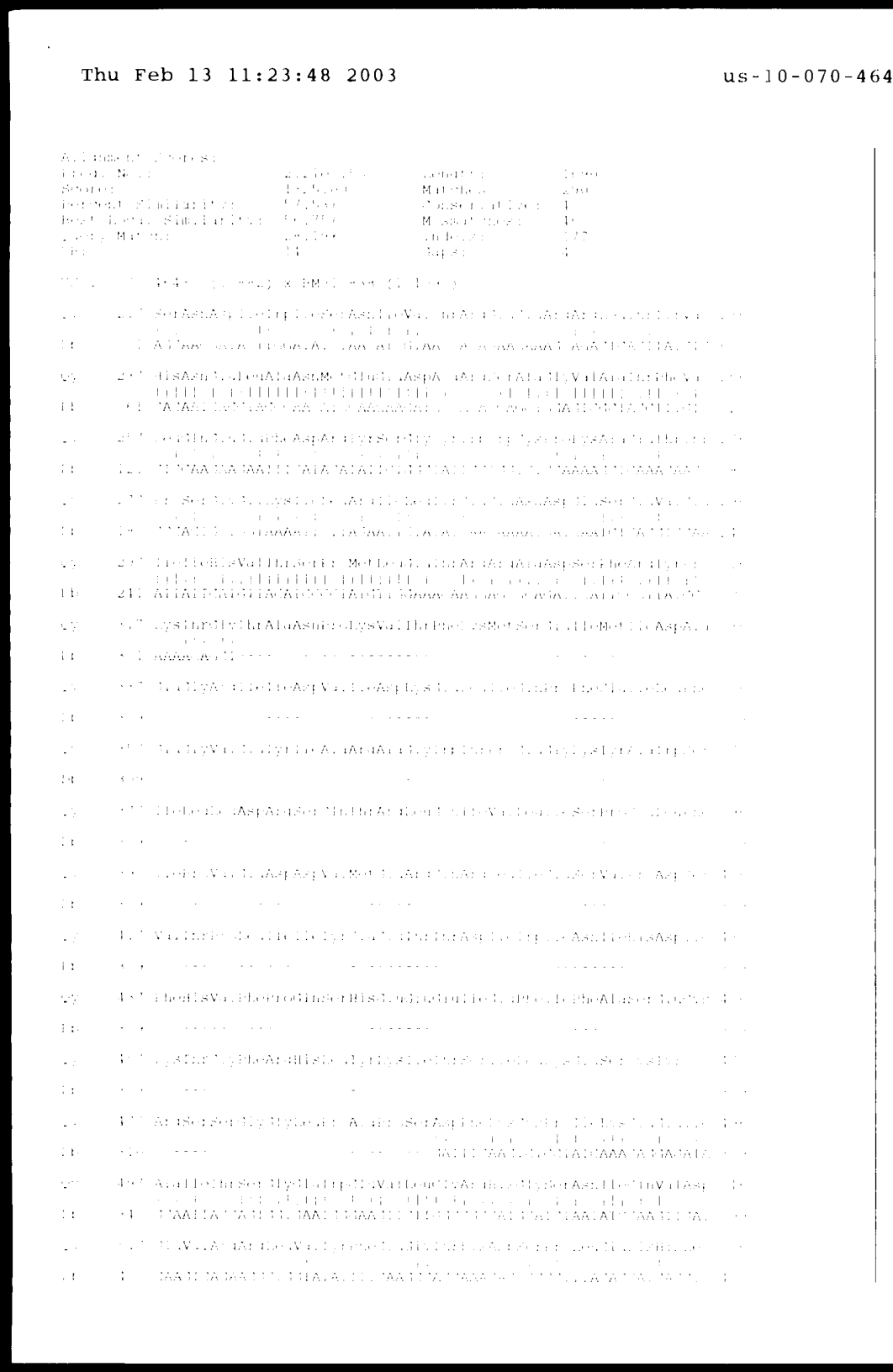


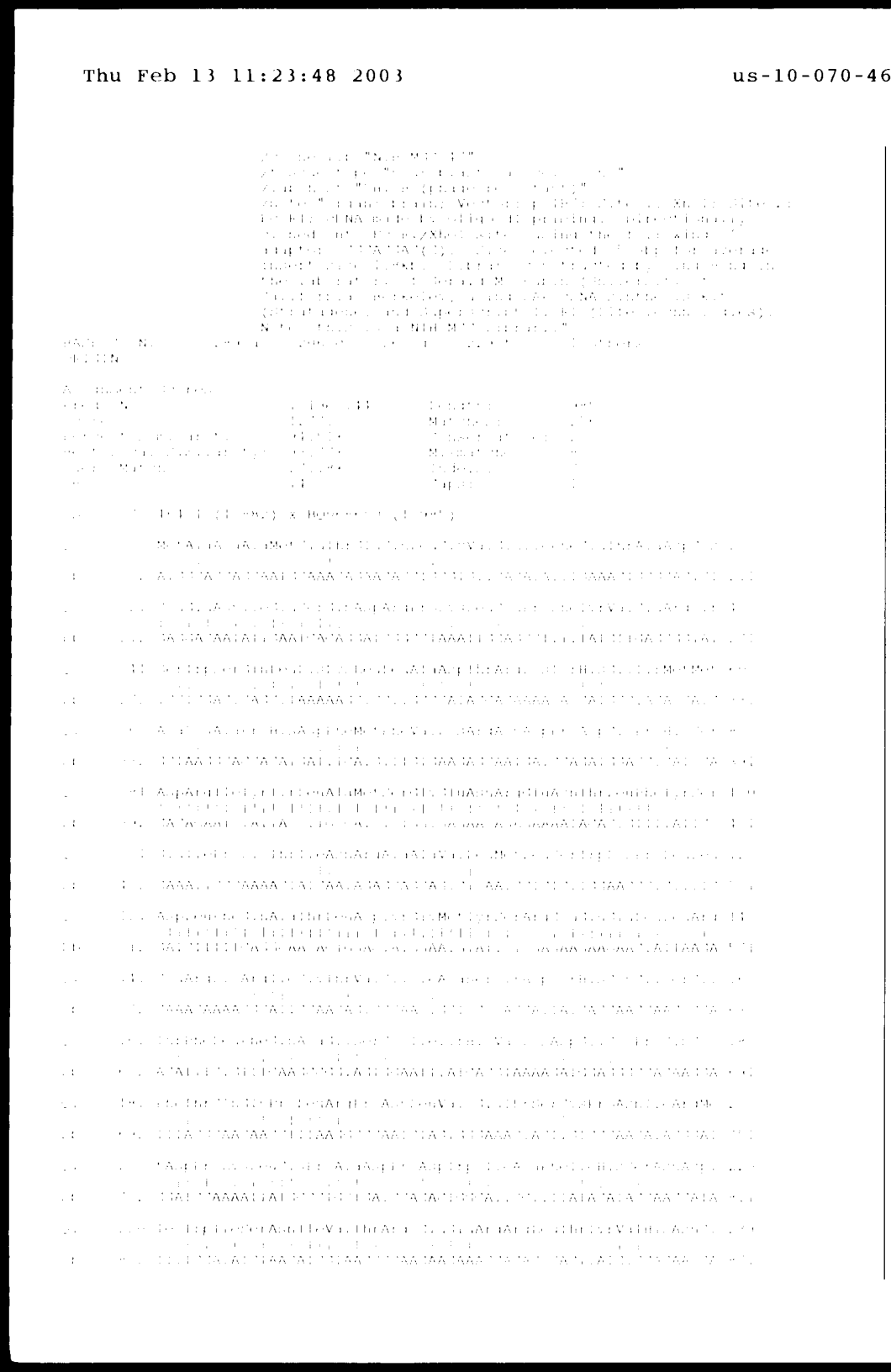


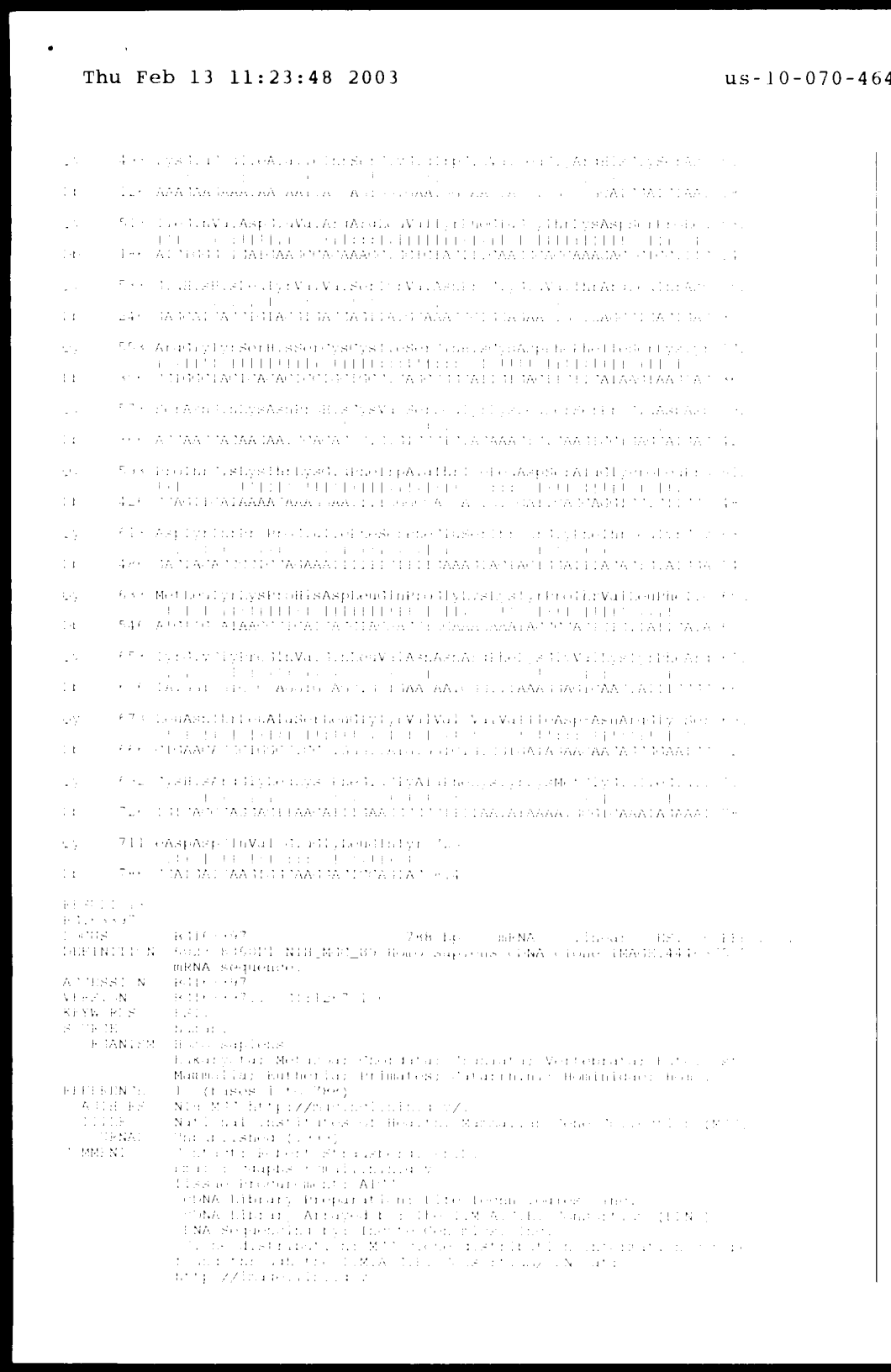


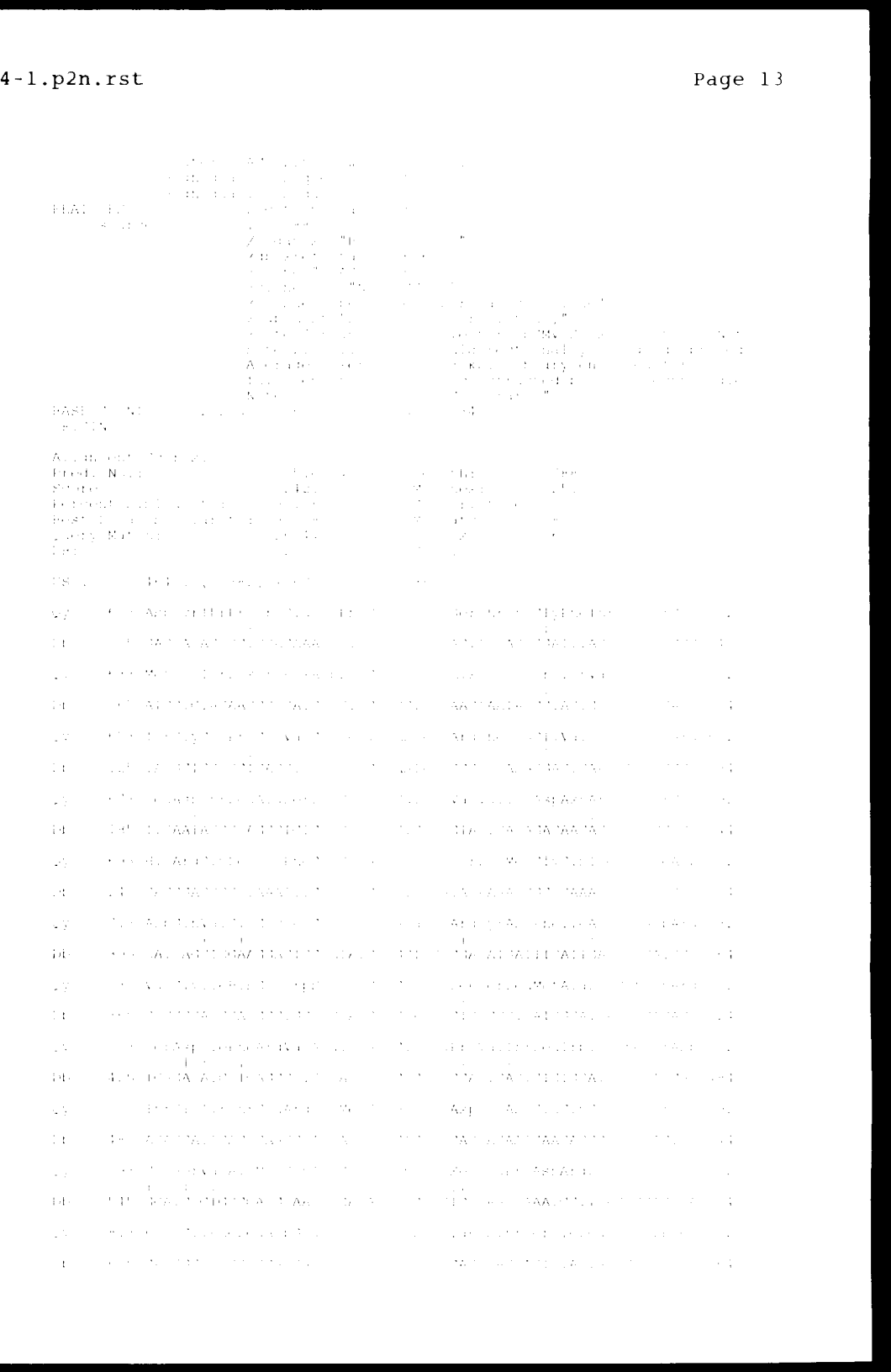


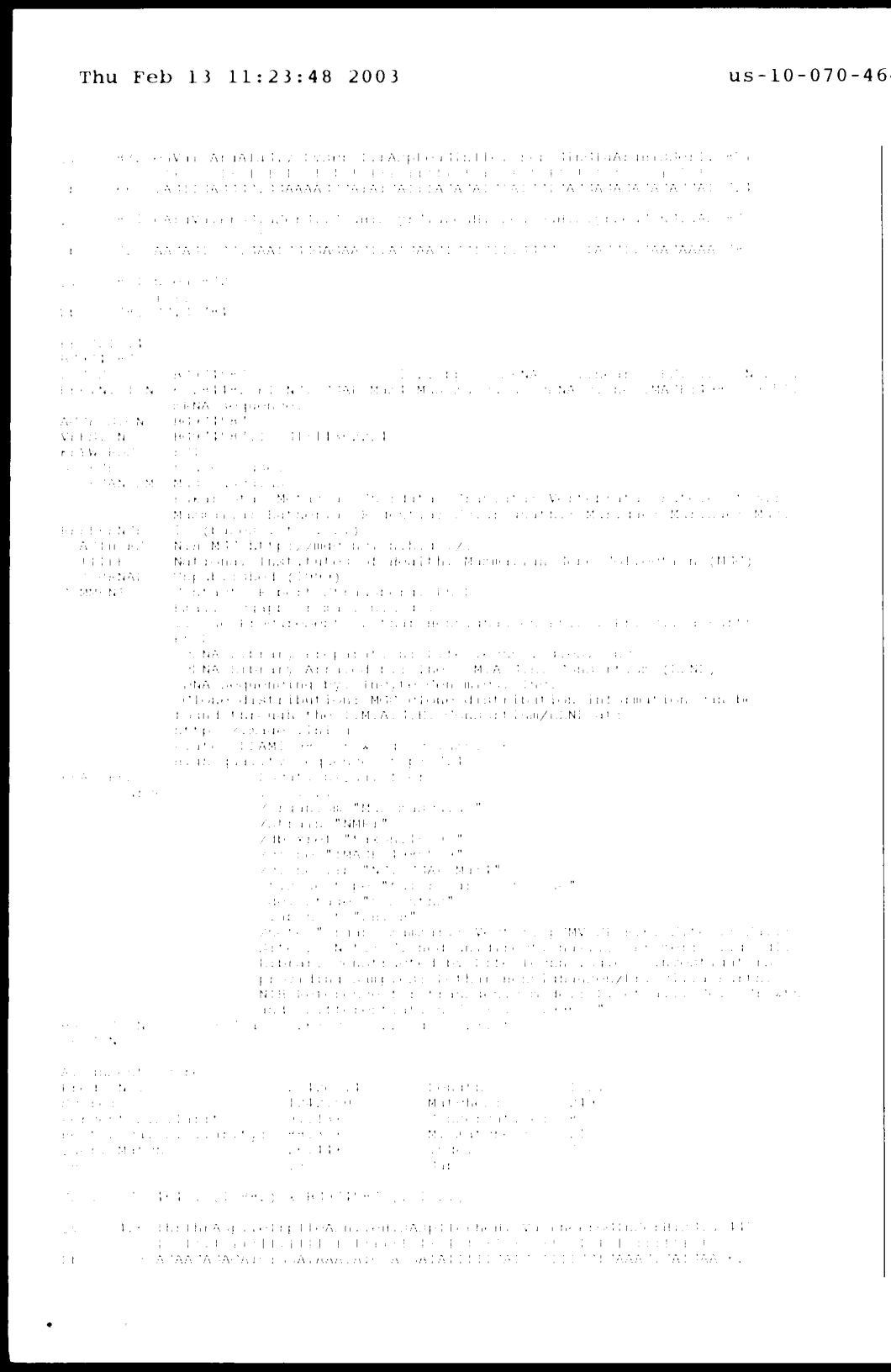


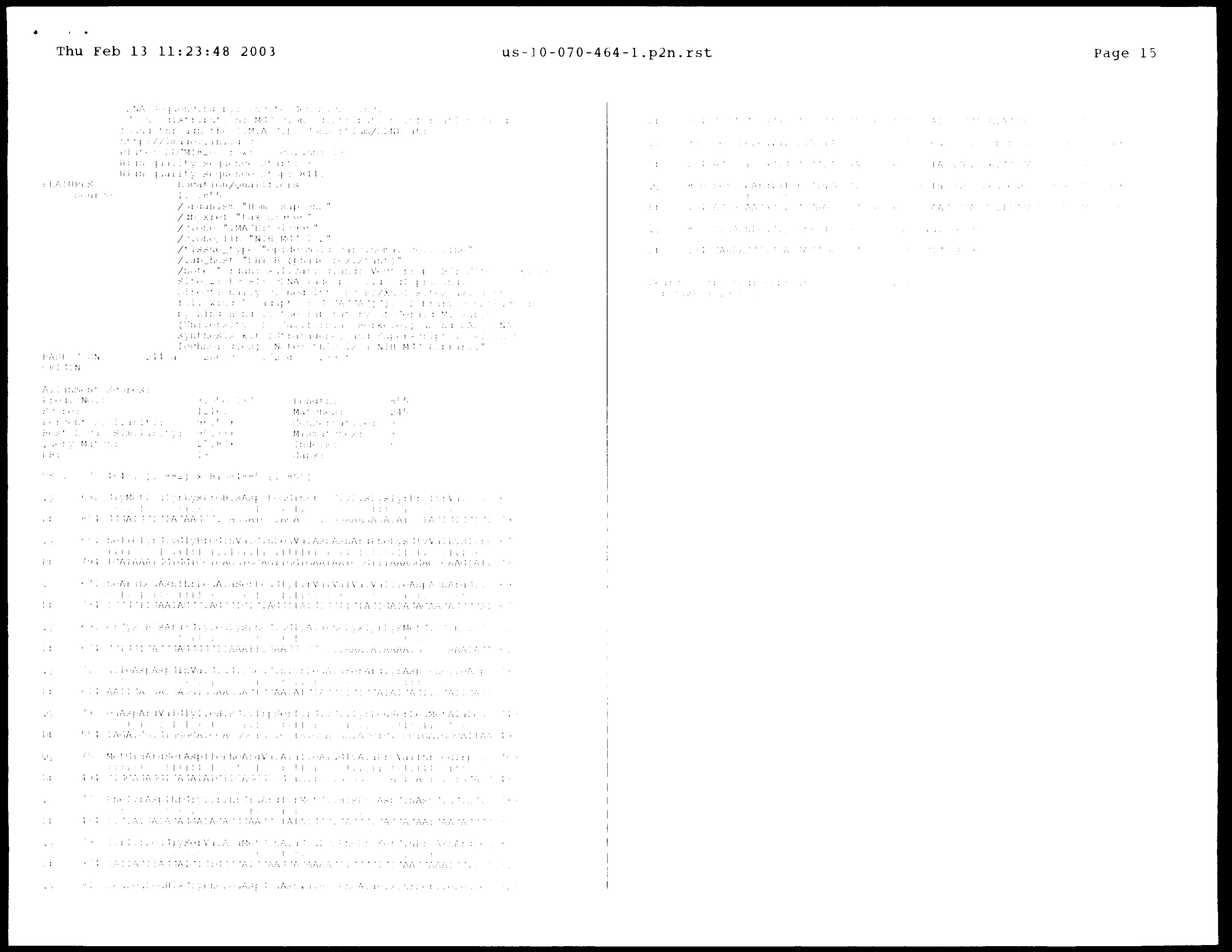


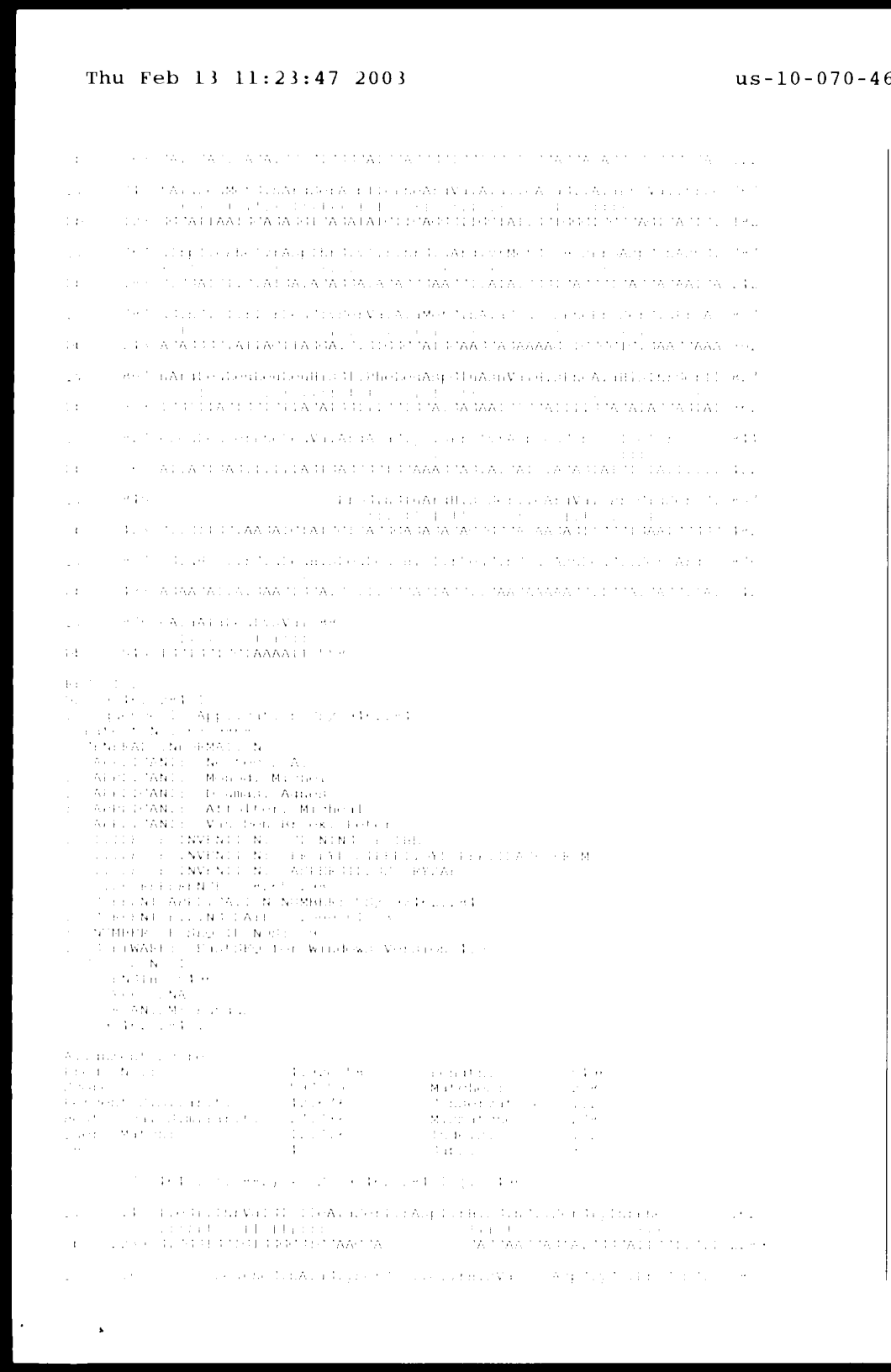


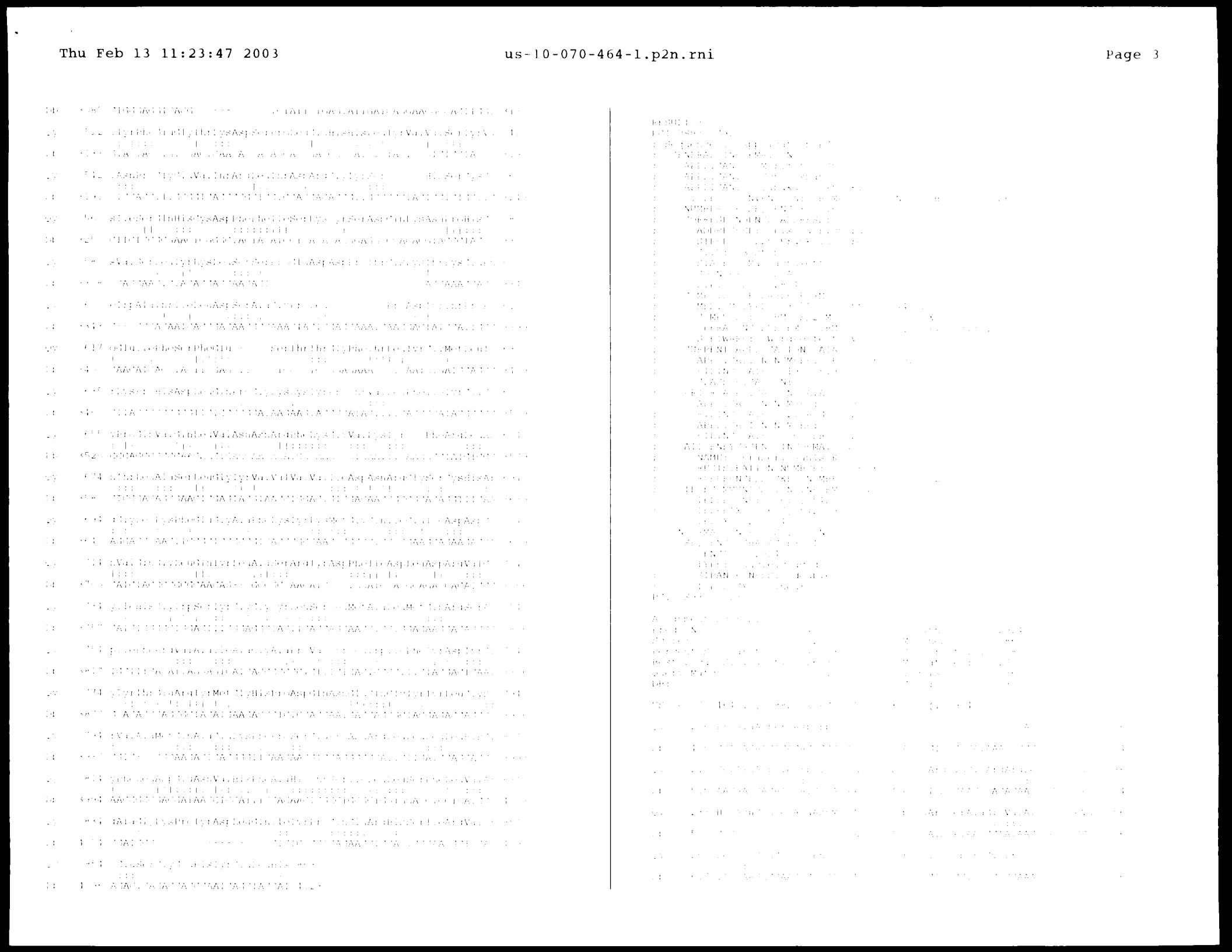


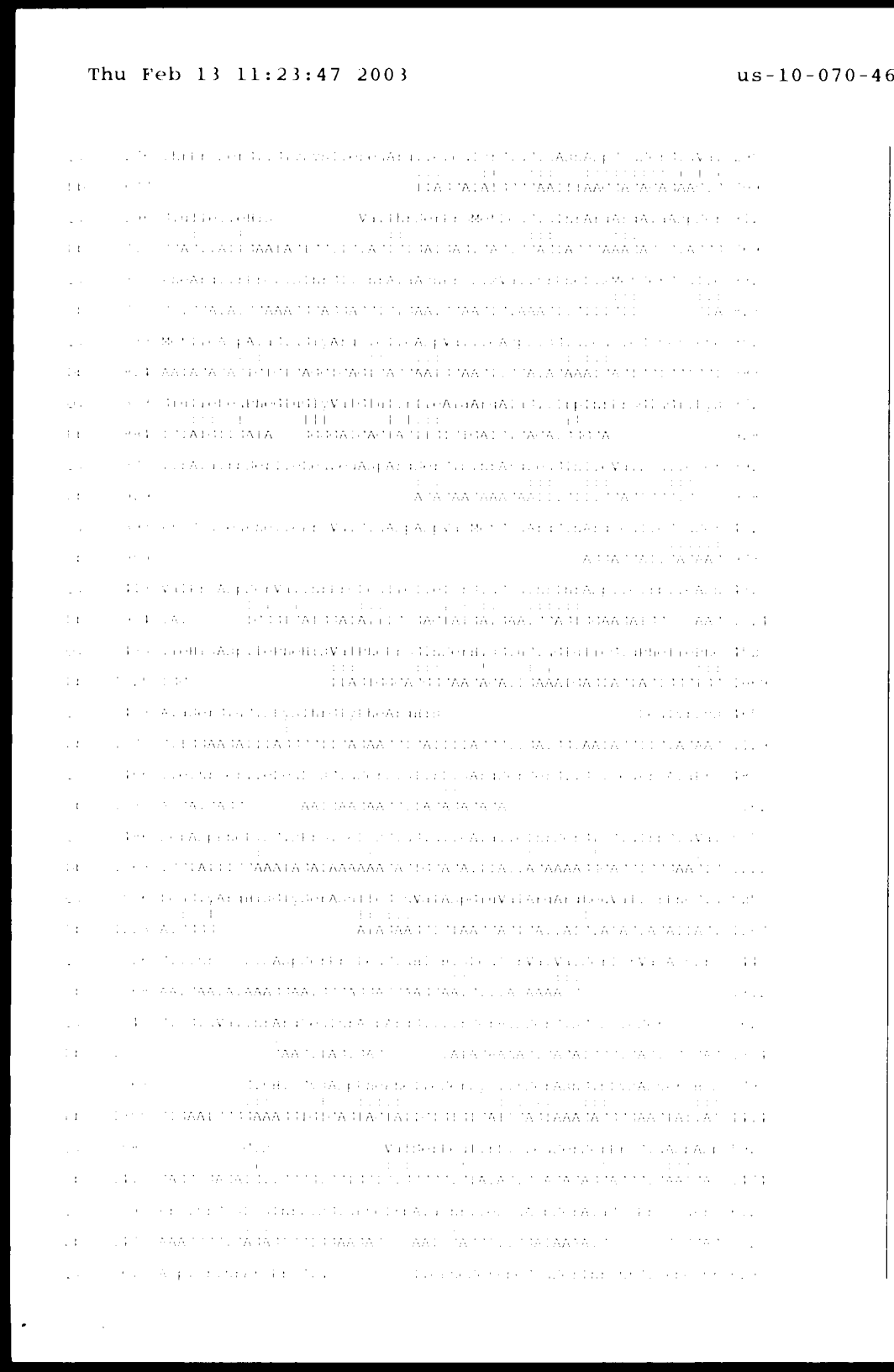


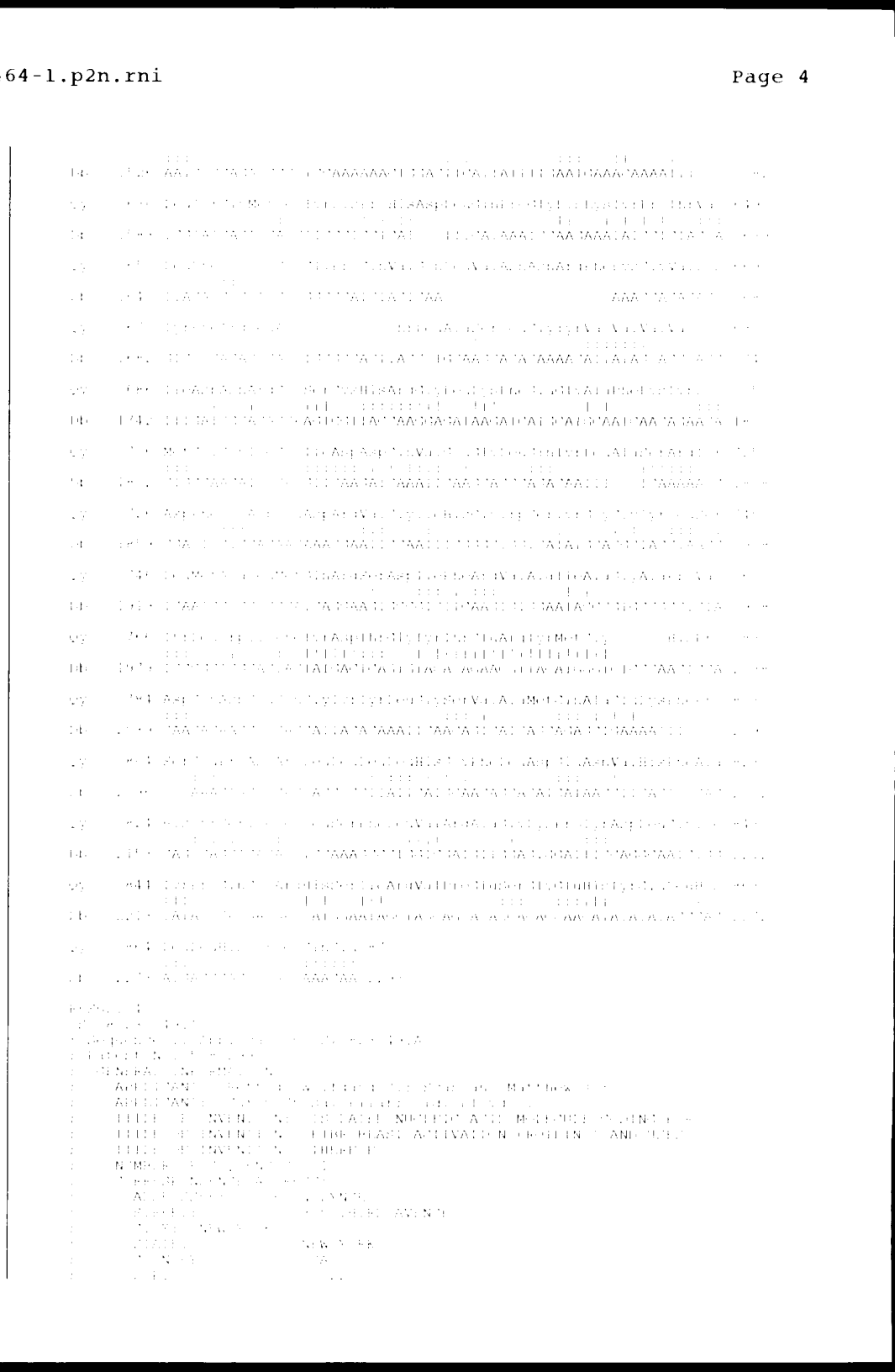


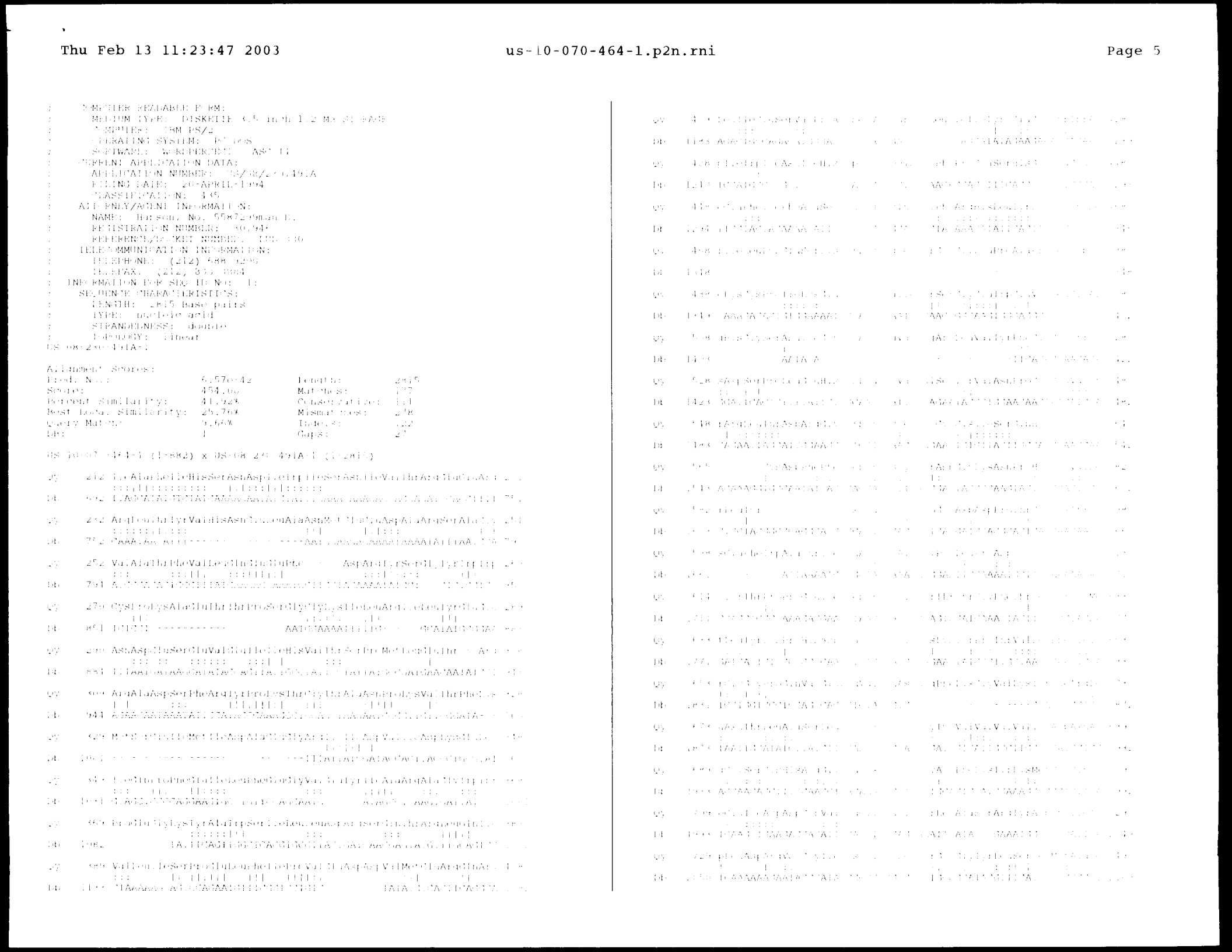


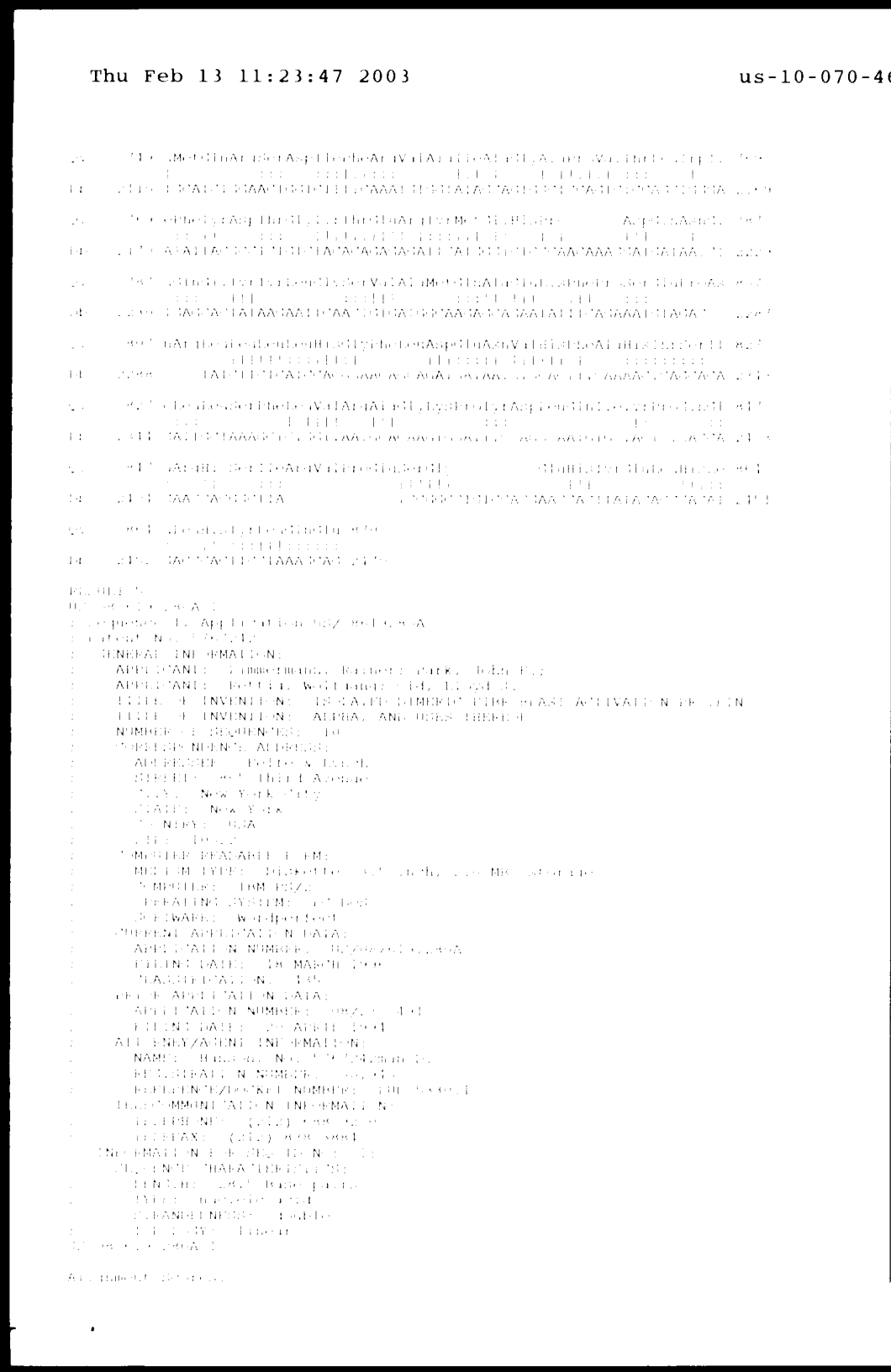


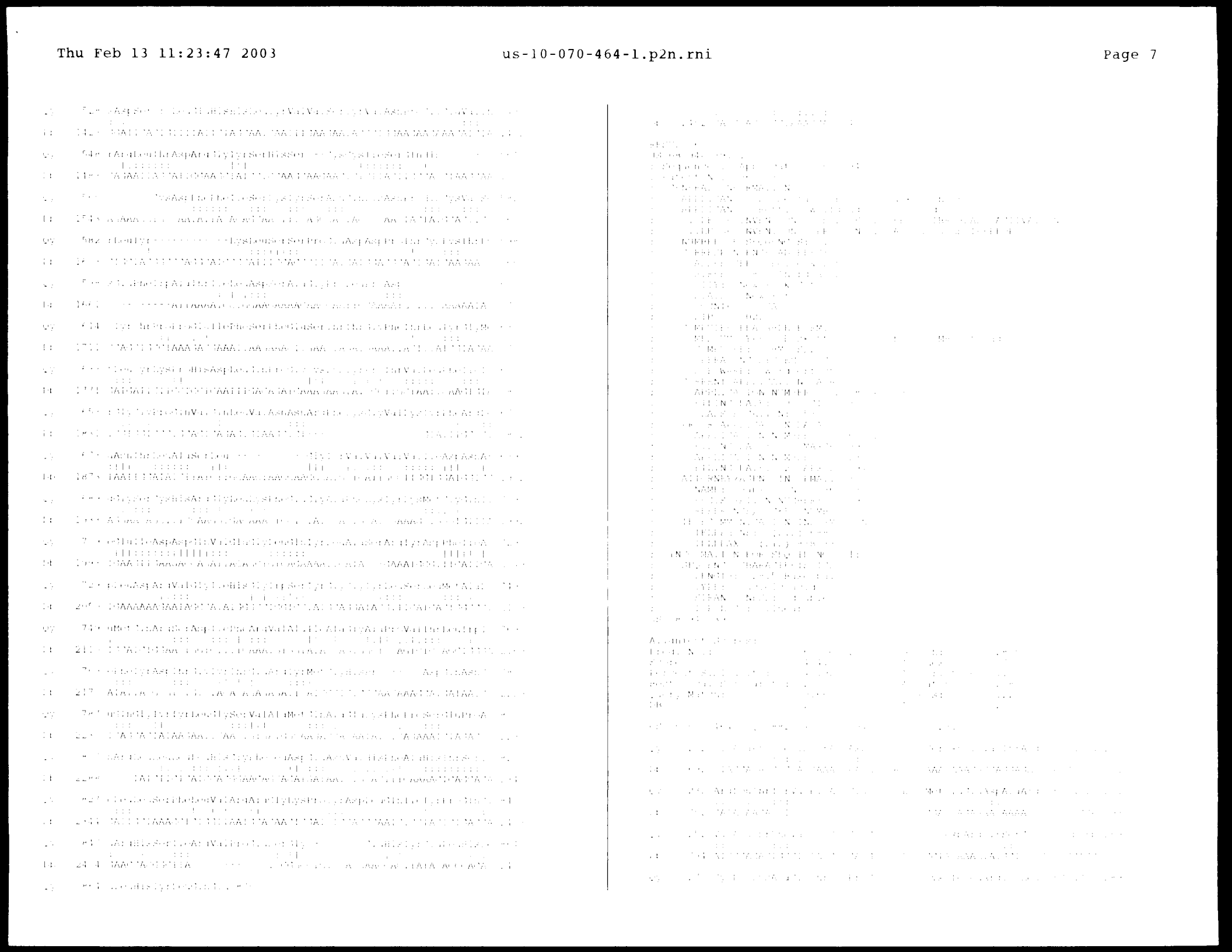


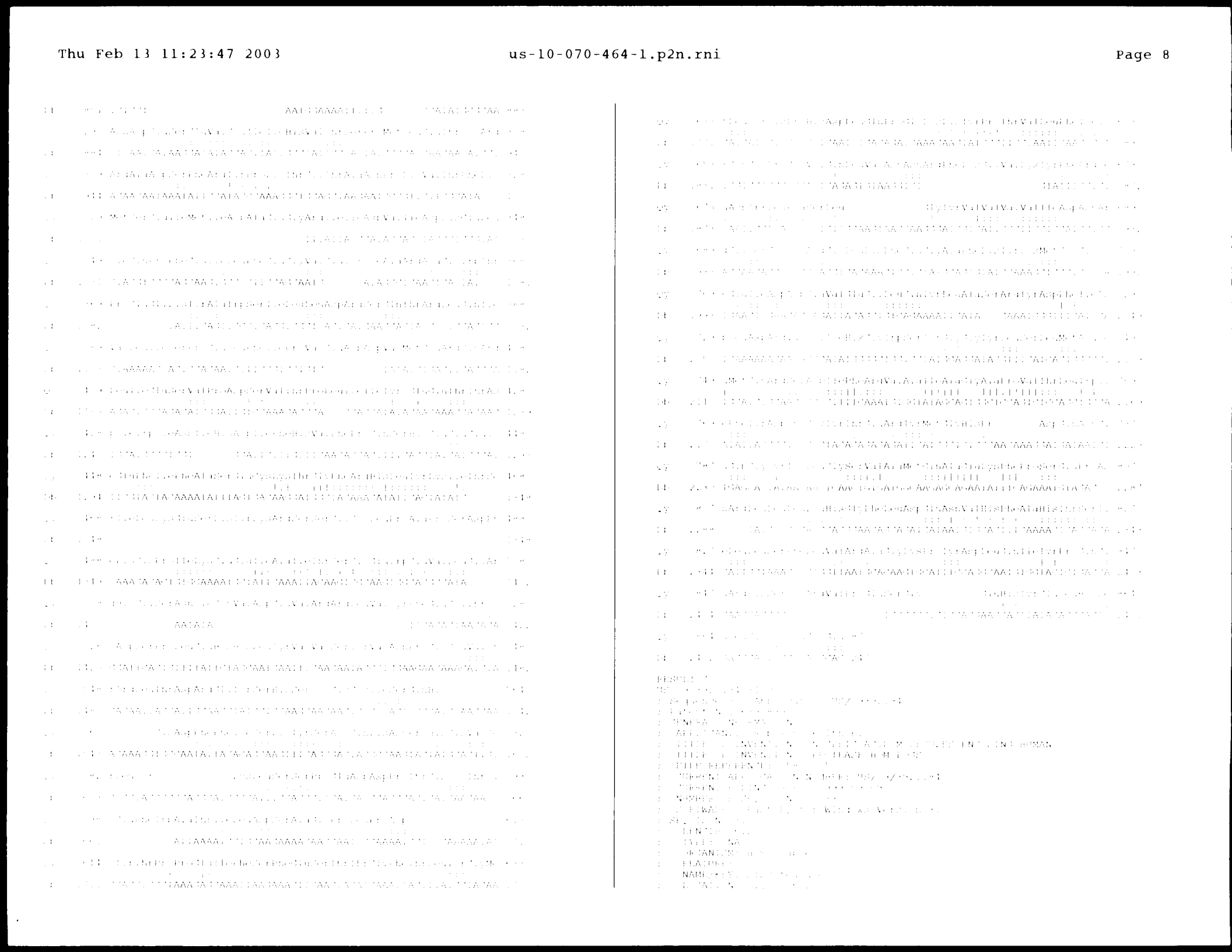


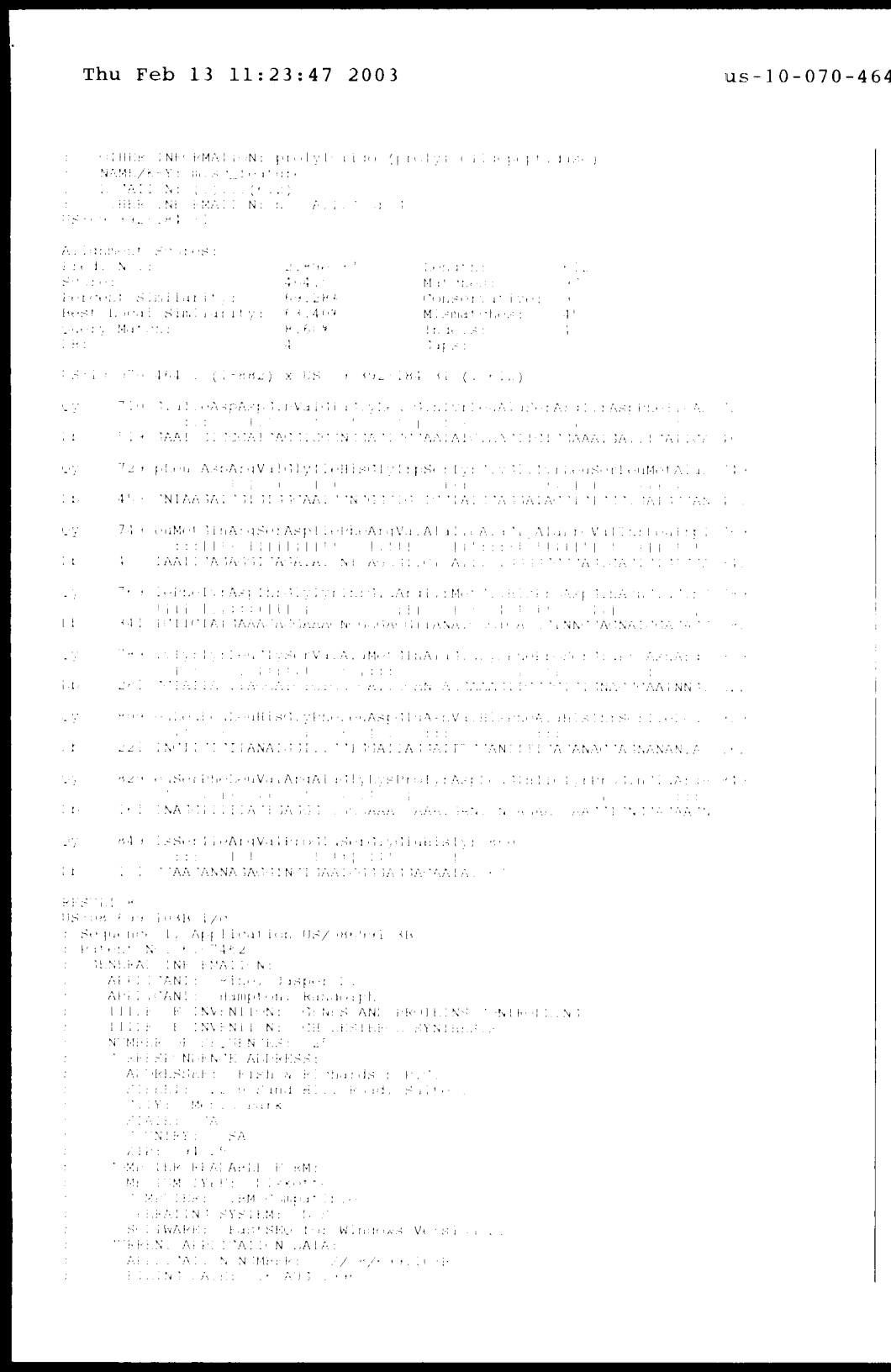


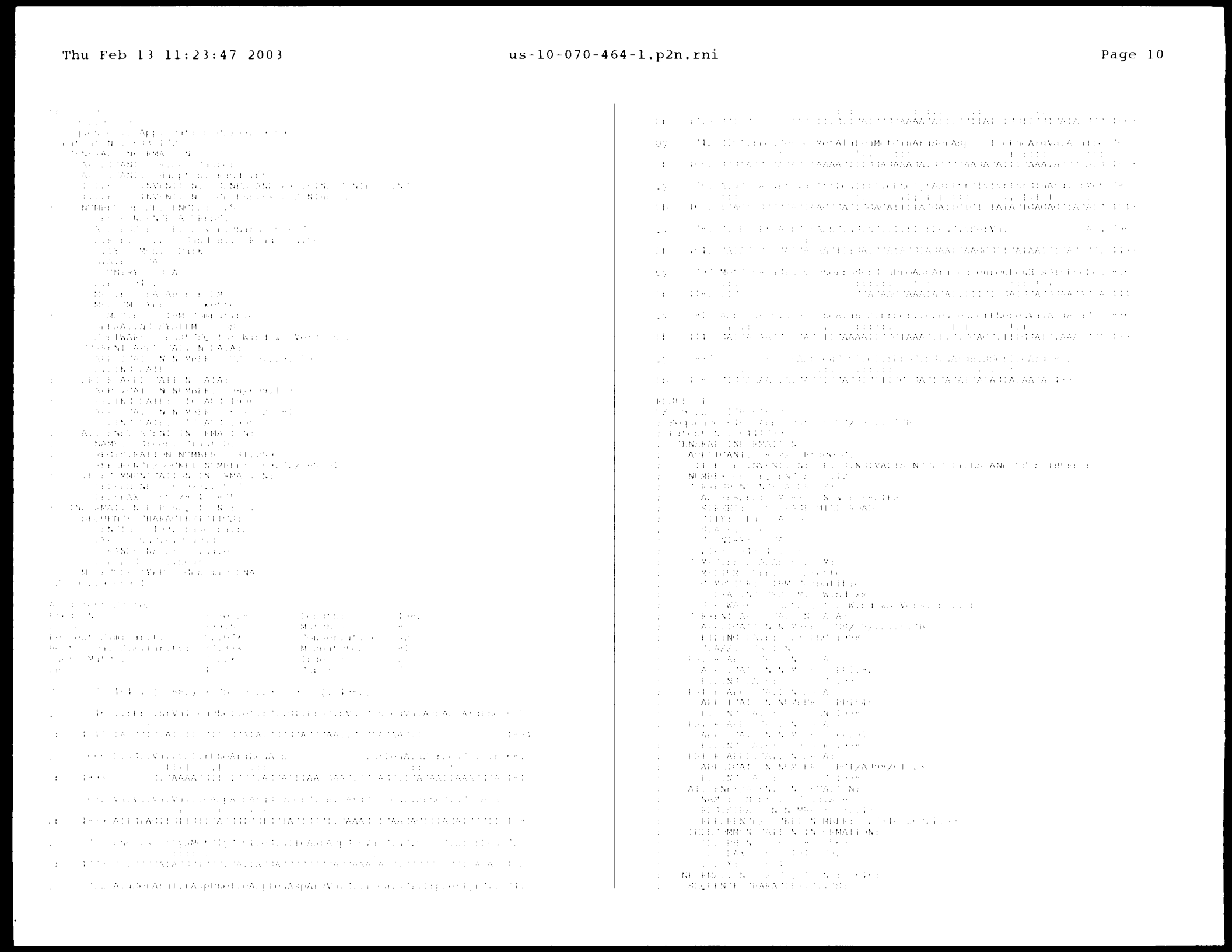


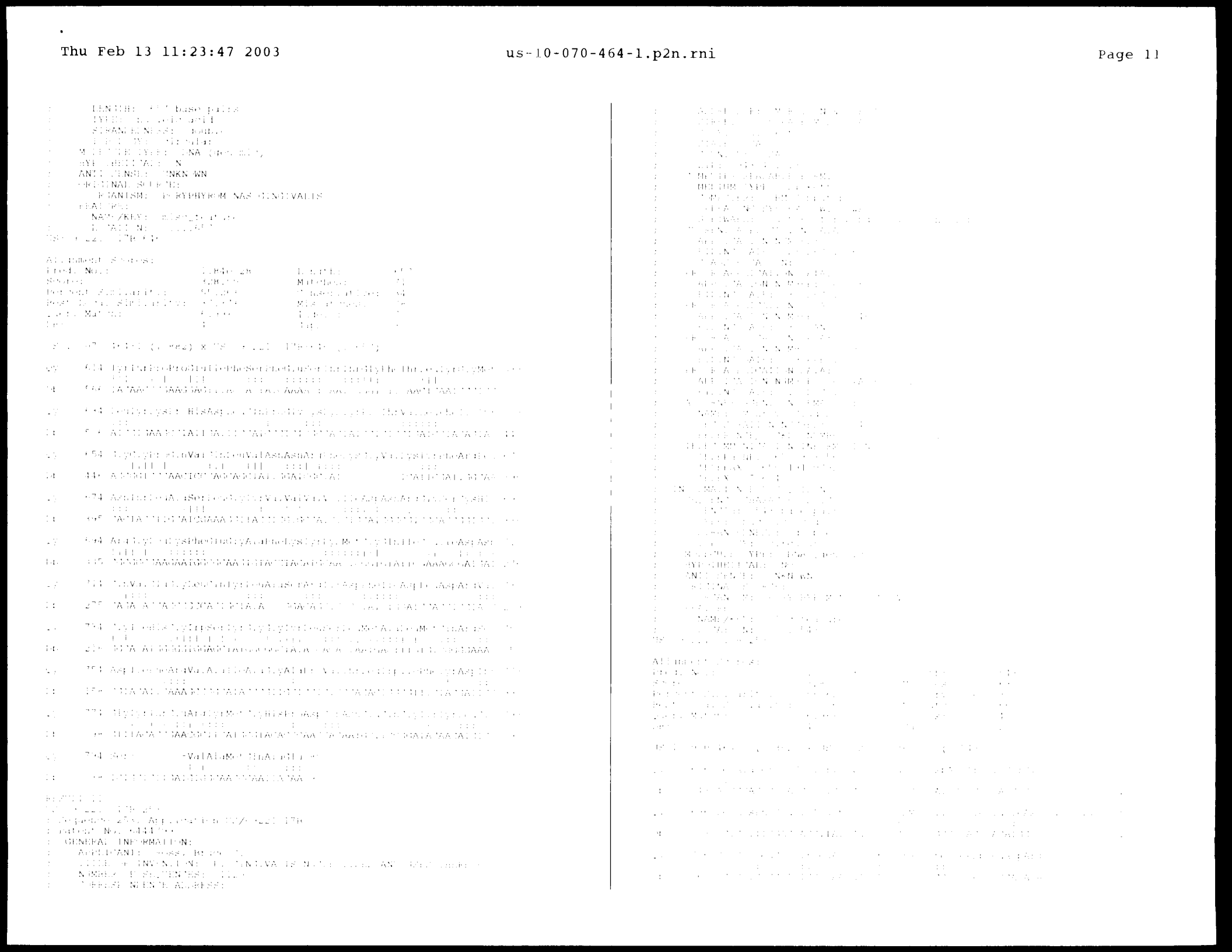


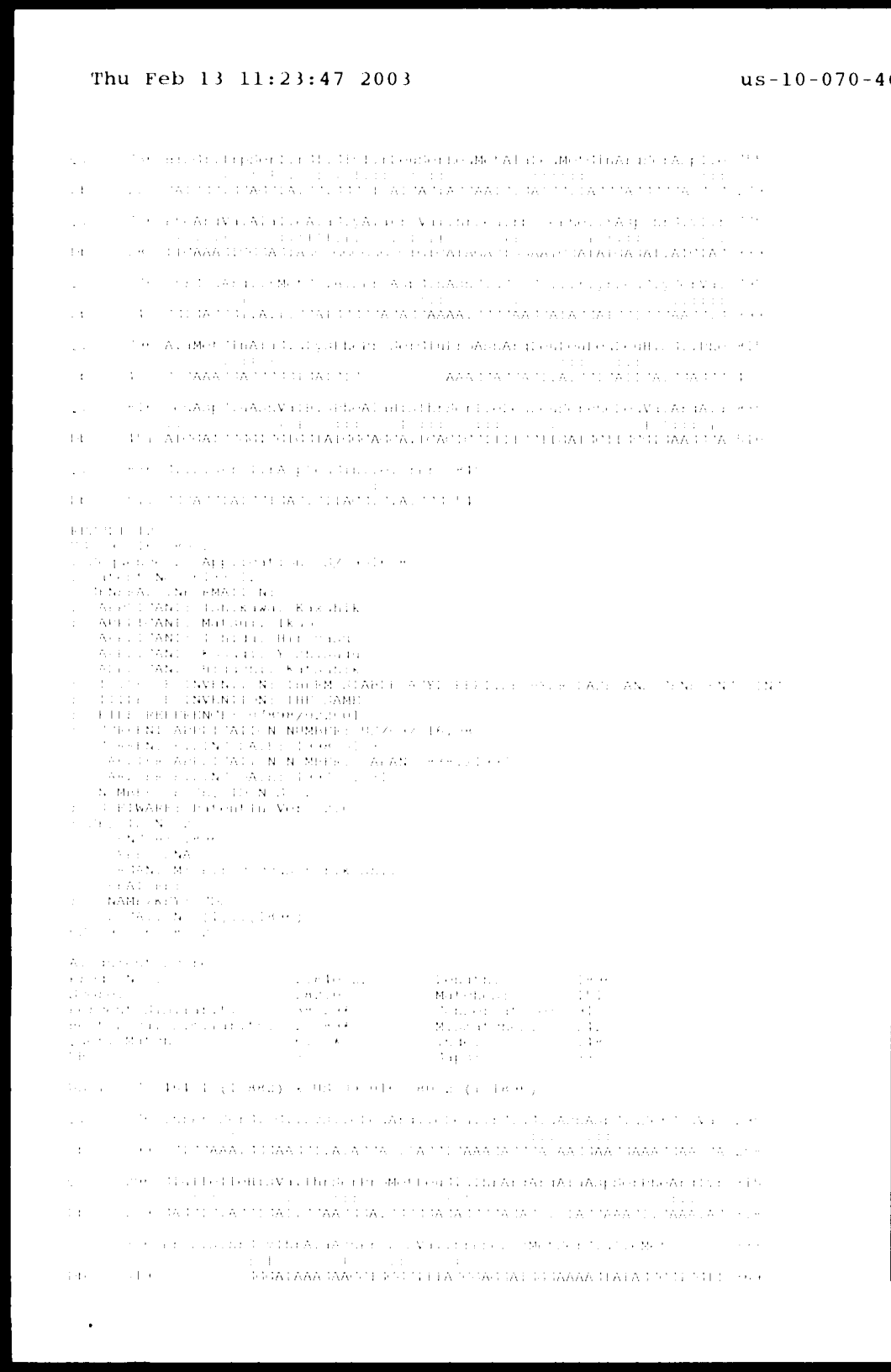


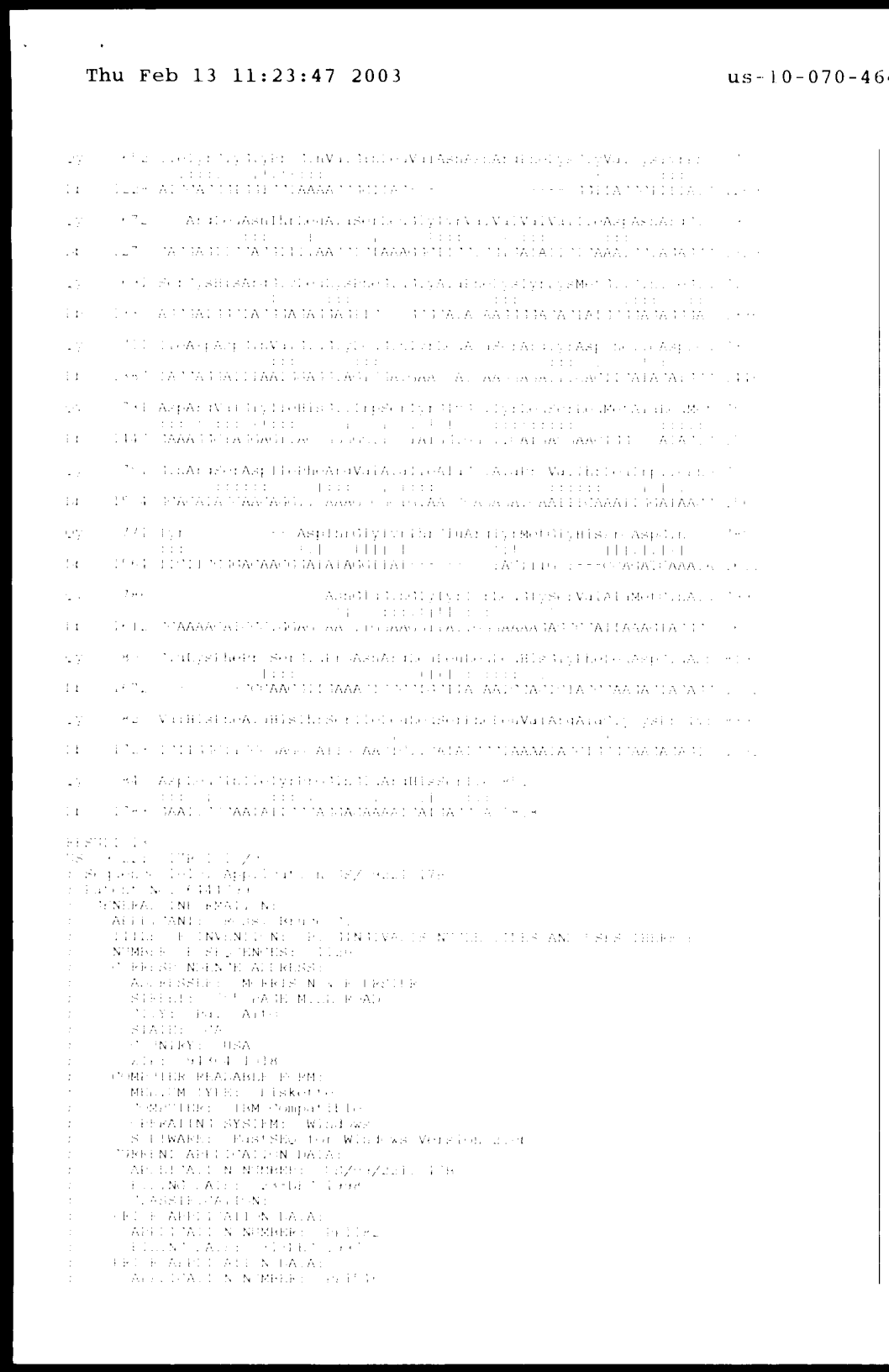


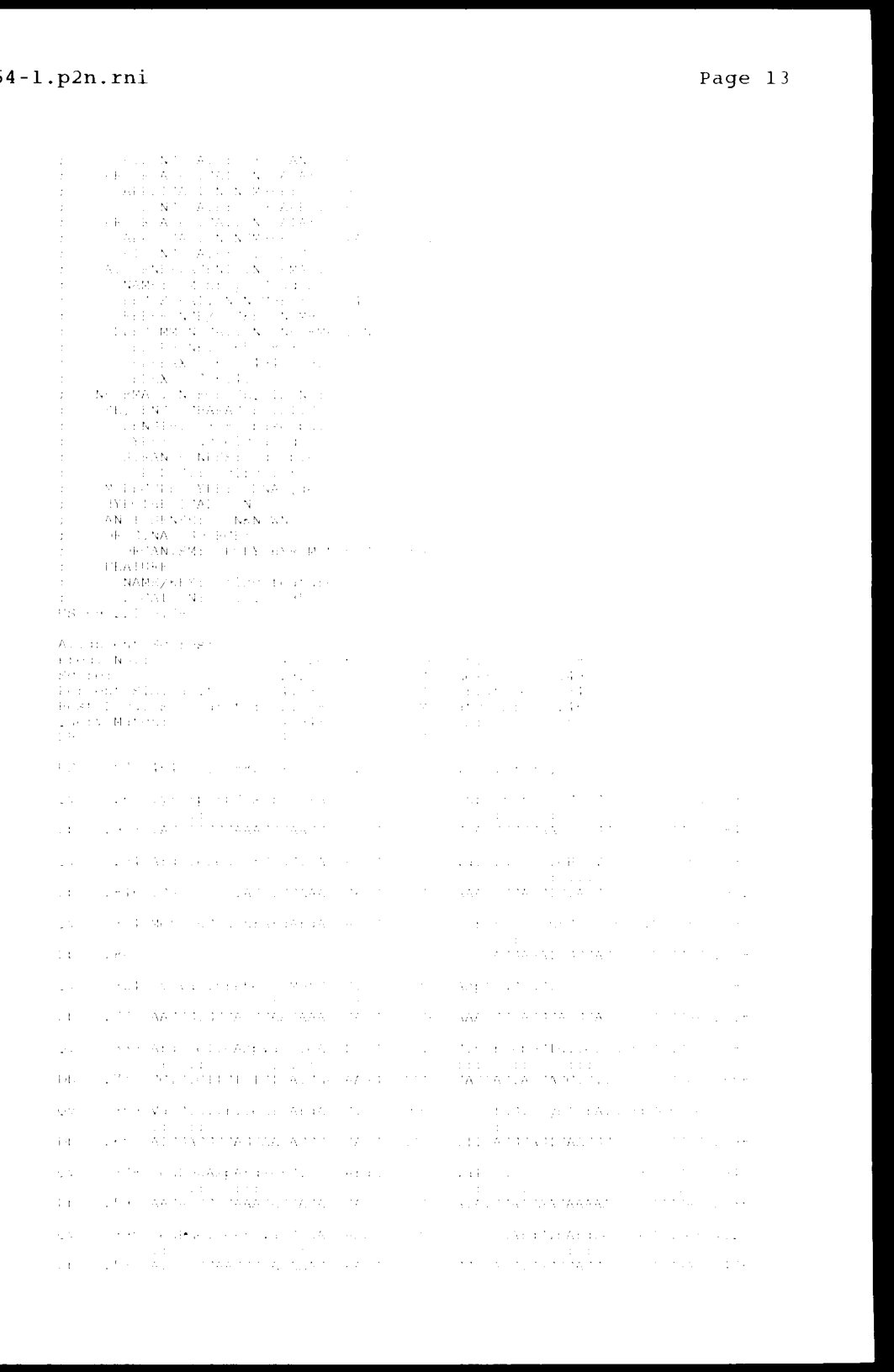


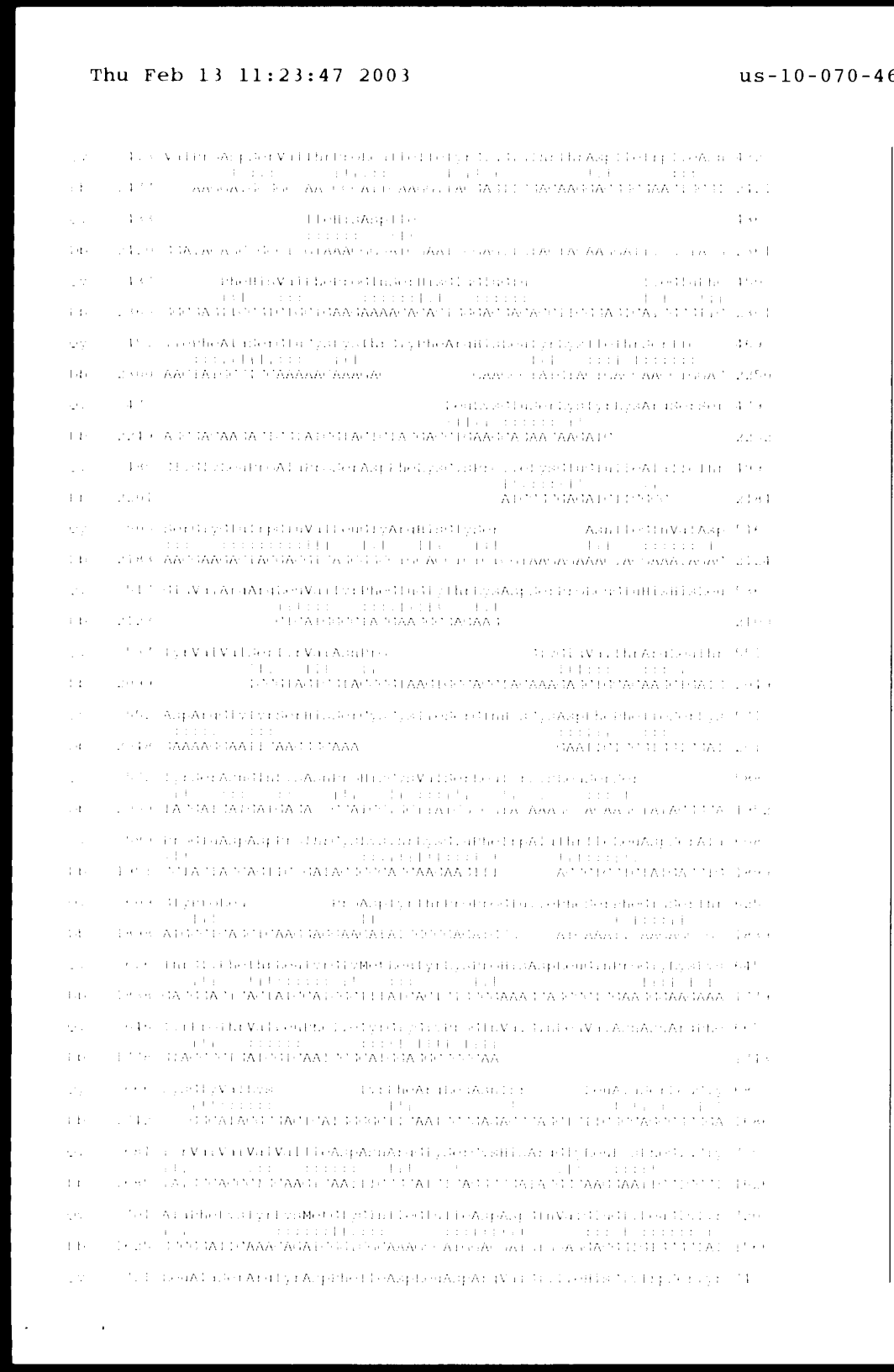


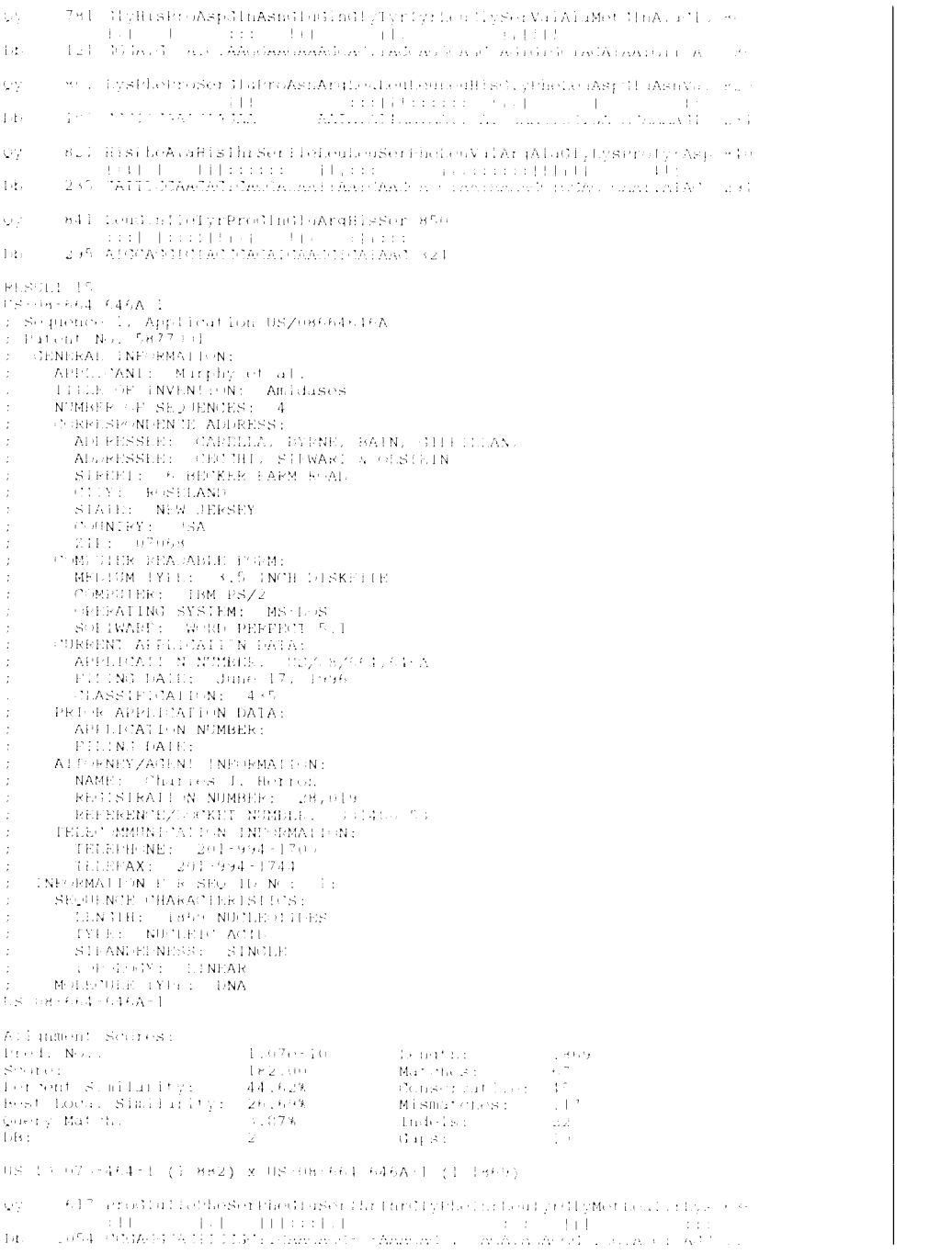










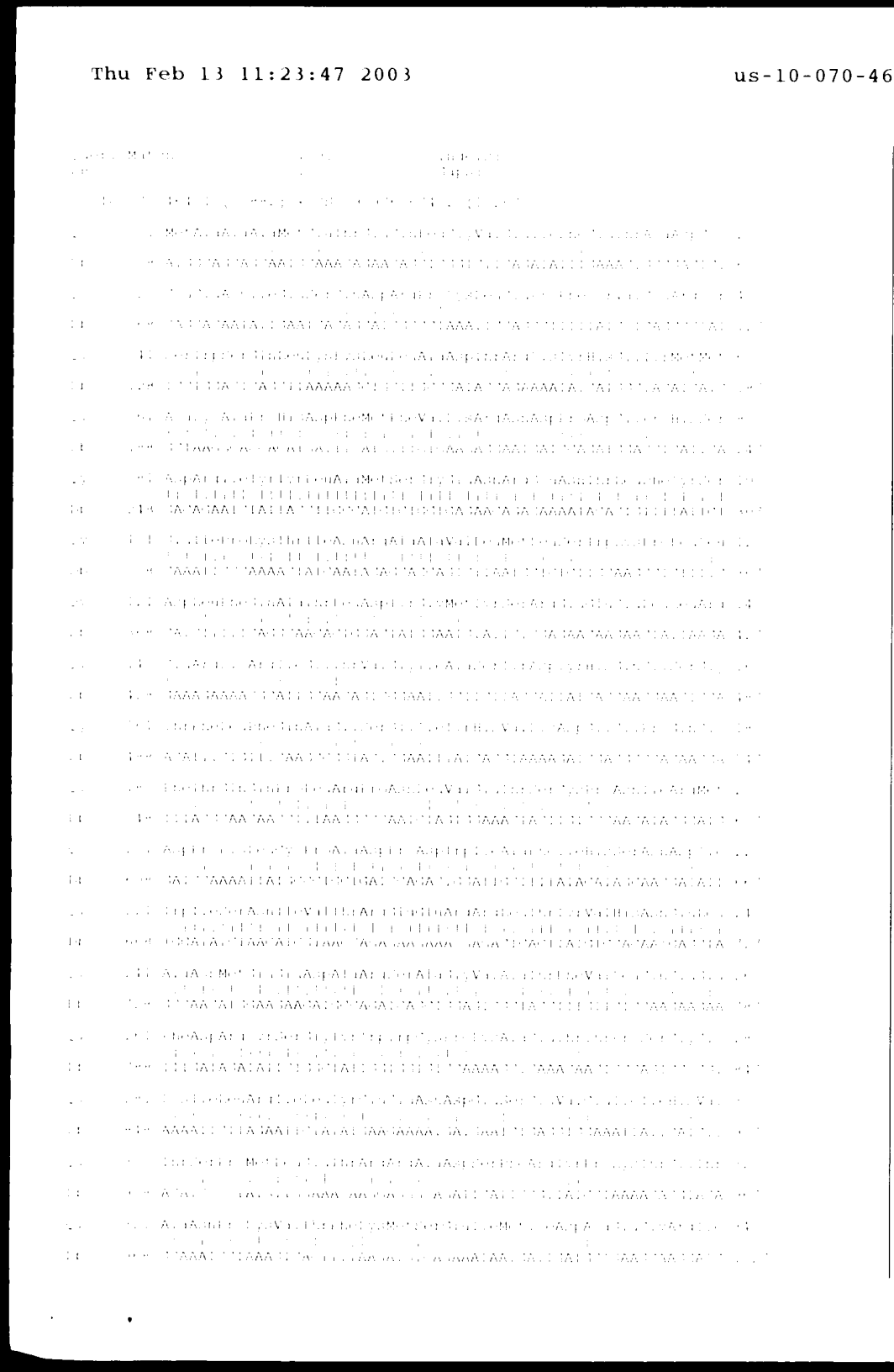


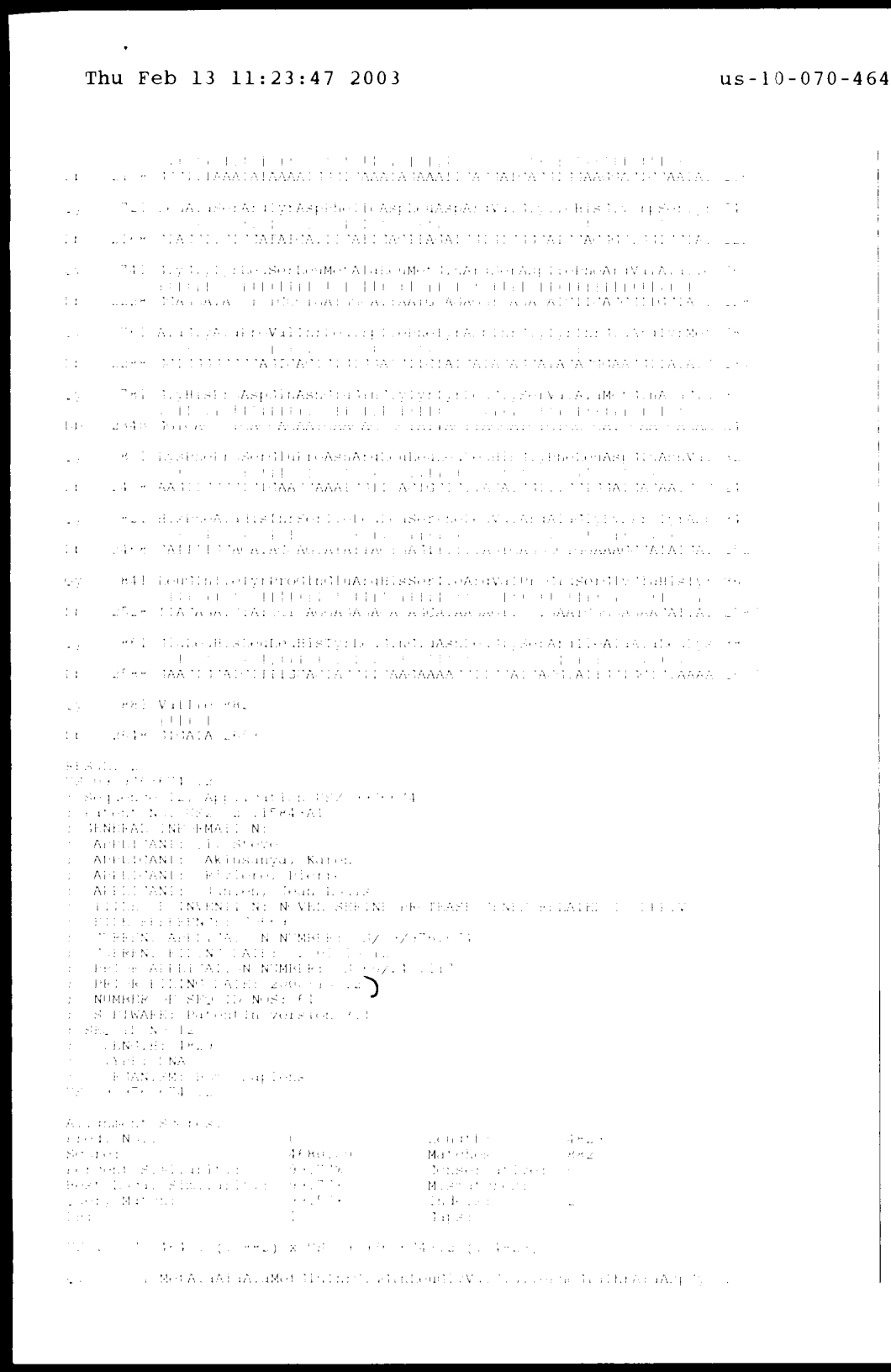
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; Sequence 1, Application US/08664646A
; Patent No. 5877010
; GENERAL INFORMATION:
; APPLICANT: Murphy et al.
; TITLE OF INVENTION: Amidases
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECIL H. STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,646A
; FILING DATE: June 17, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles J. Bertoz
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 12345-53
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1850 NUCLEOTIDES
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: DNA
US-08-664-646A-1

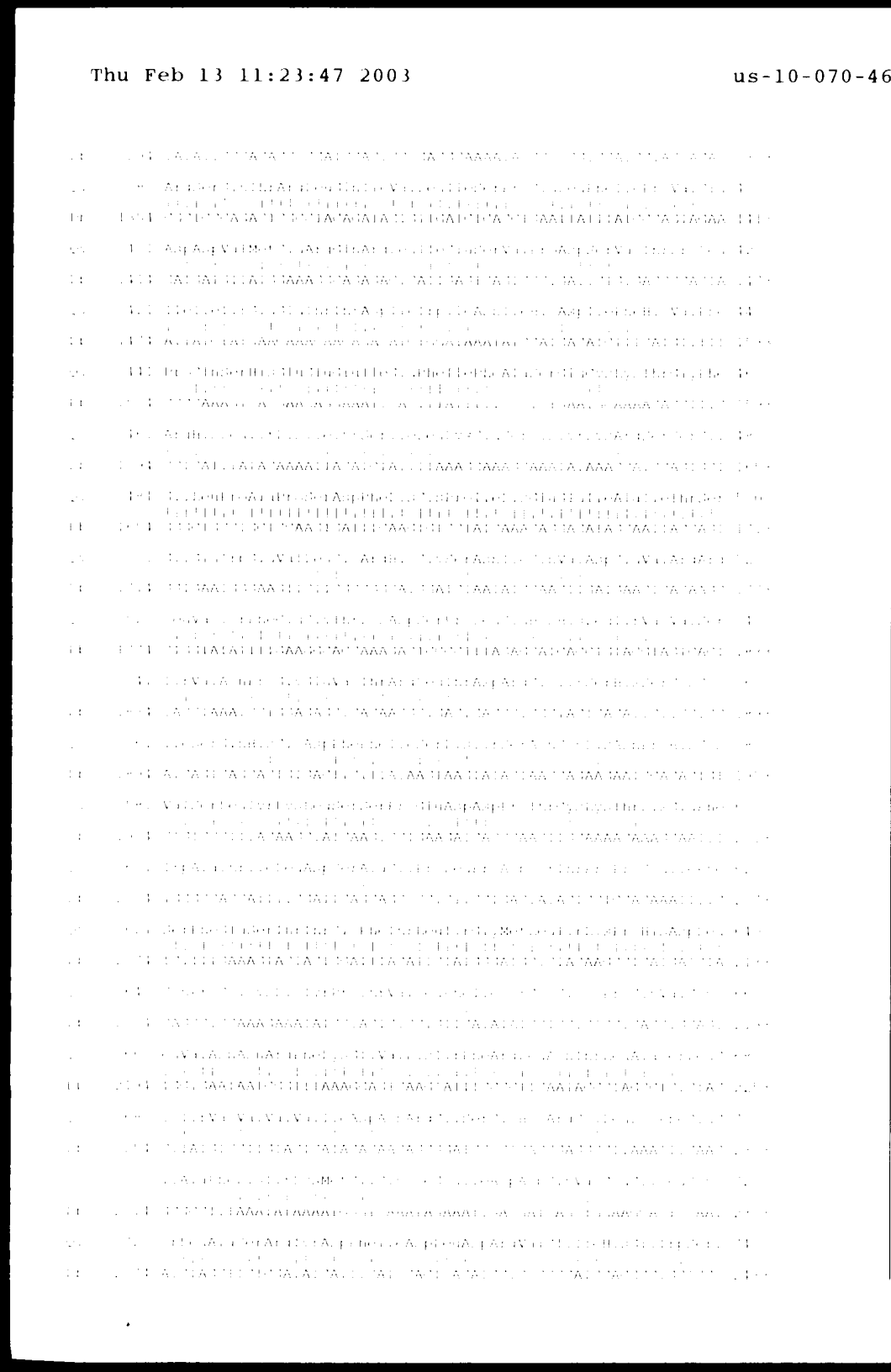
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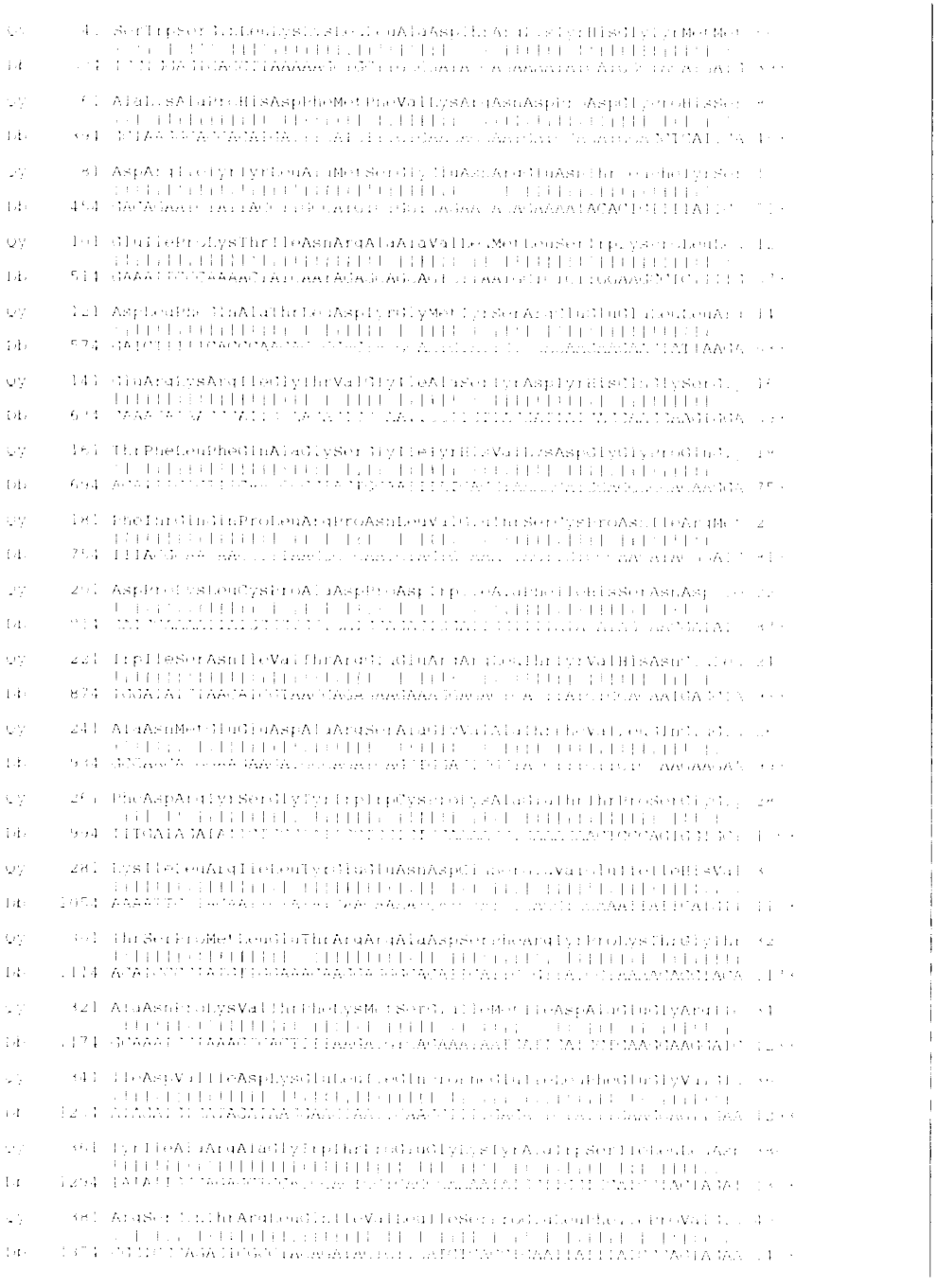
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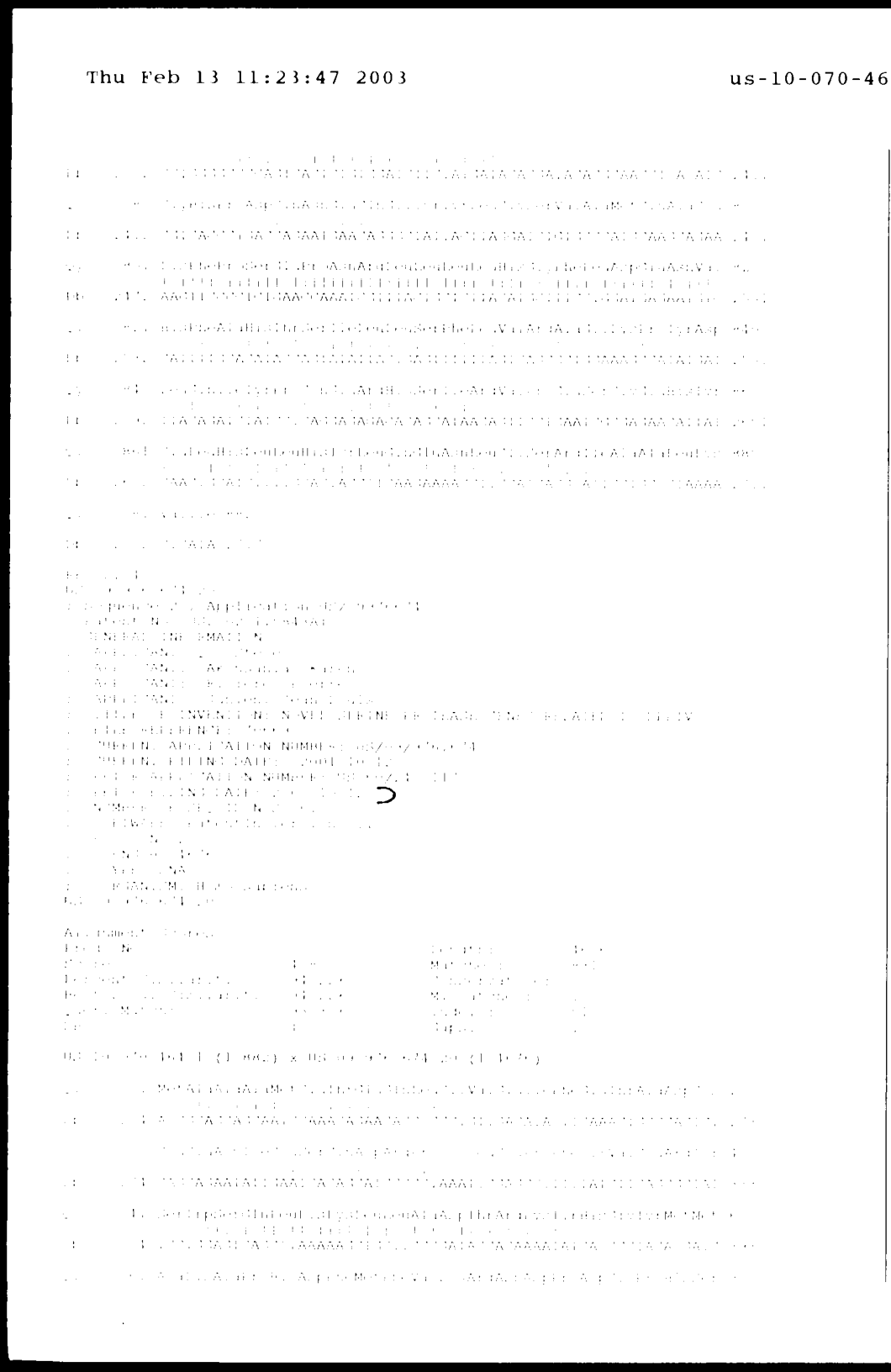
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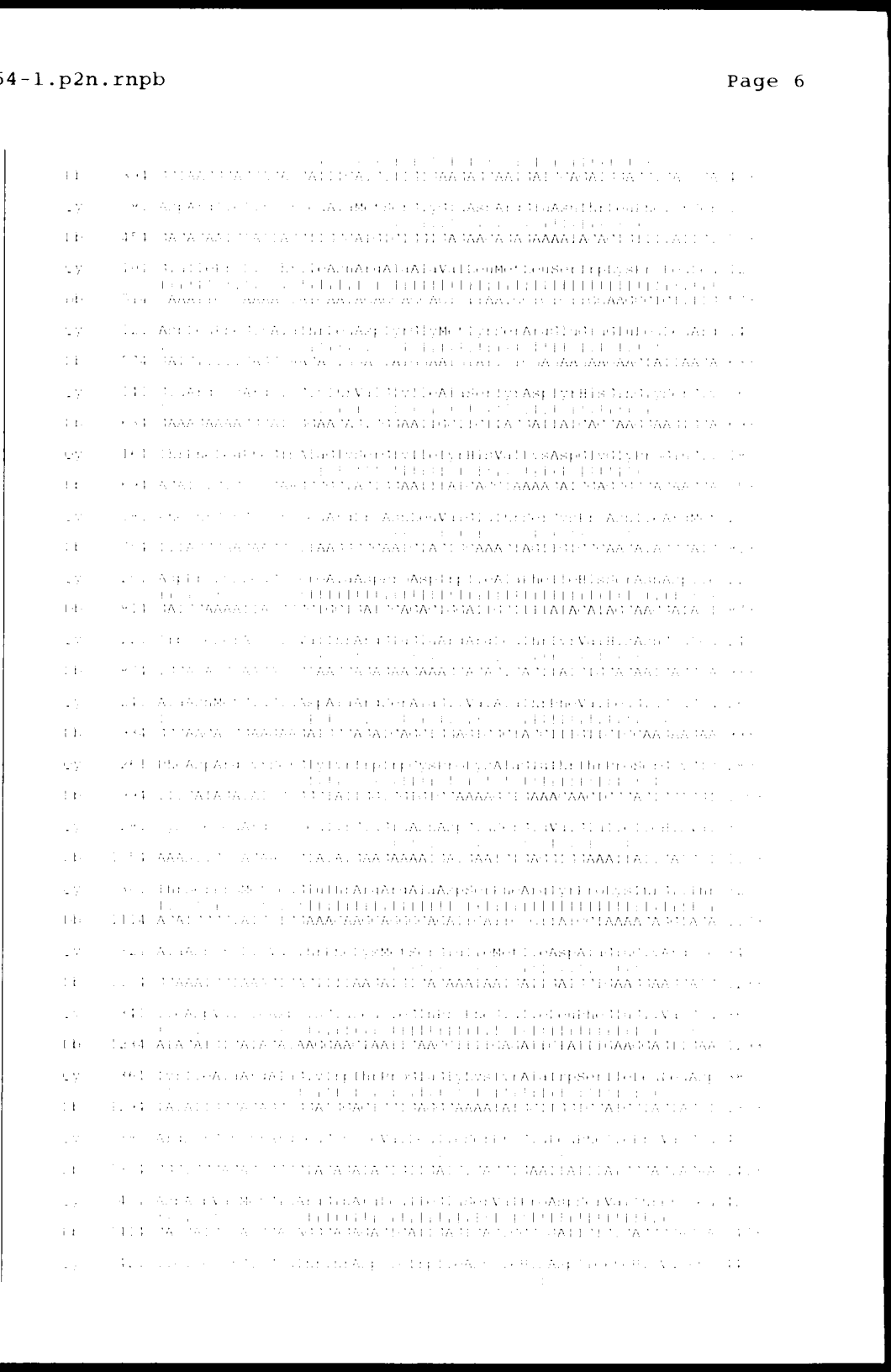


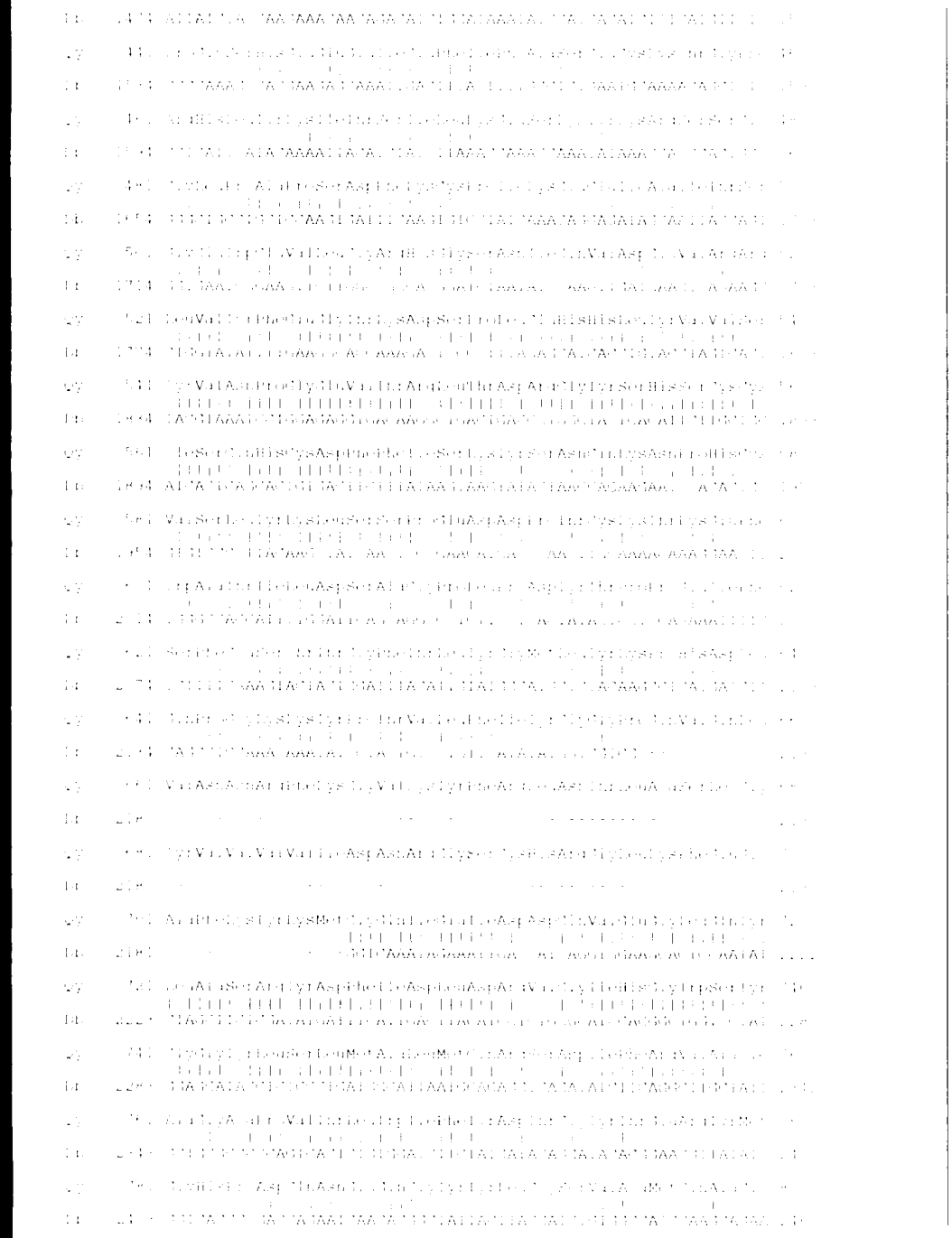


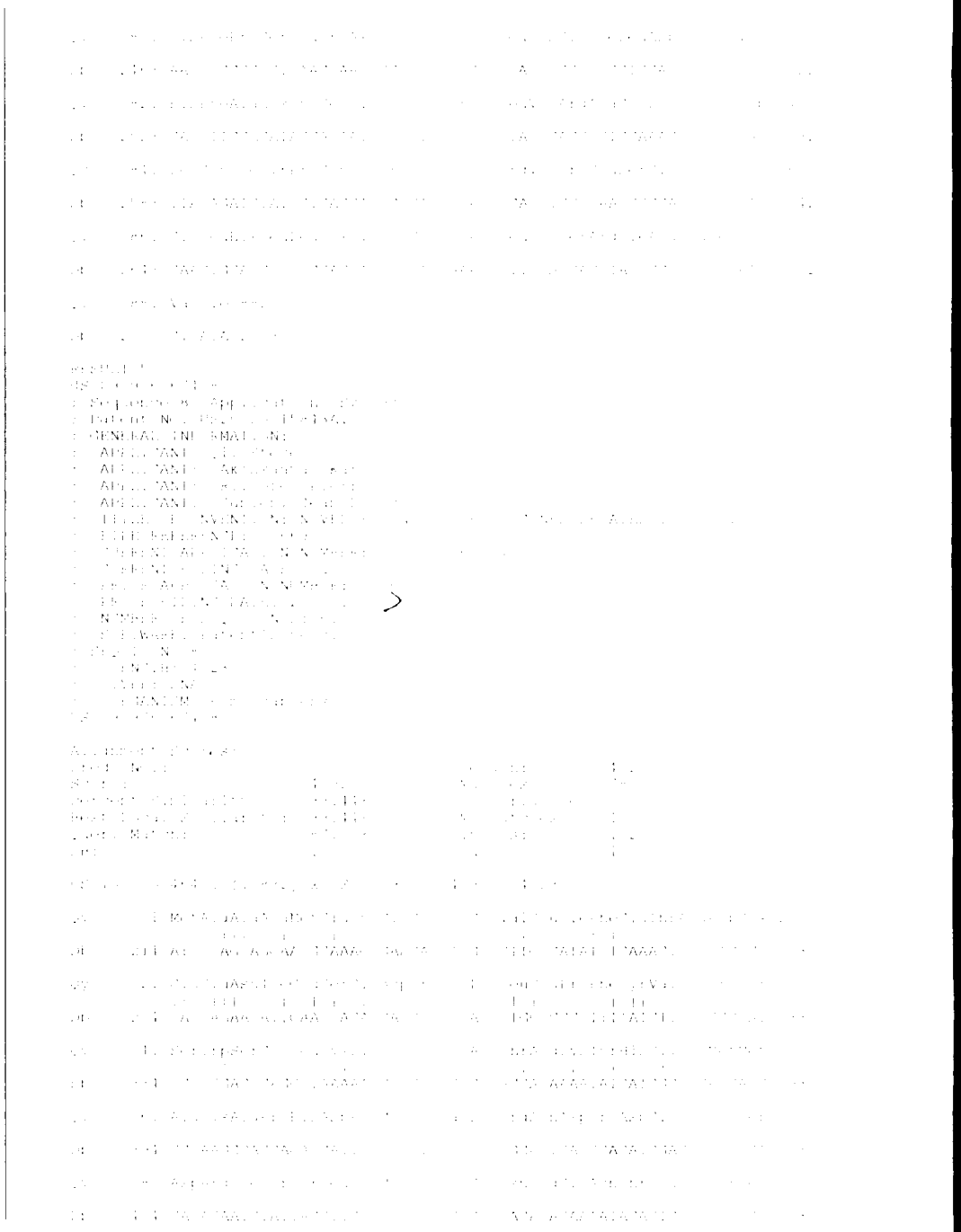


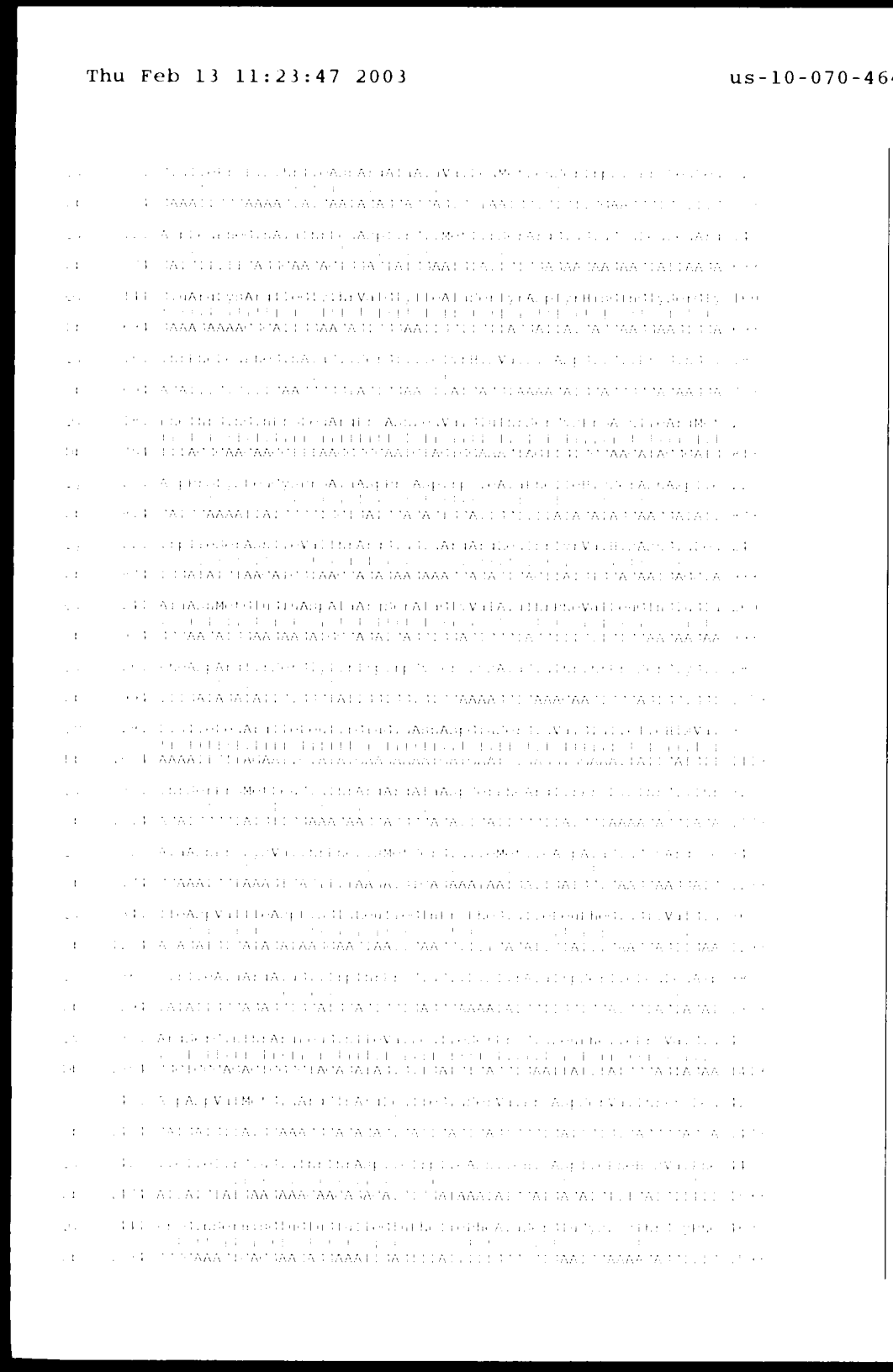


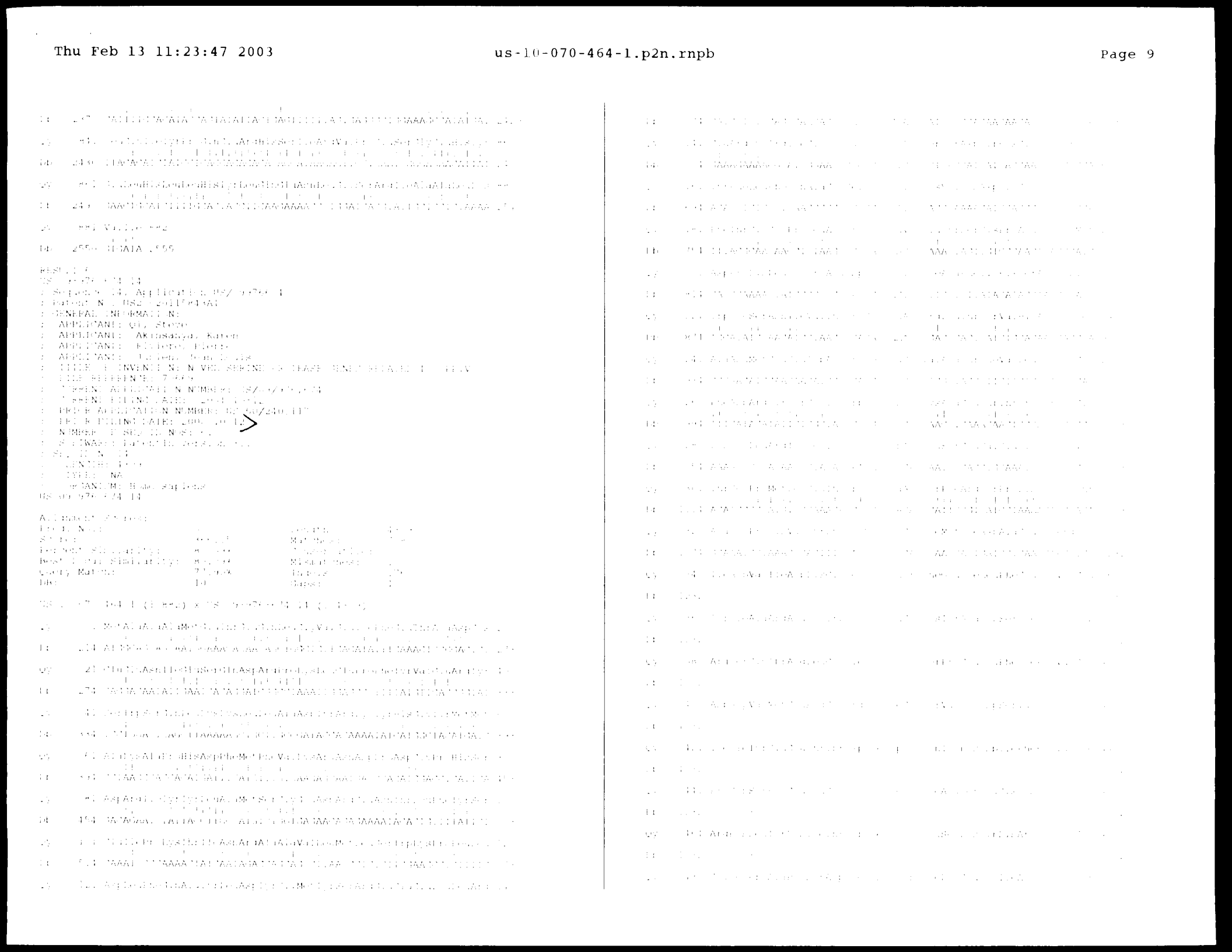


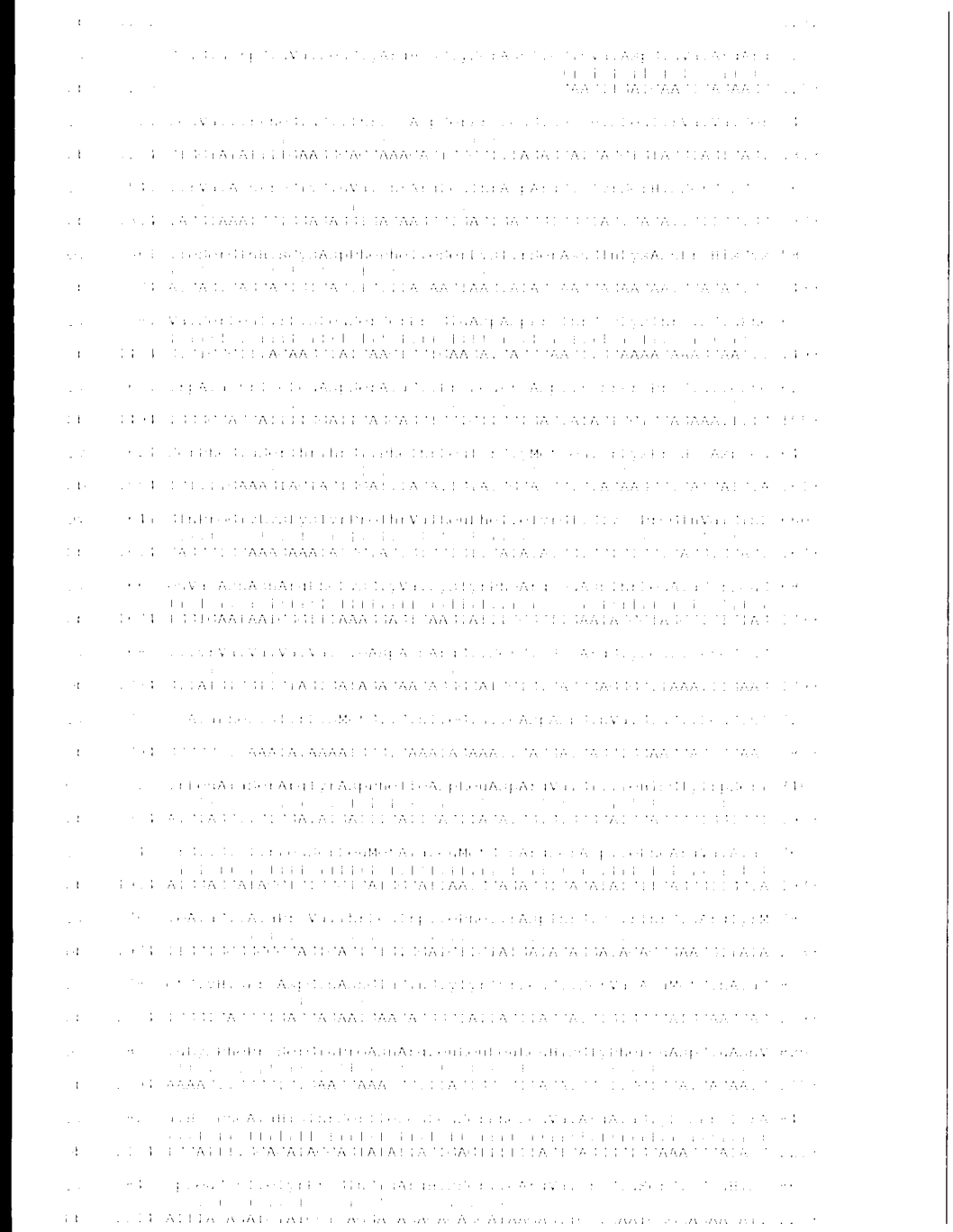


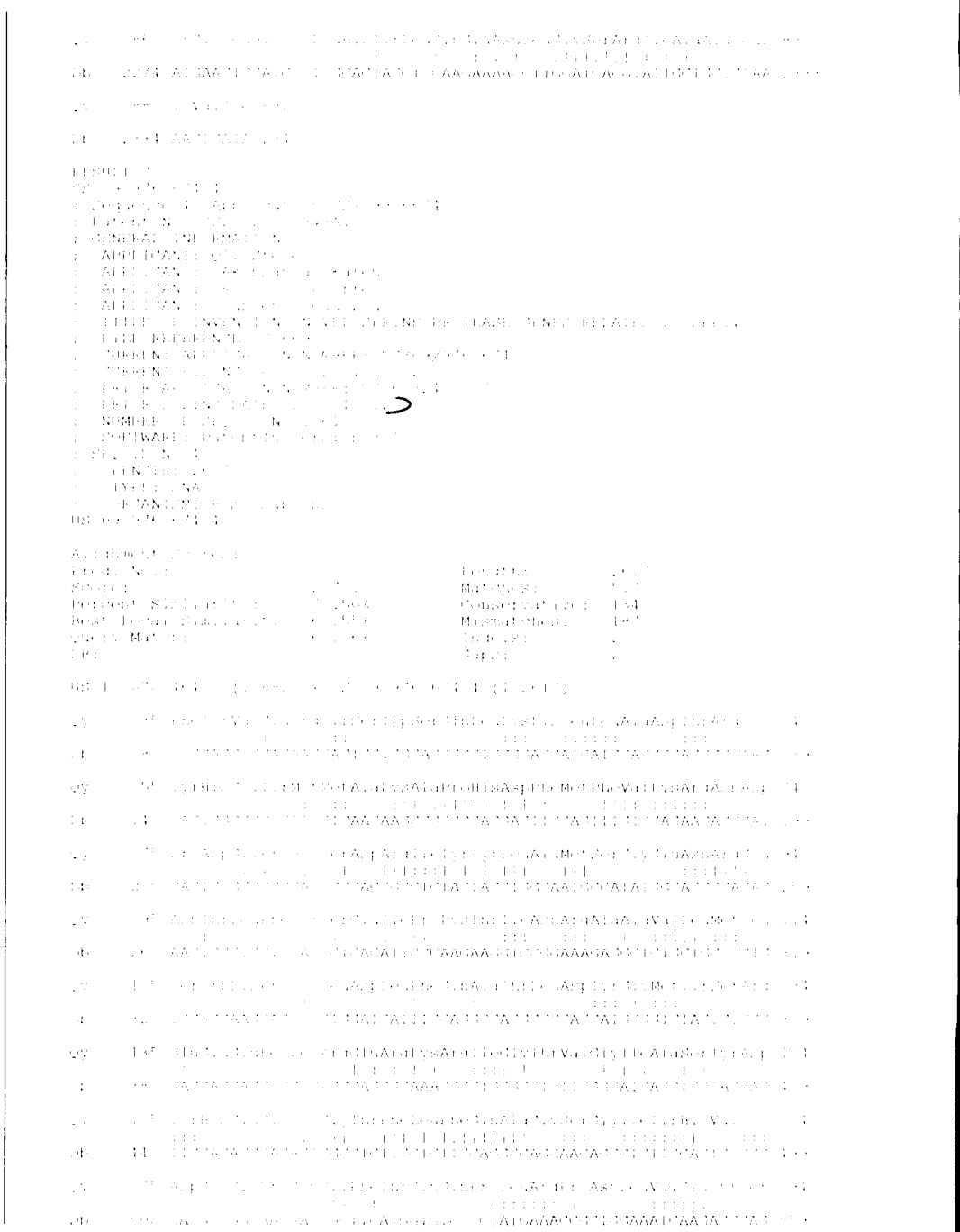


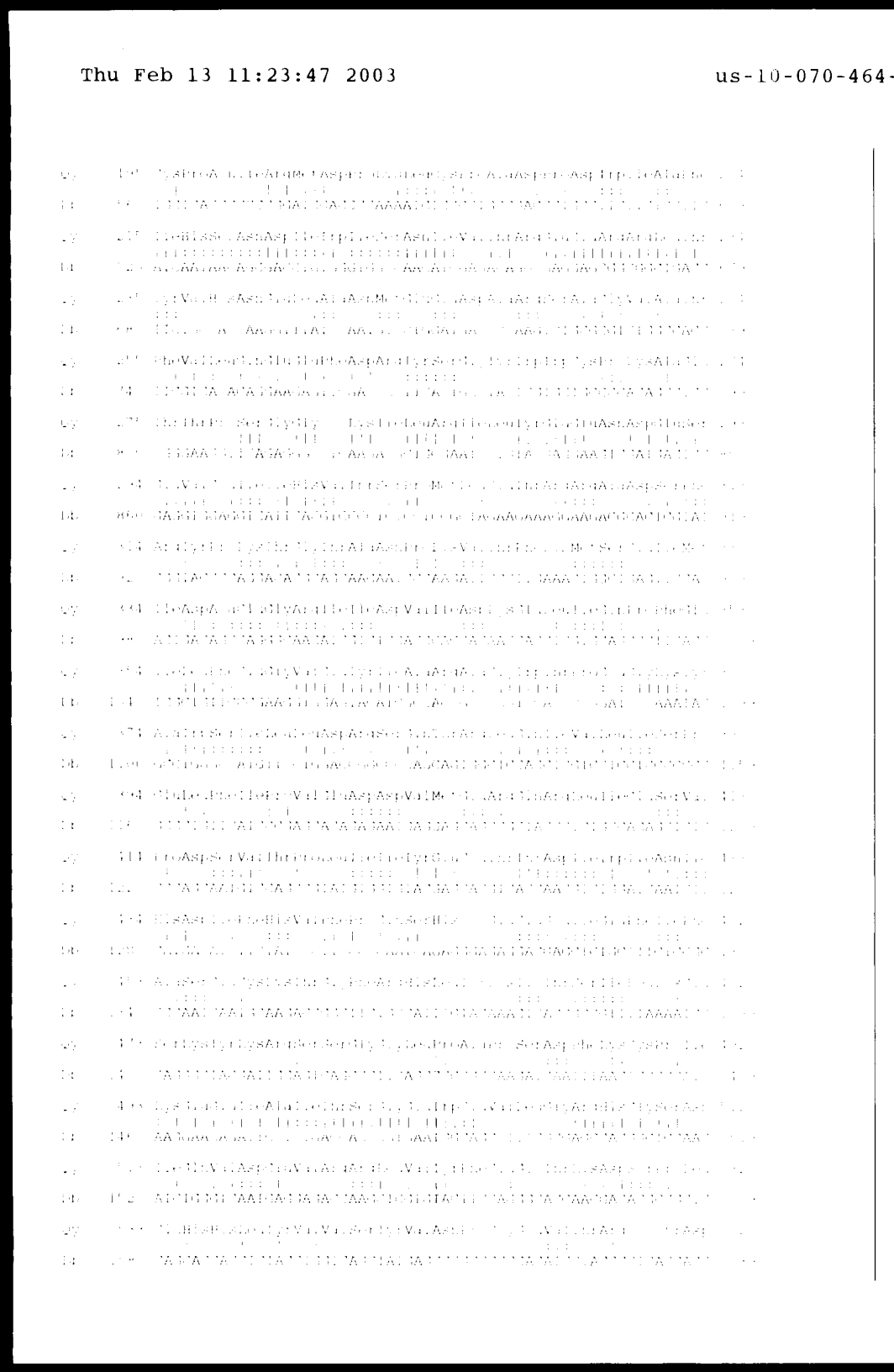


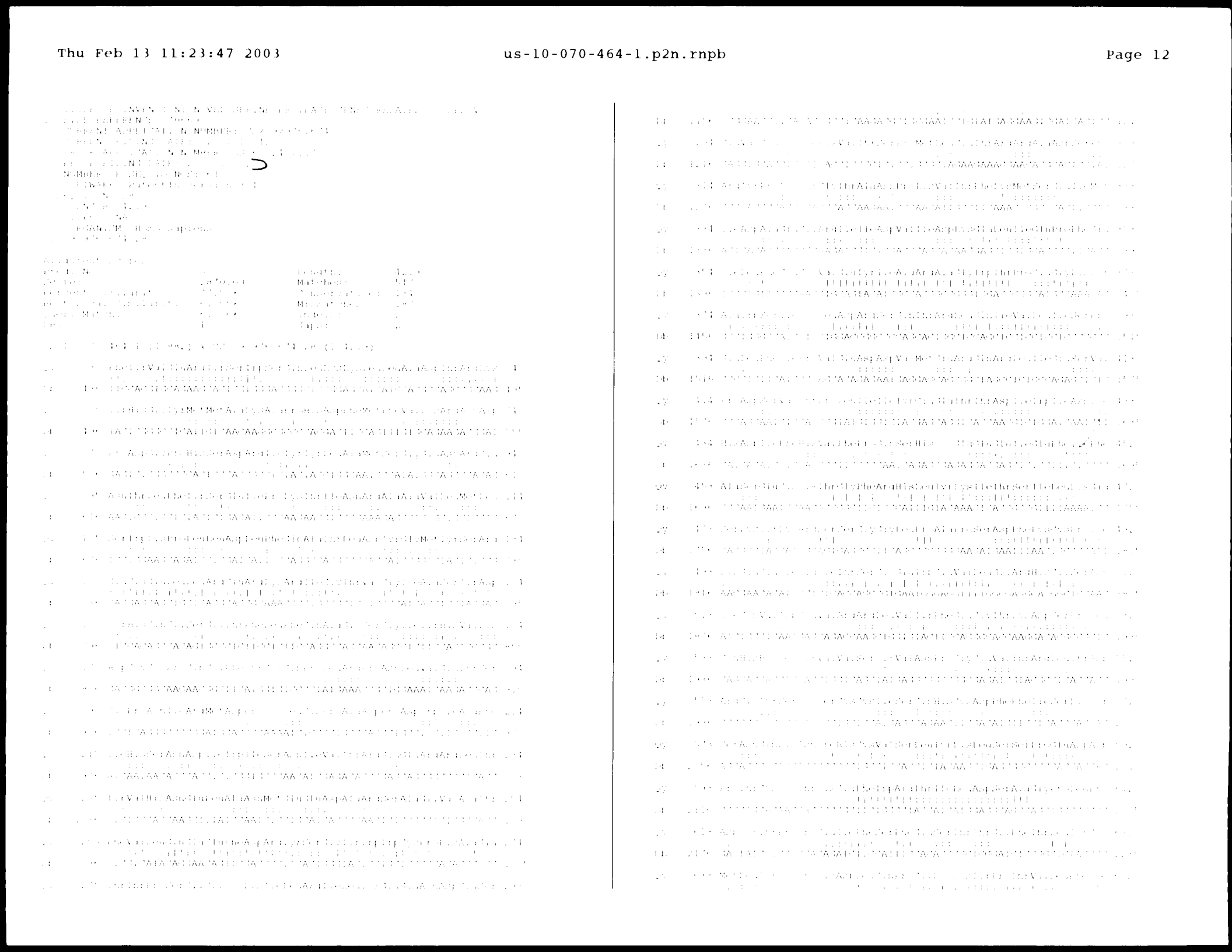


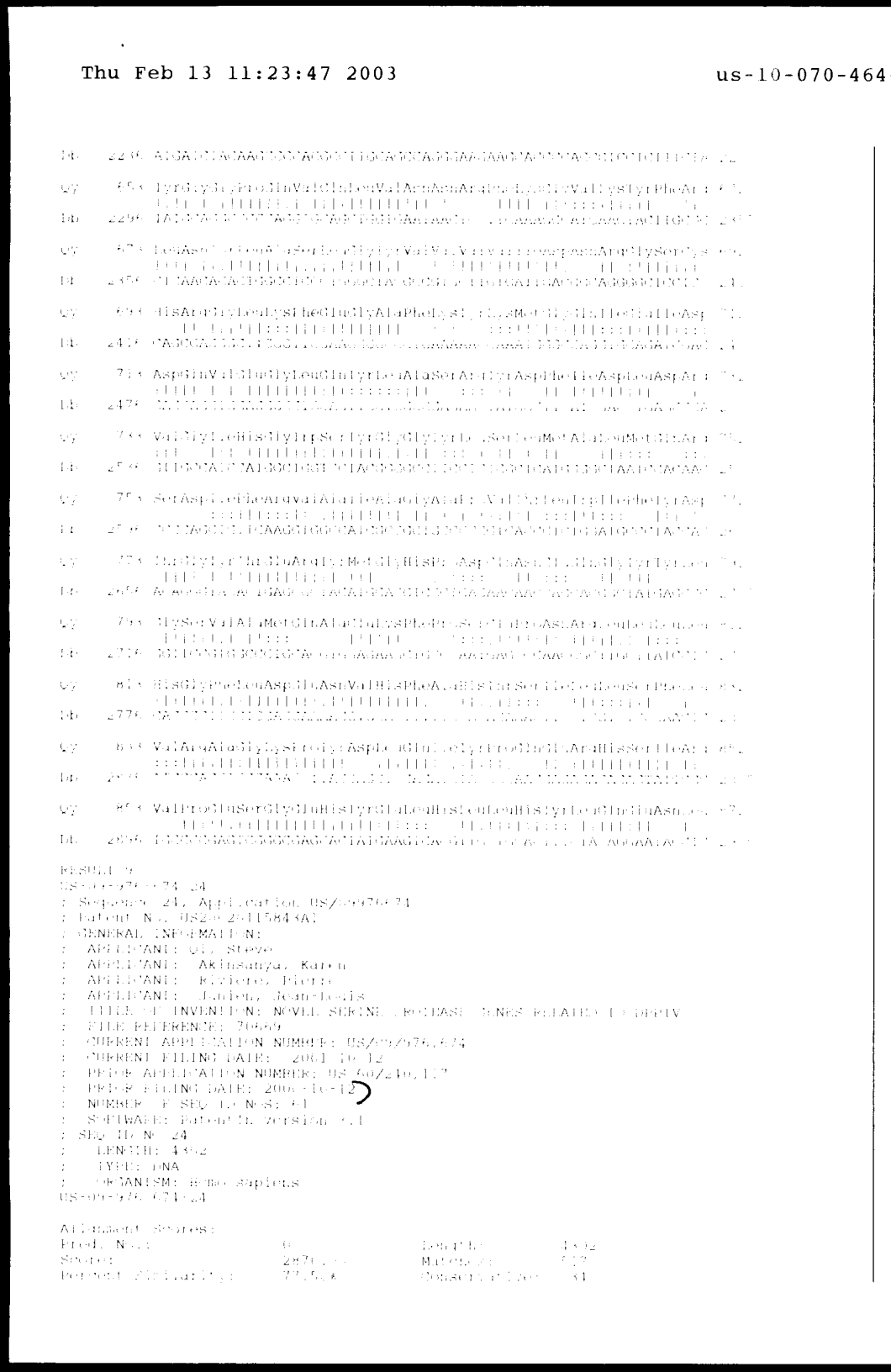






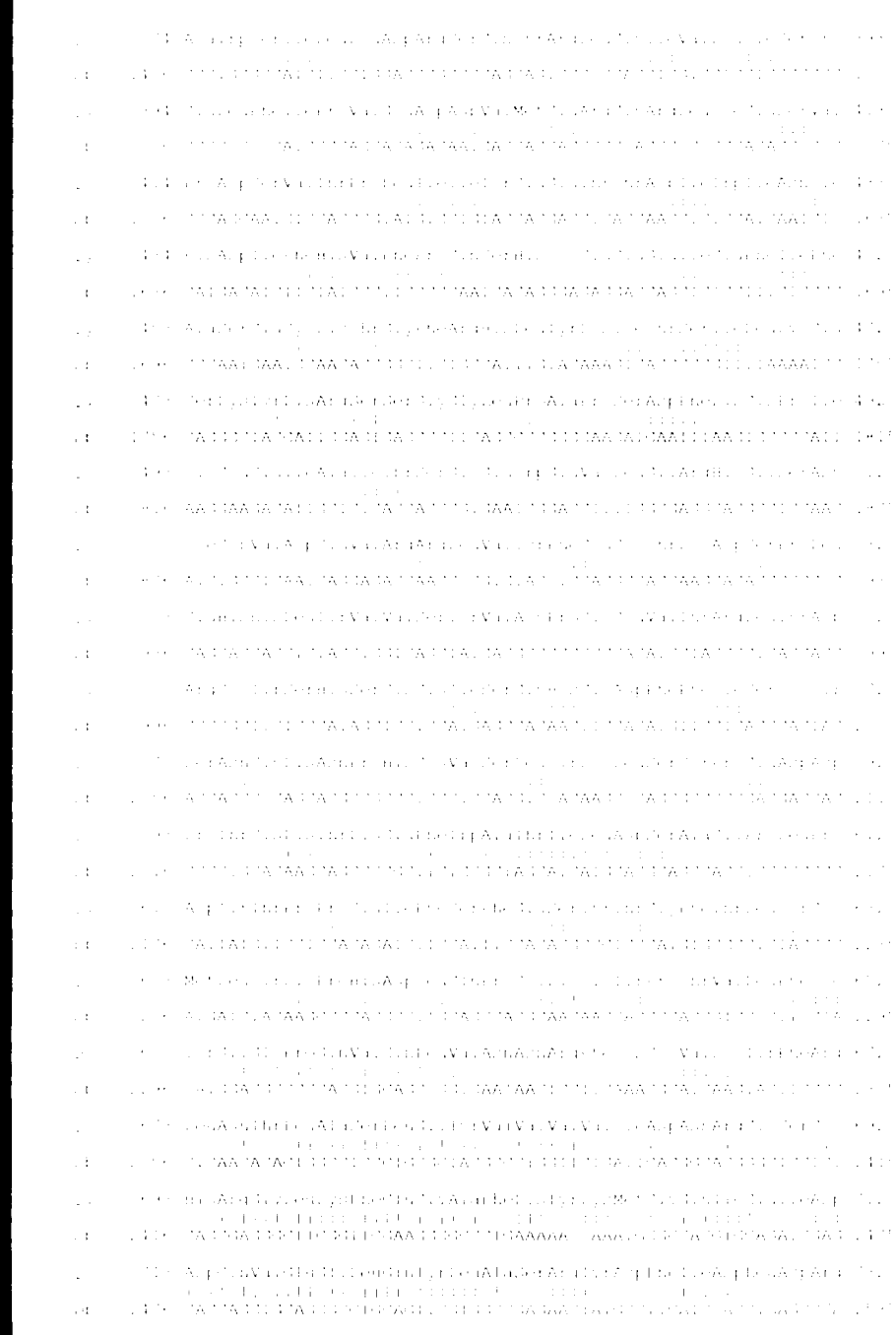


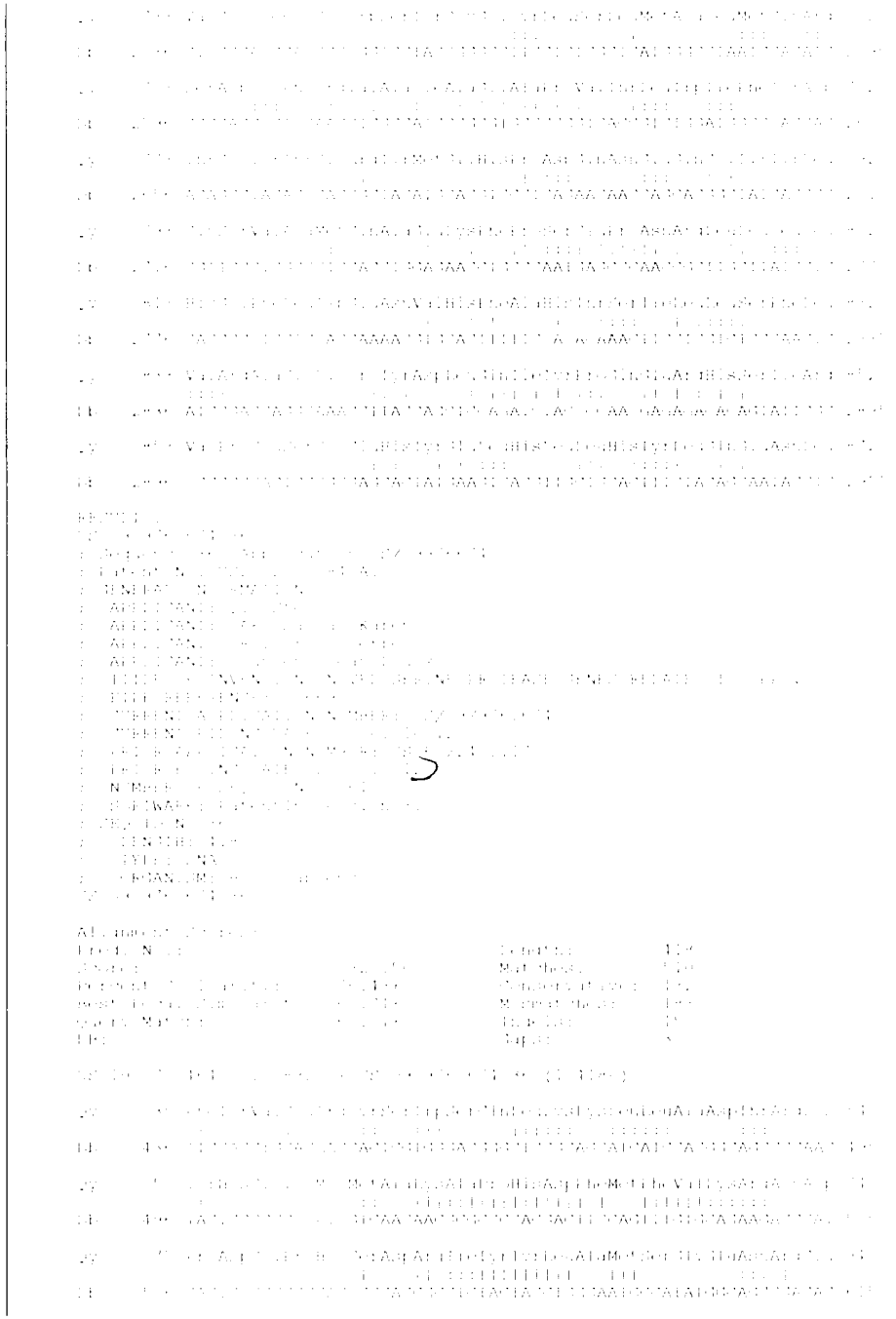


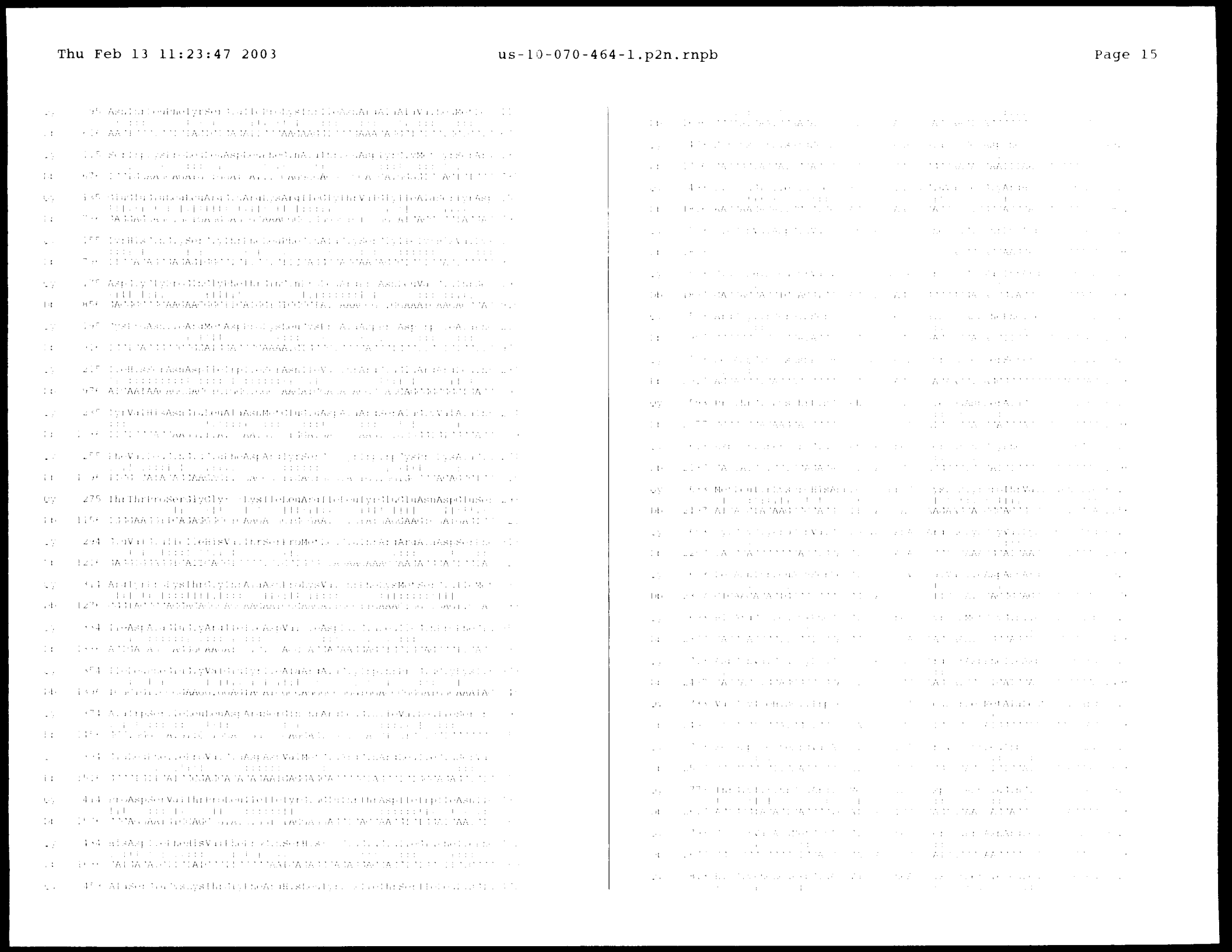


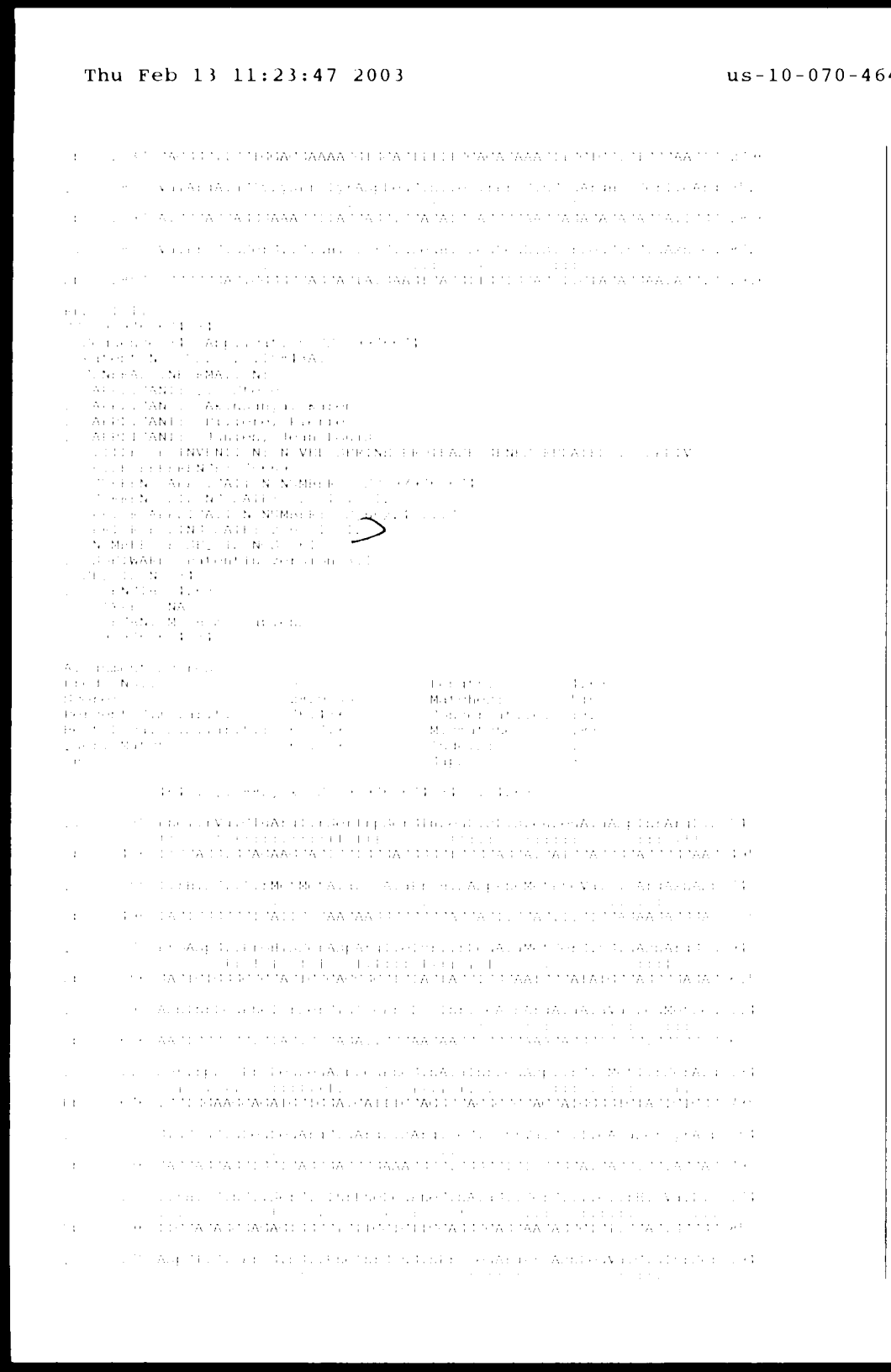
RESULT 2
US-10-070-464-24
; Sequence 24, Application US/10070464
; Patent No. US20040115843A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Steve
; APPLICANT: Akinsanya, Karen
; APPLICANT: Rozier, Pierre
; APPLICANT: Linden, Jean-Denis
; TITLE OF INVENTION: NOVEL SERINE PROTEASE RELATED POLYPEPTIDES
; FILE REFERENCE: 20669
; CURRENT APPLICATION NUMBER: US/10/070,464
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/218,117
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-070-464-24

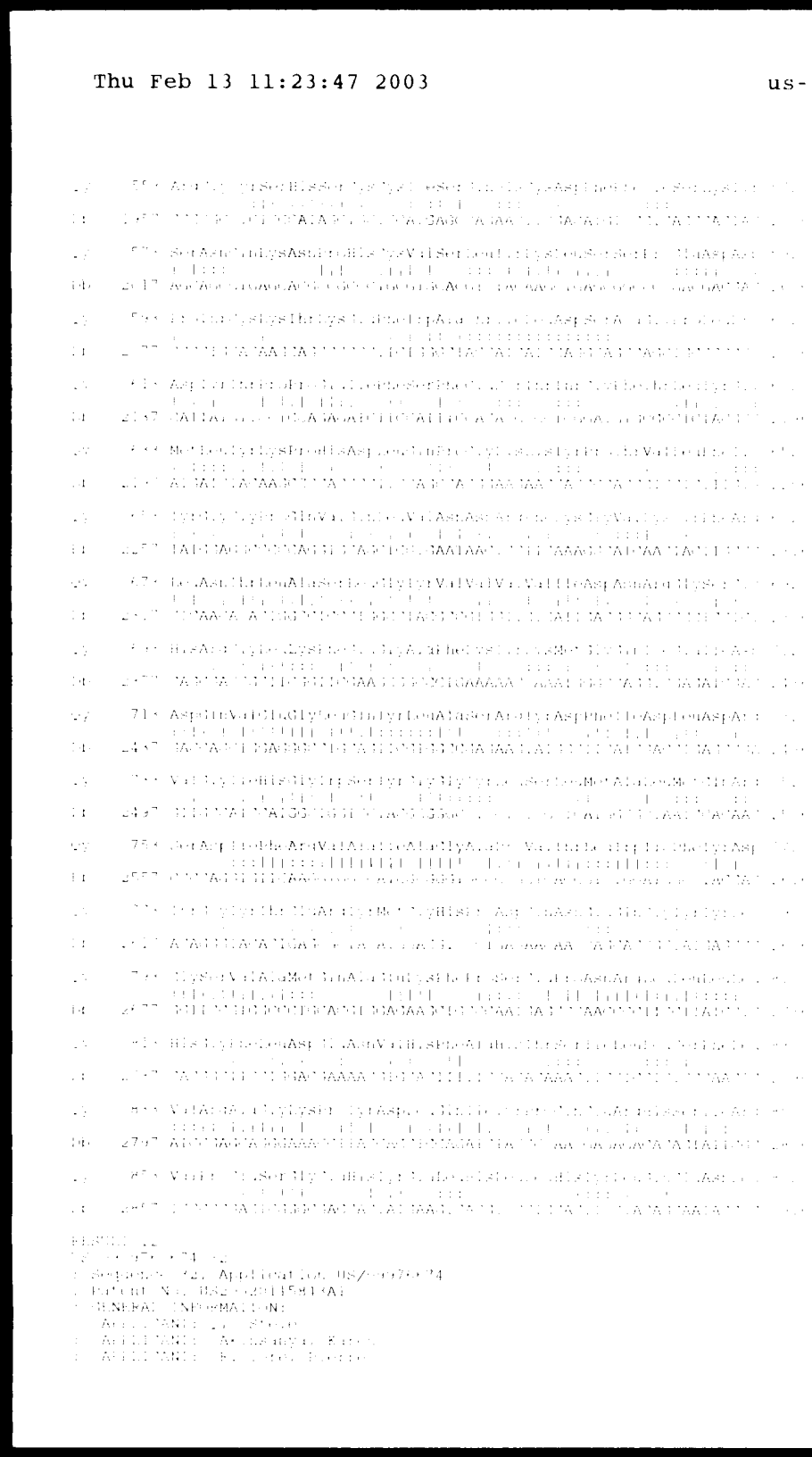
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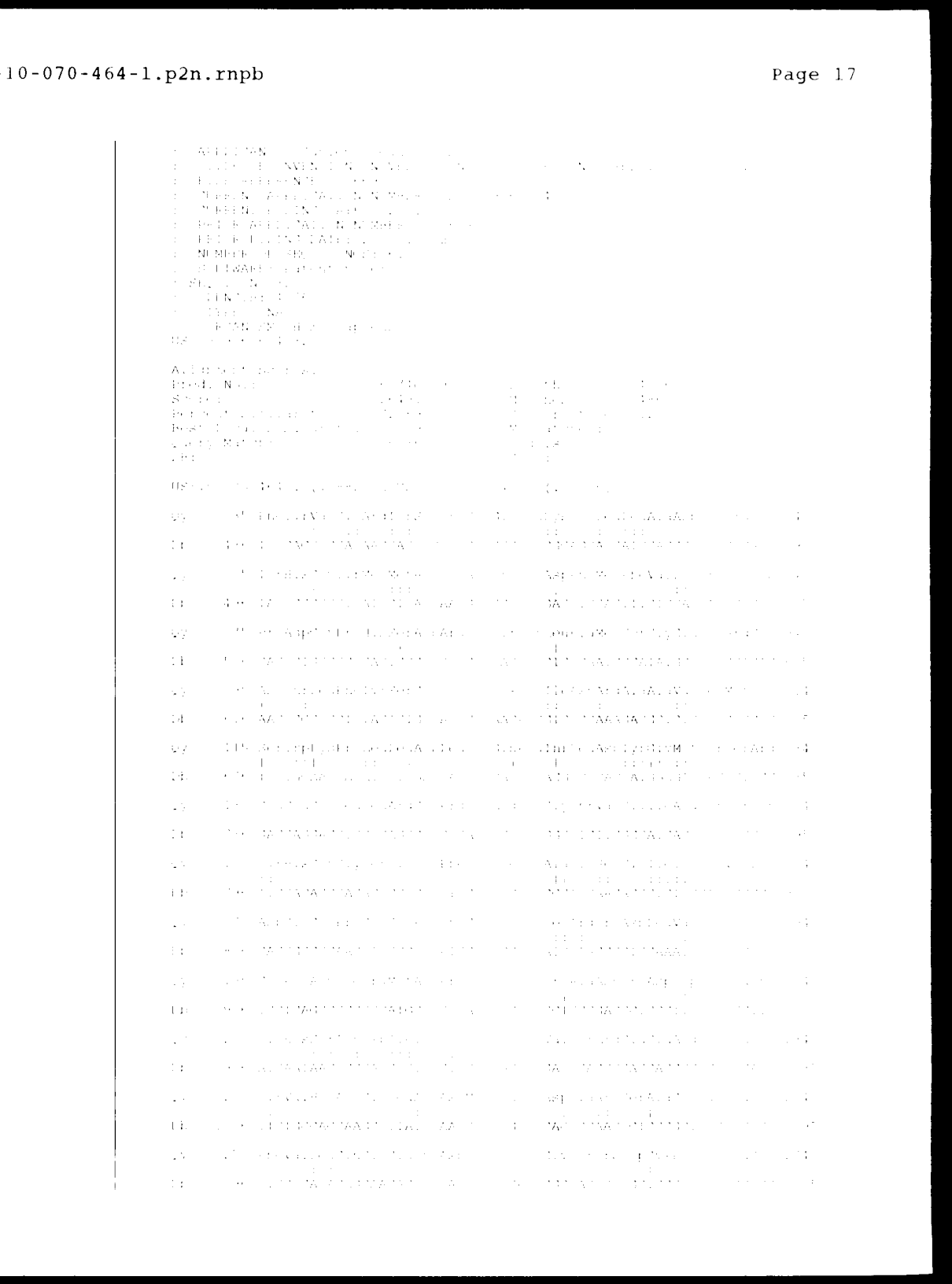


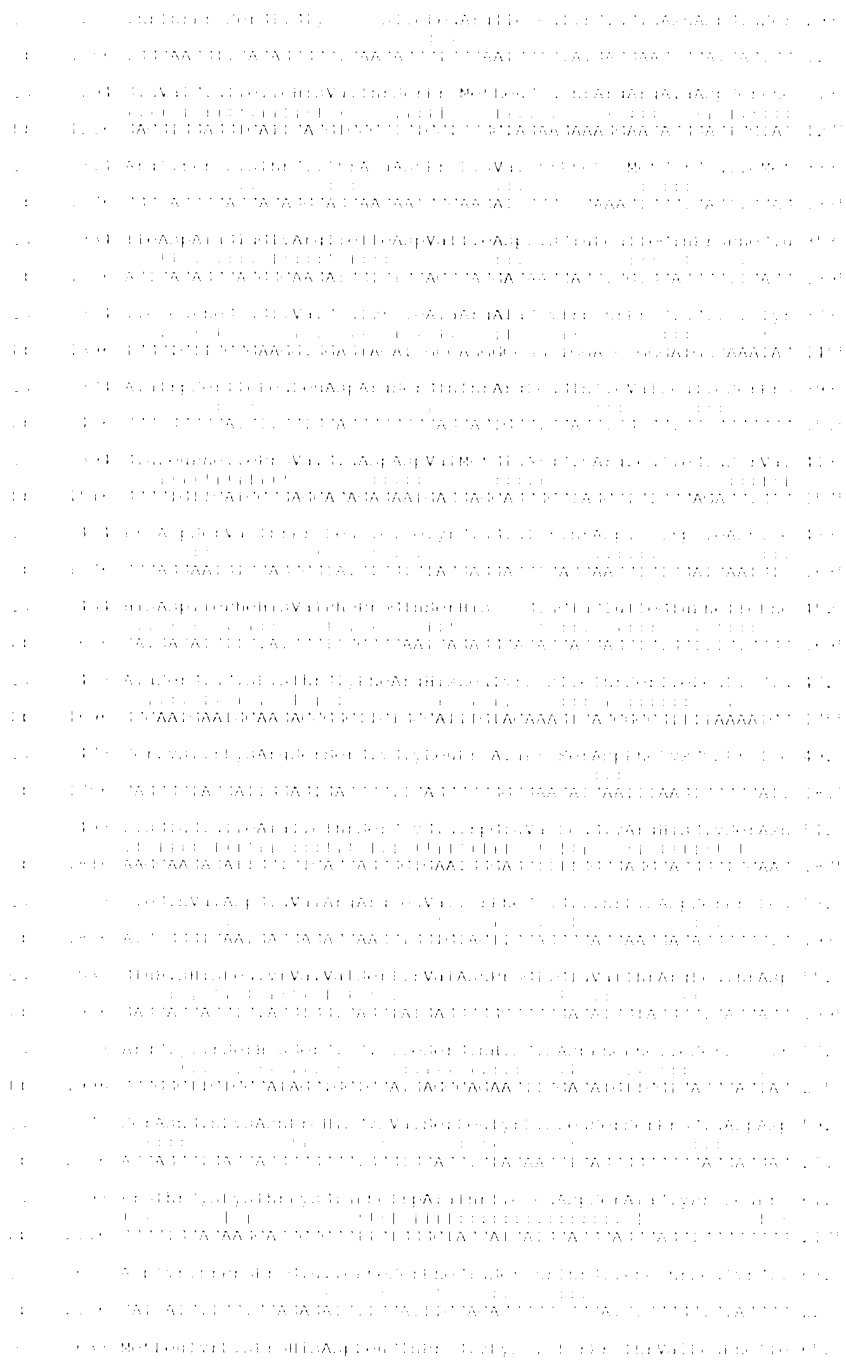


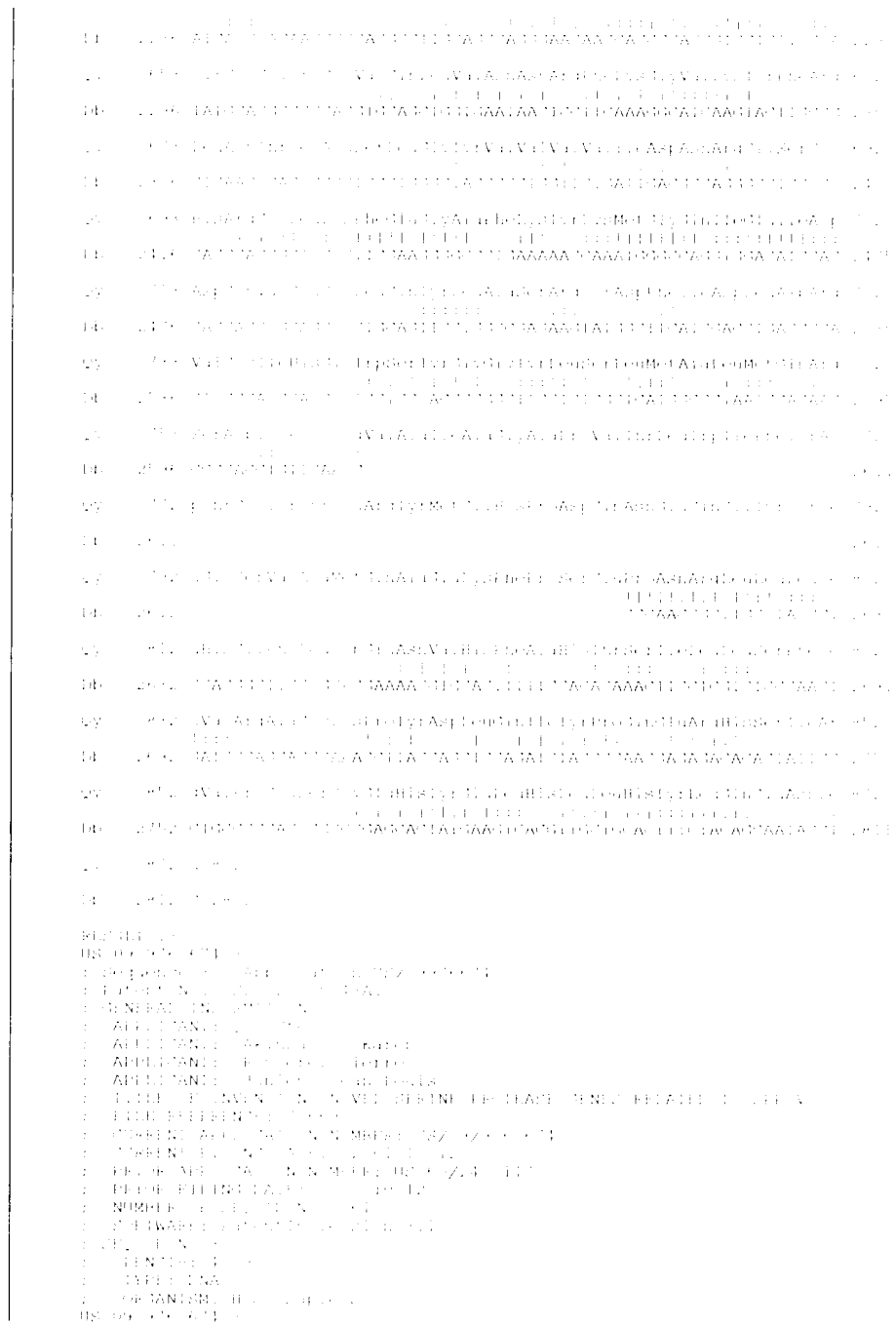


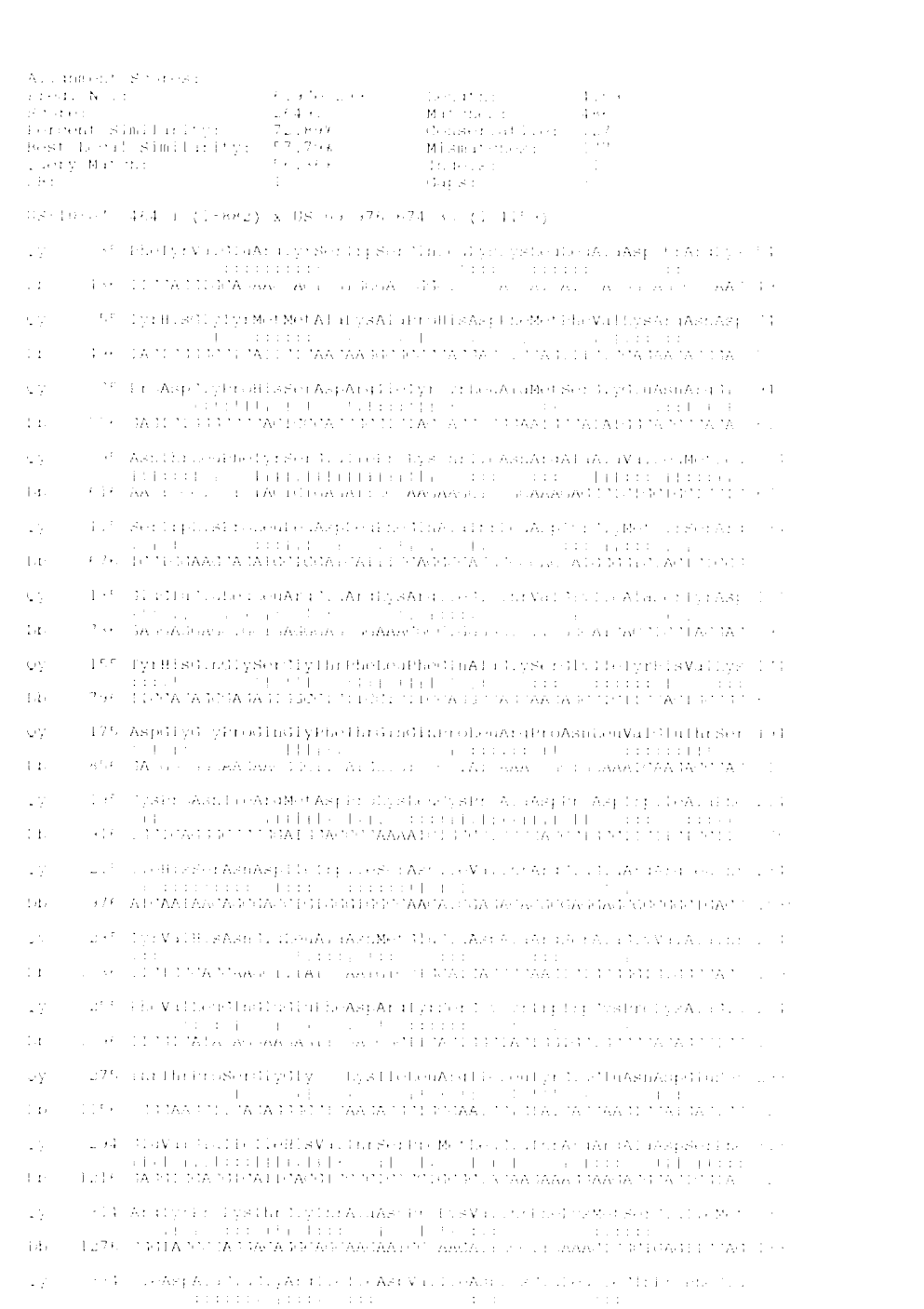


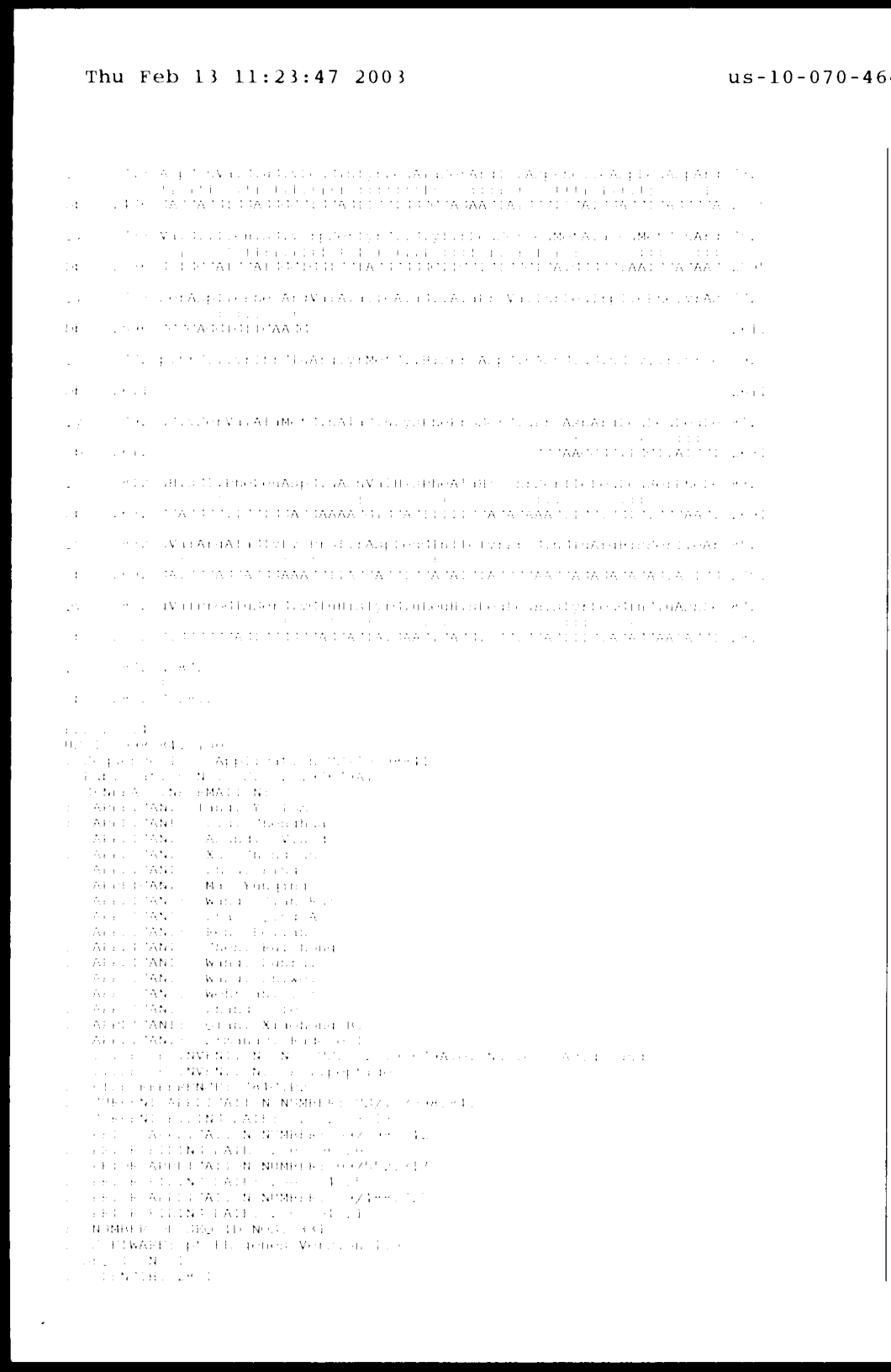


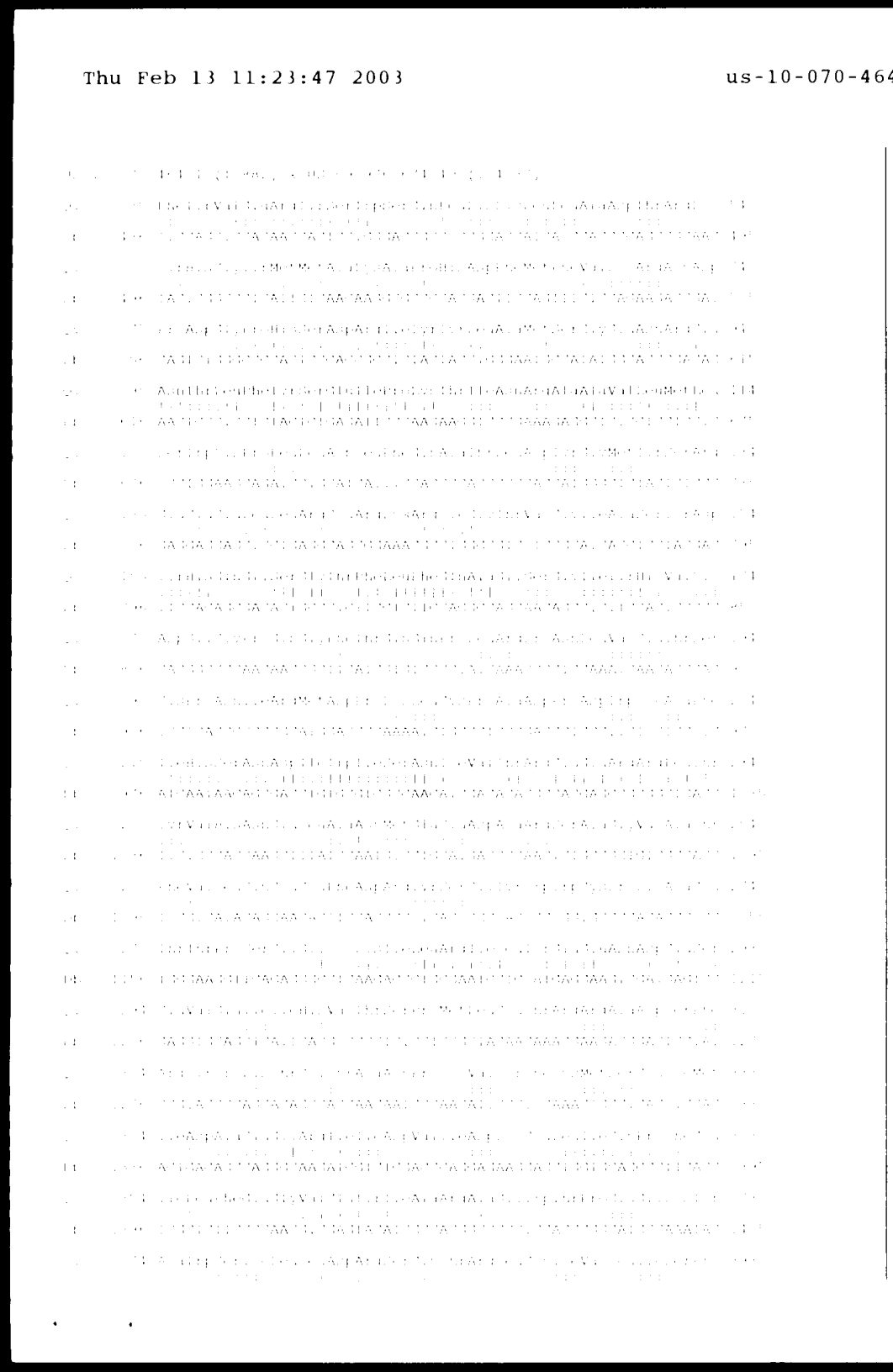


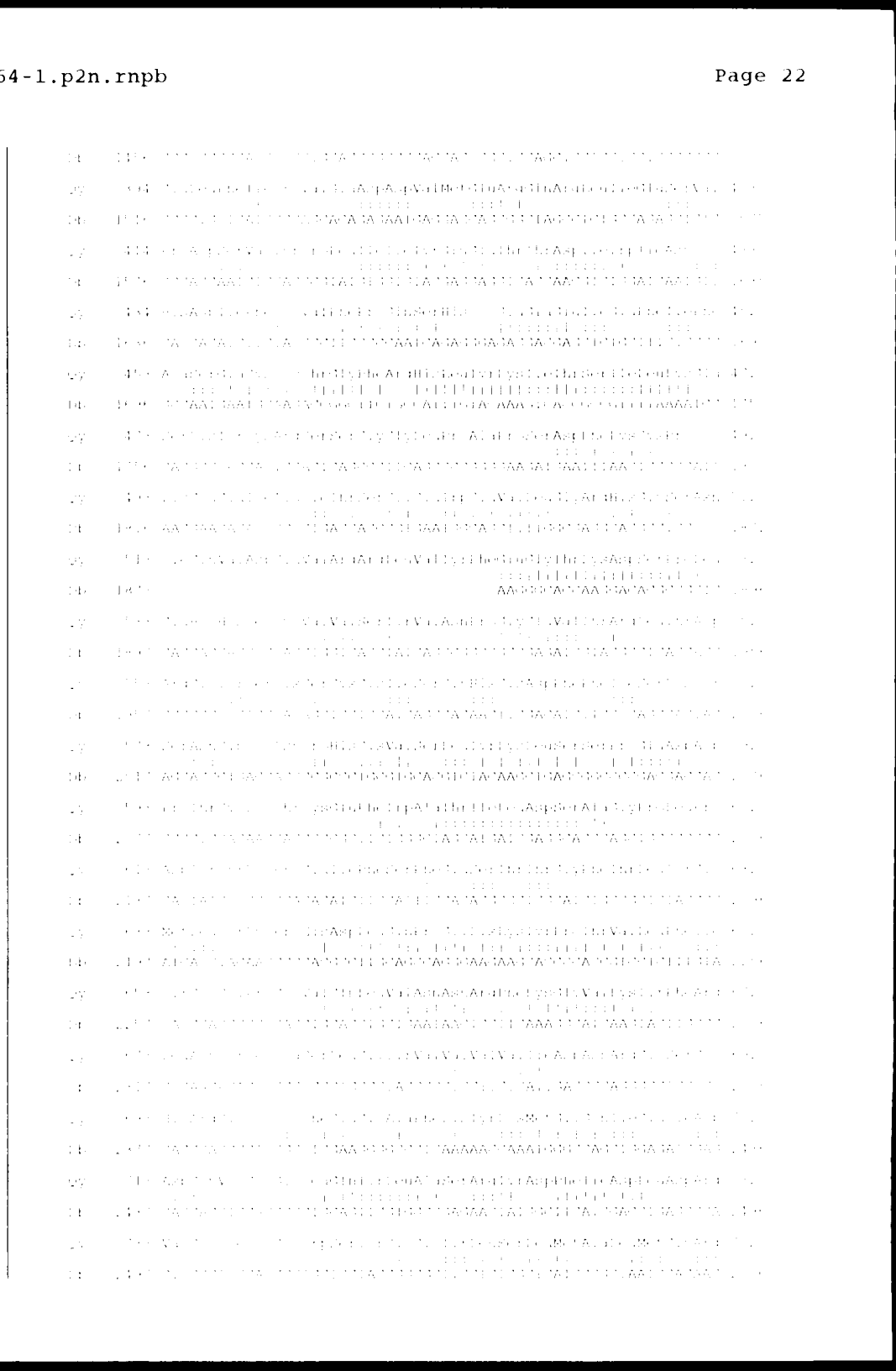


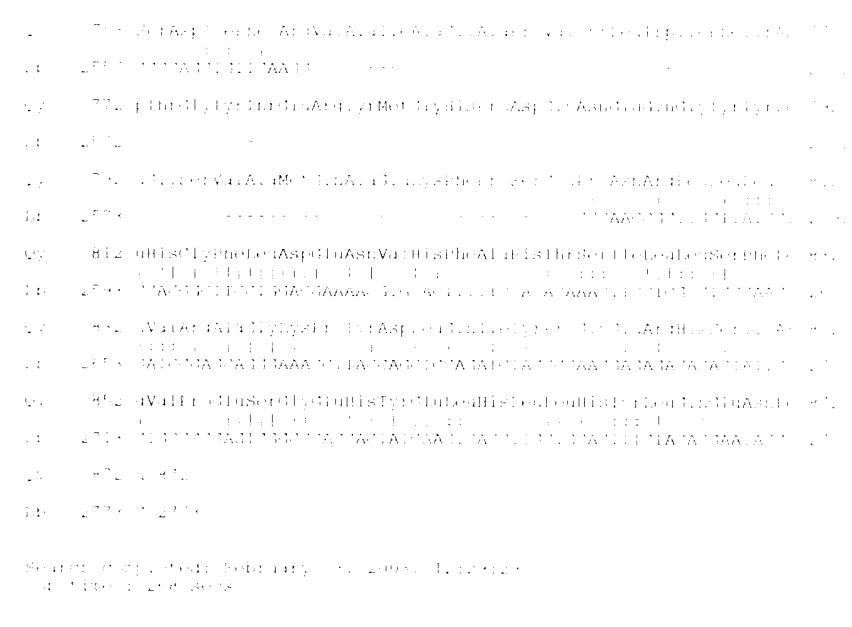


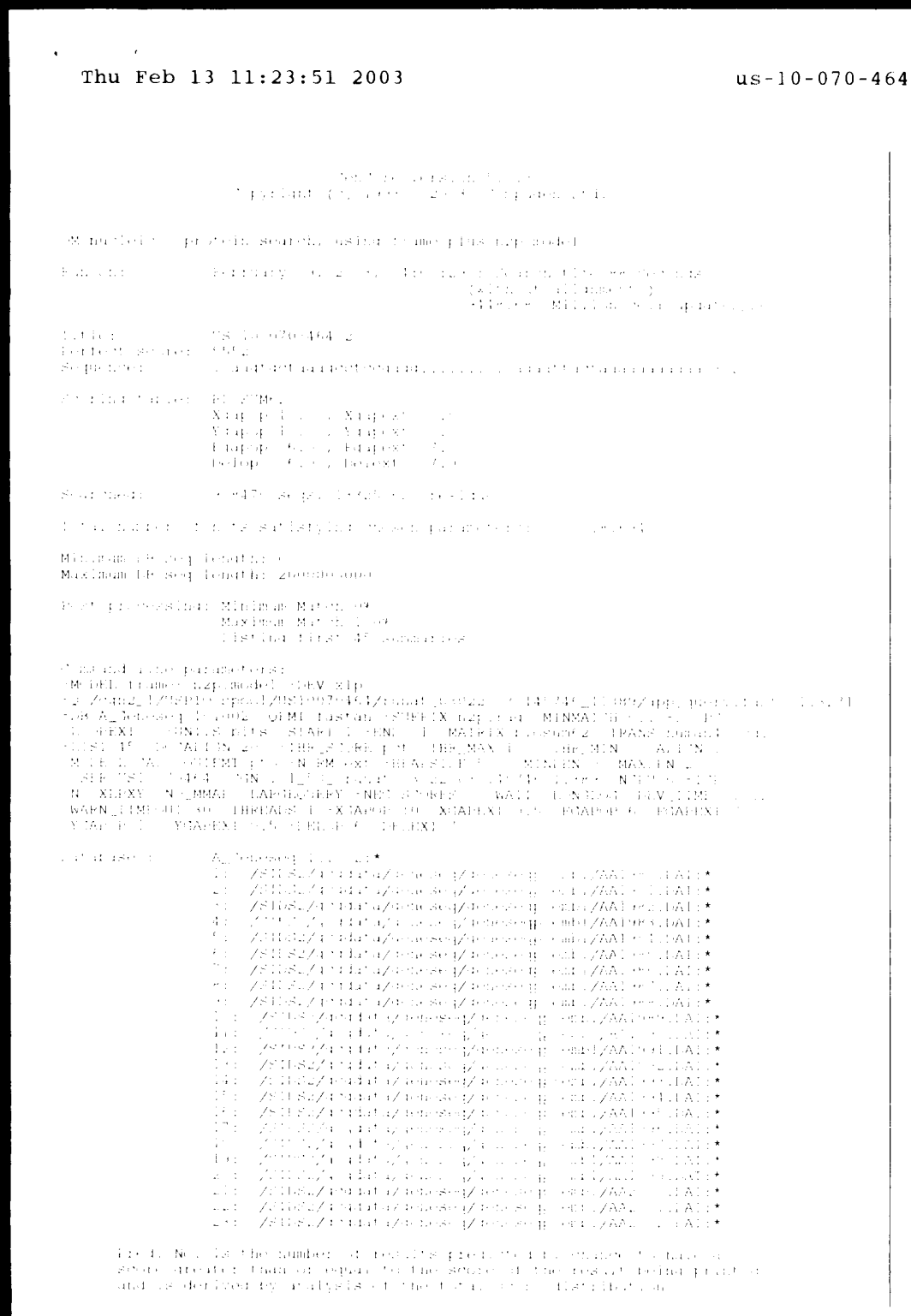


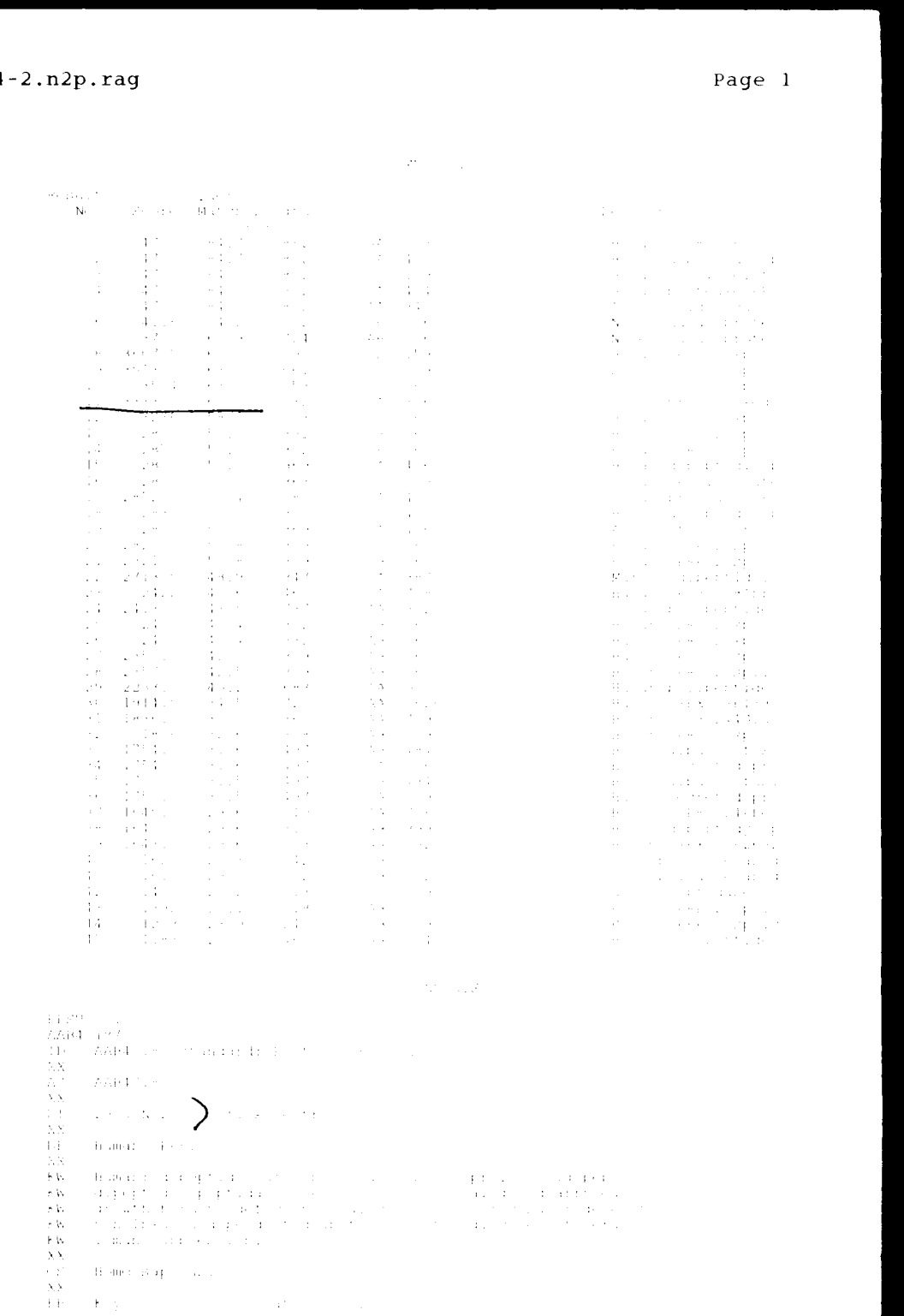


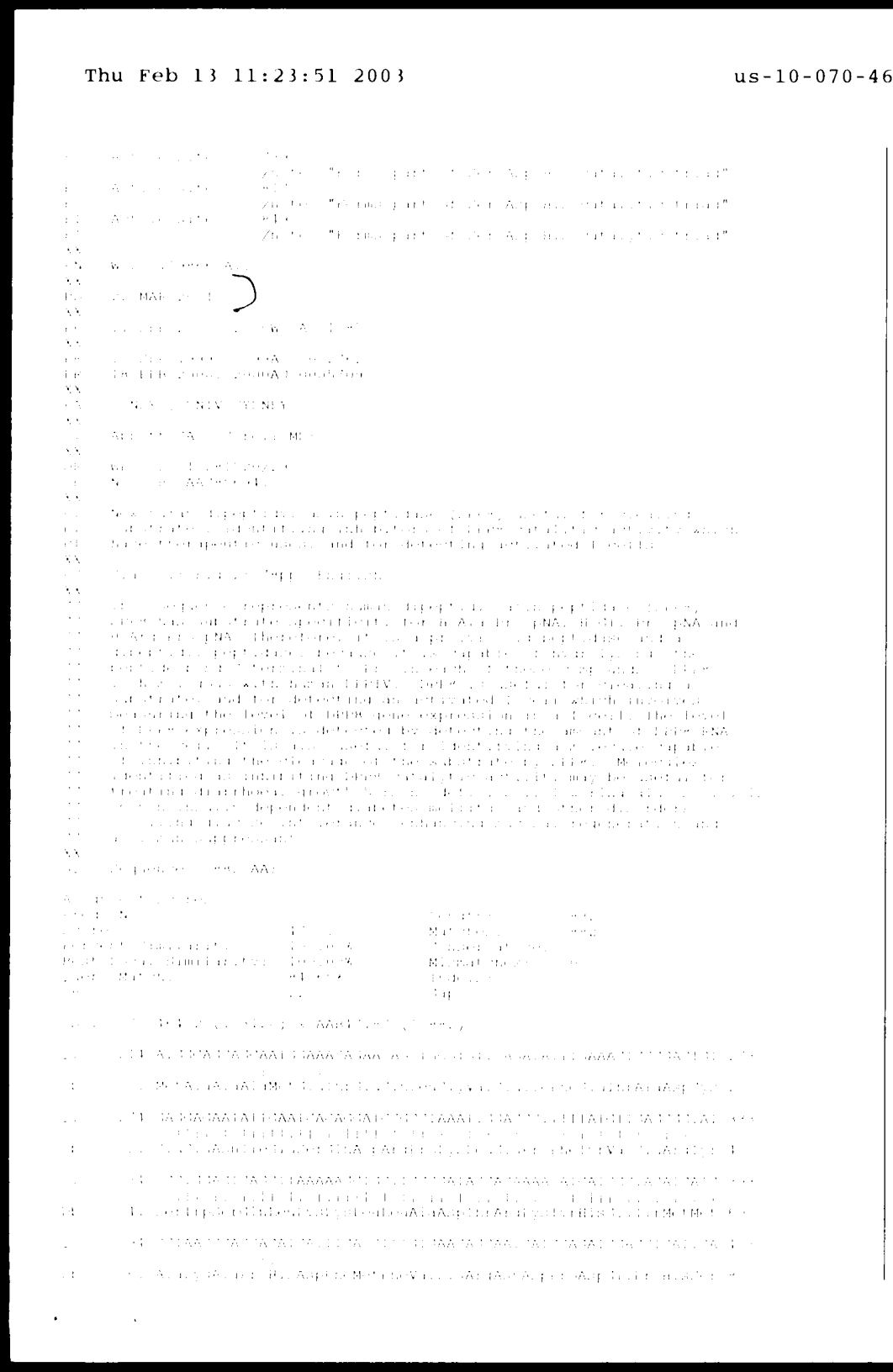


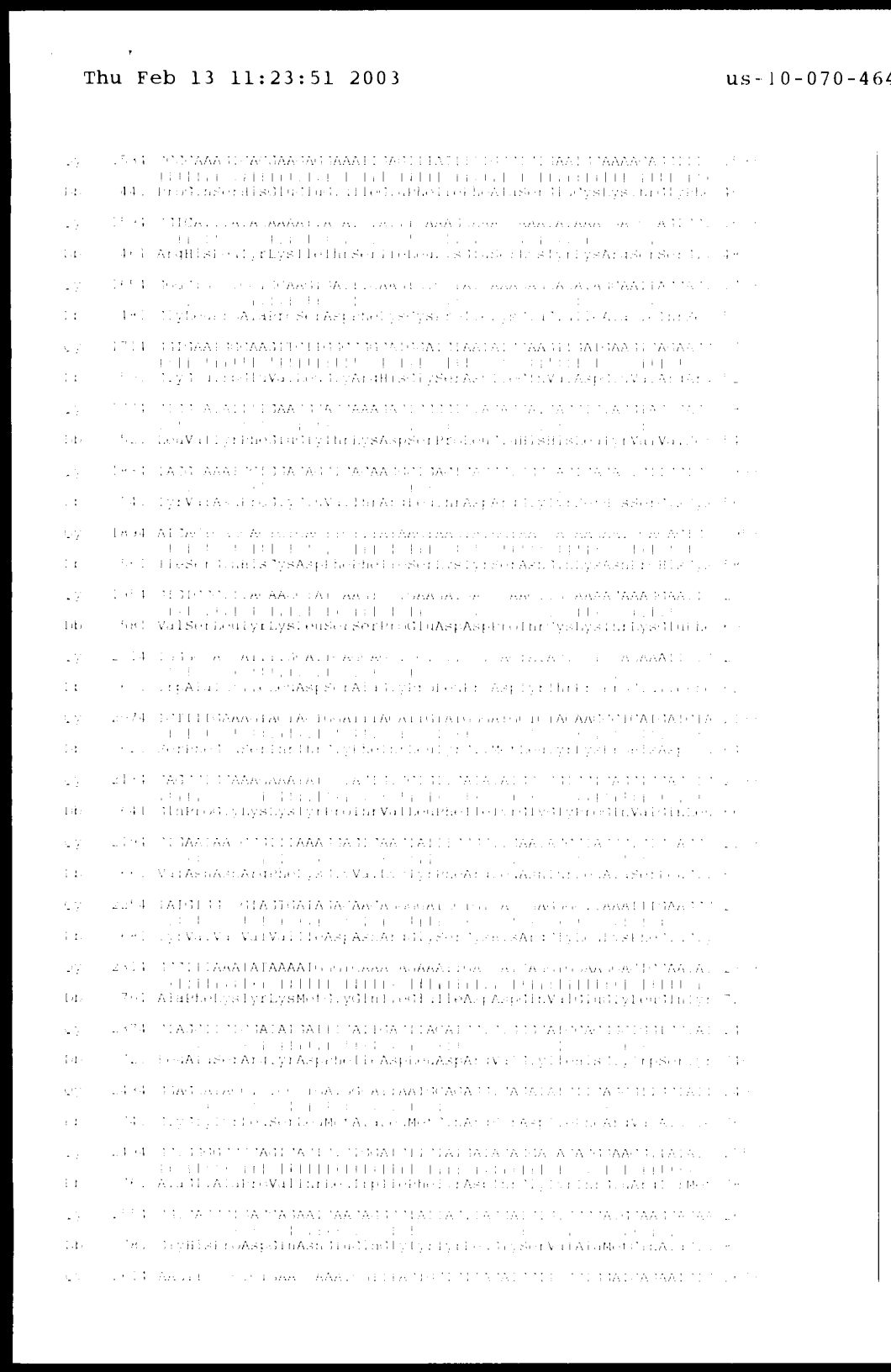


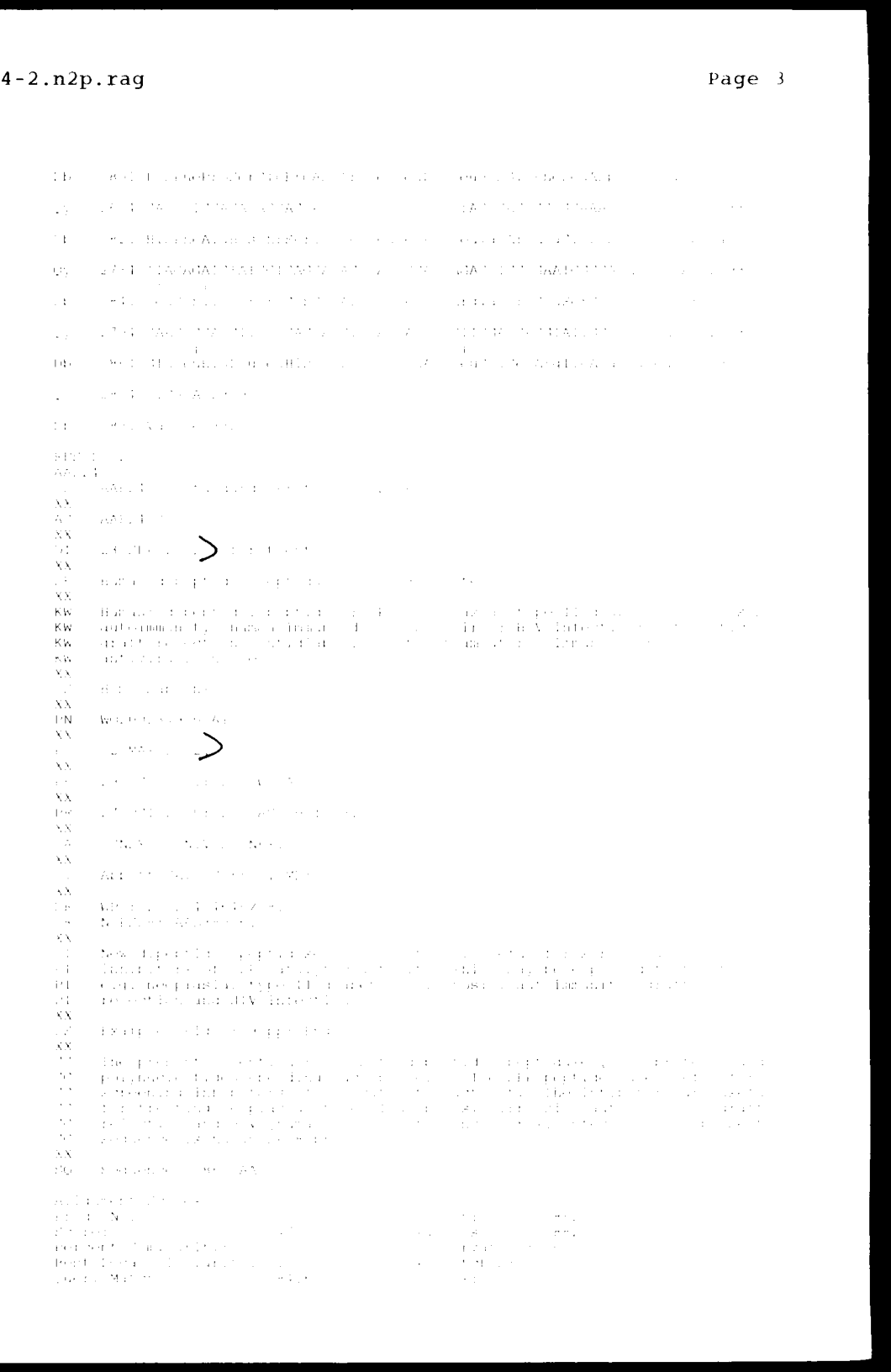


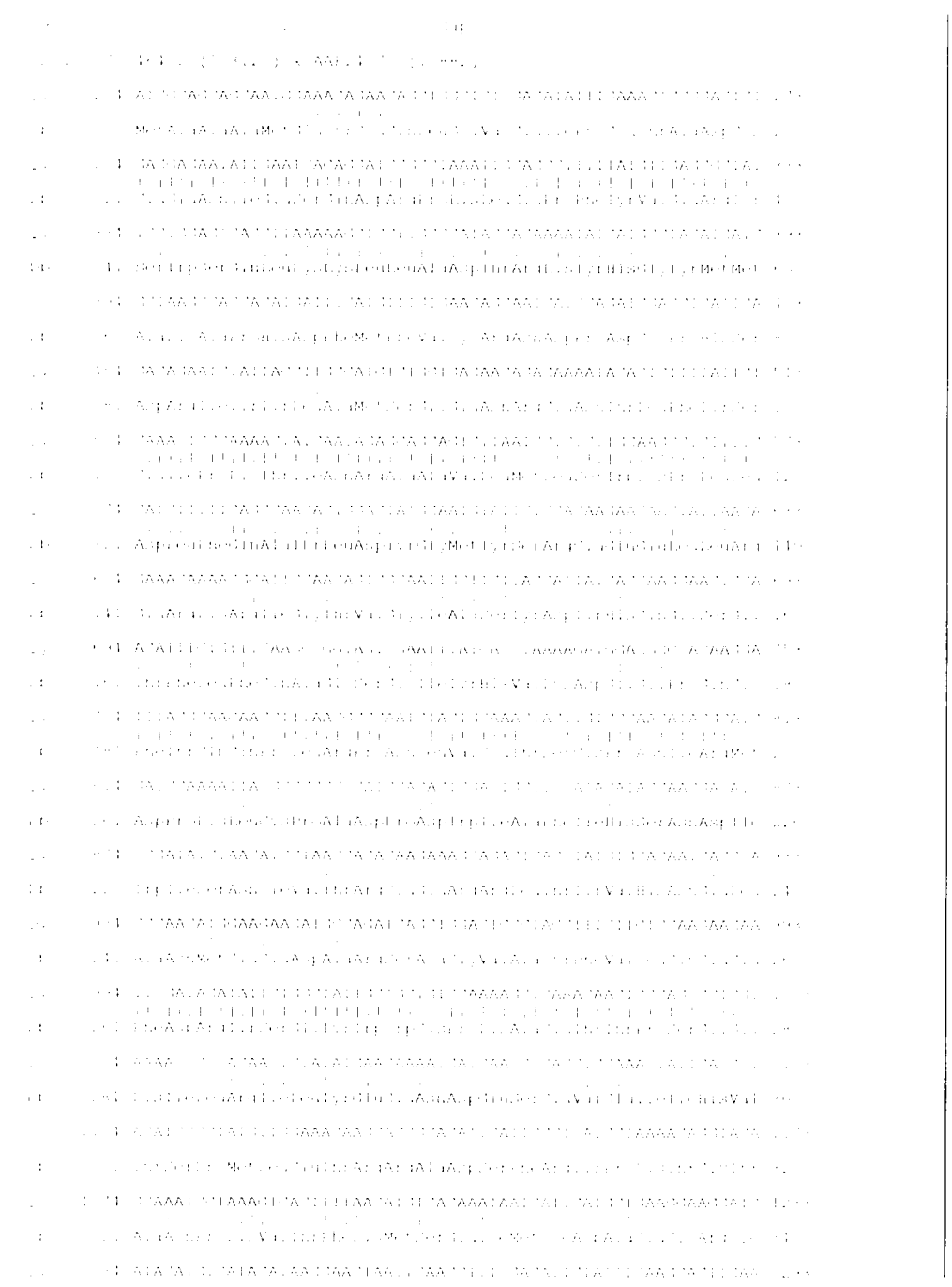


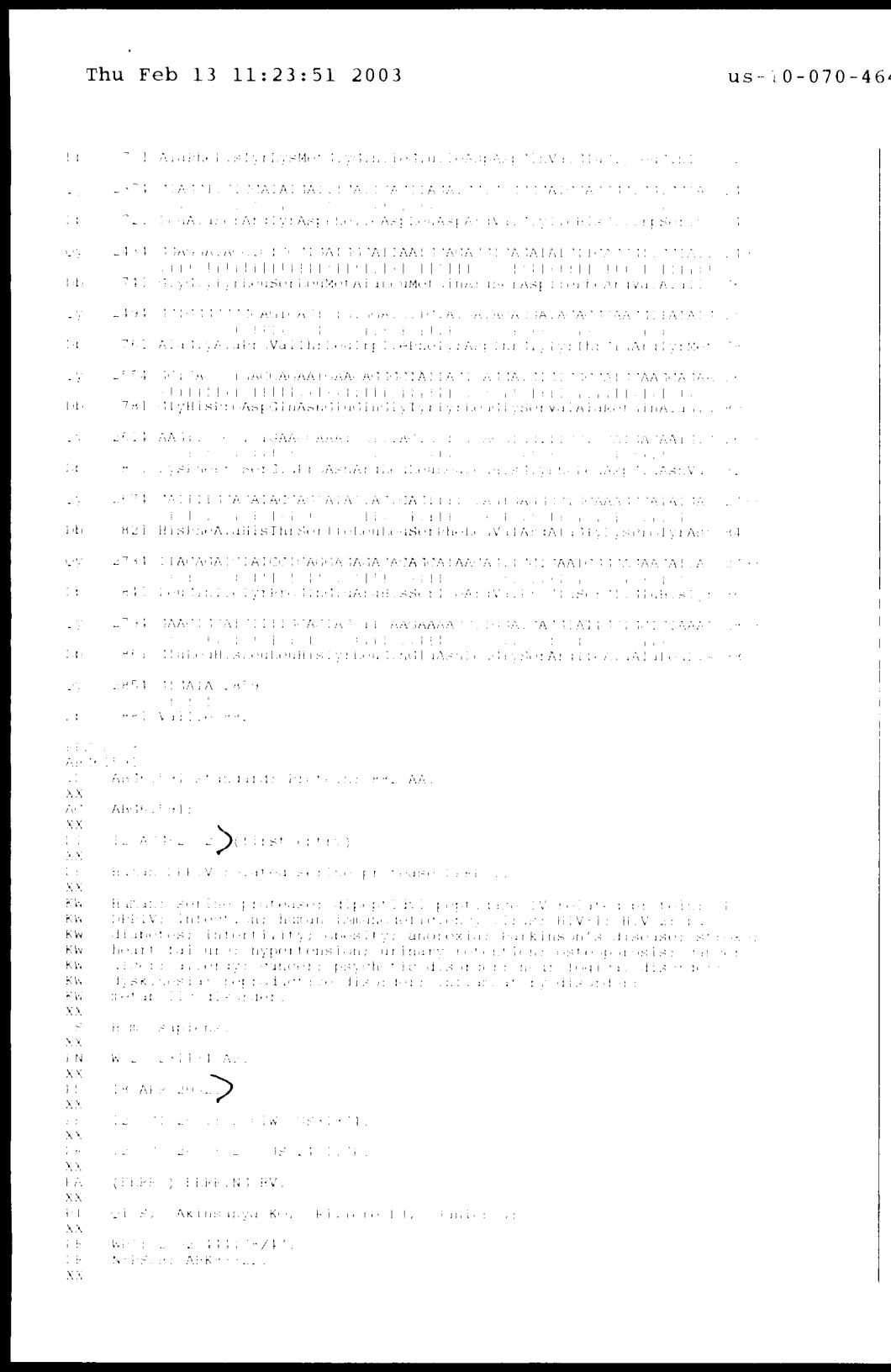


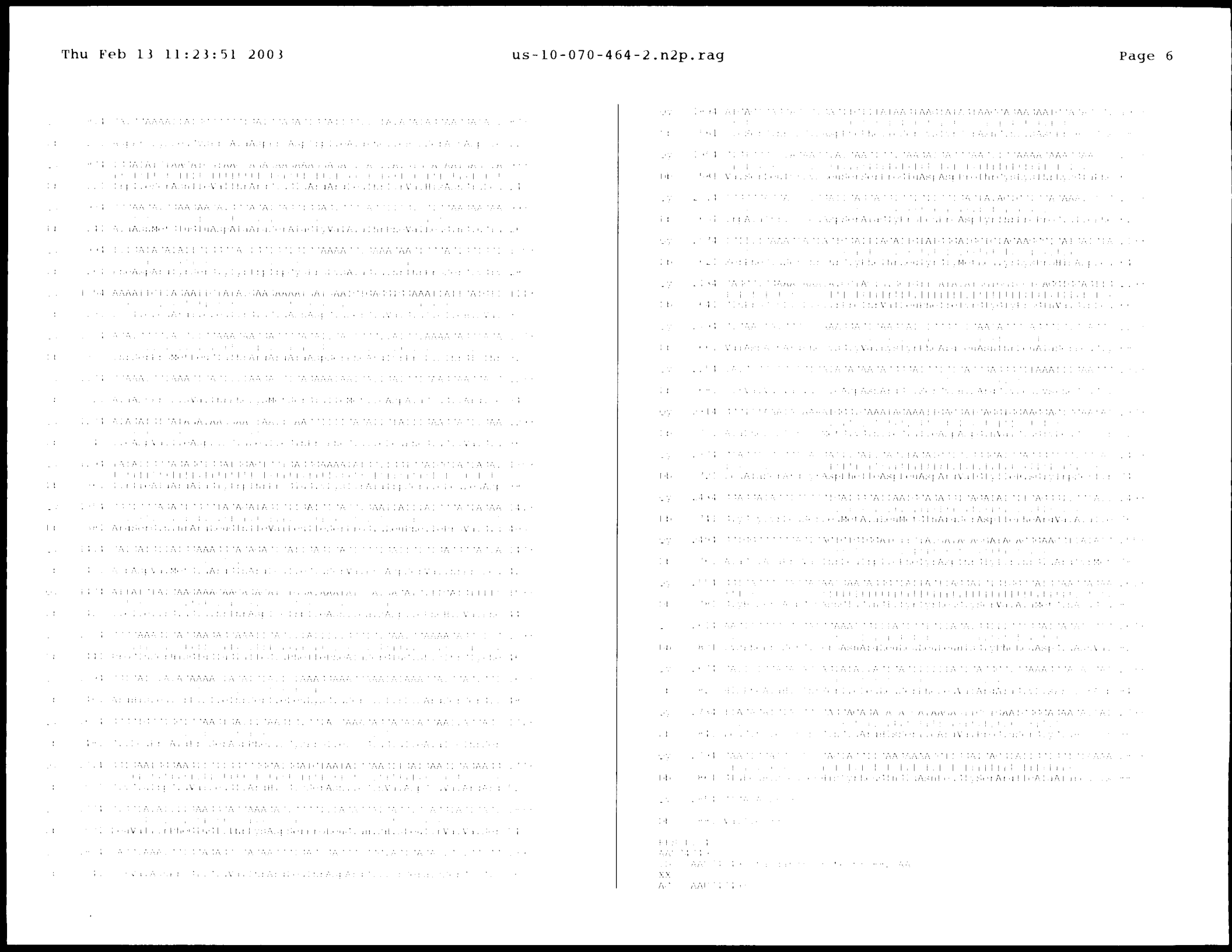


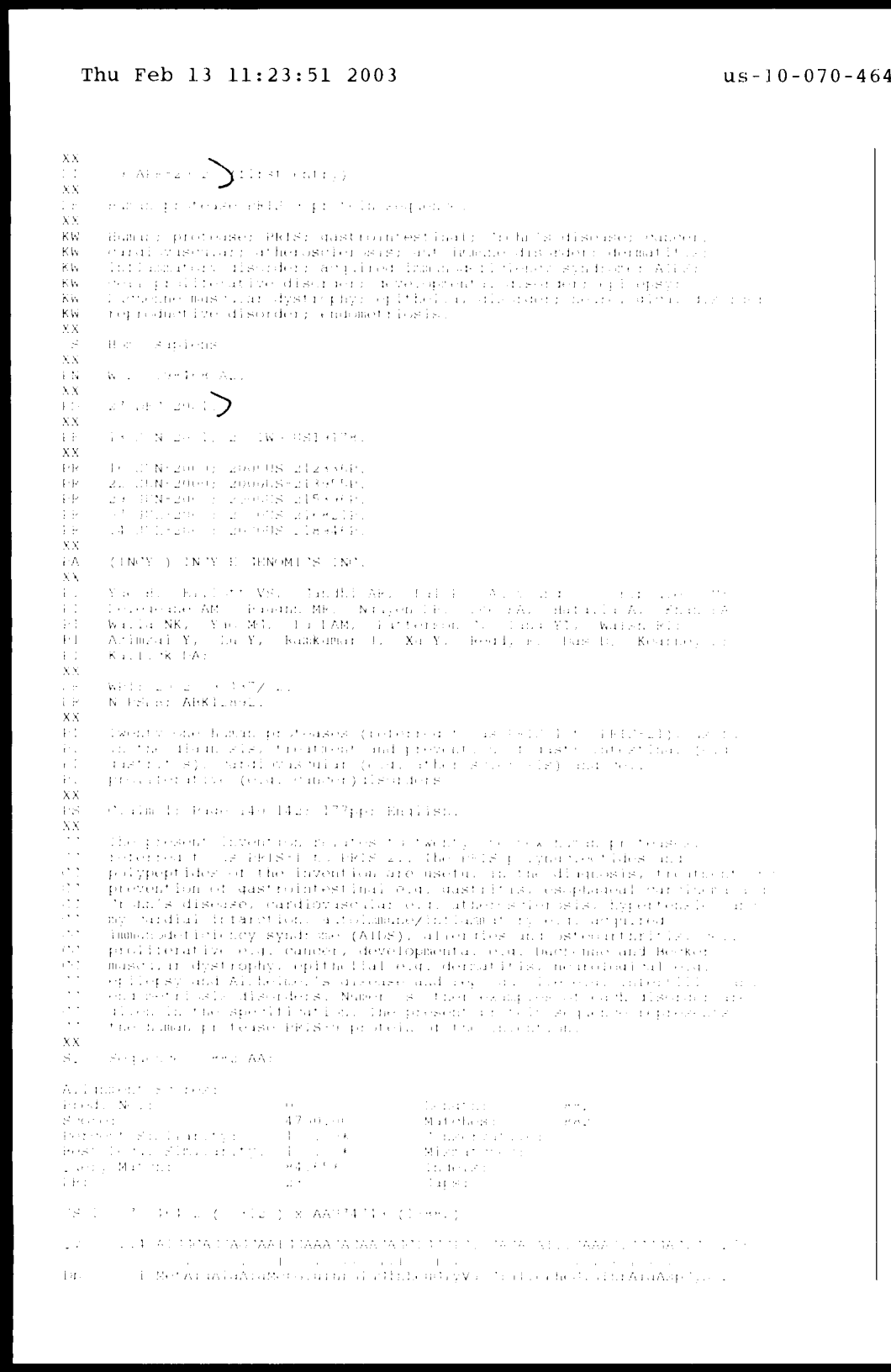


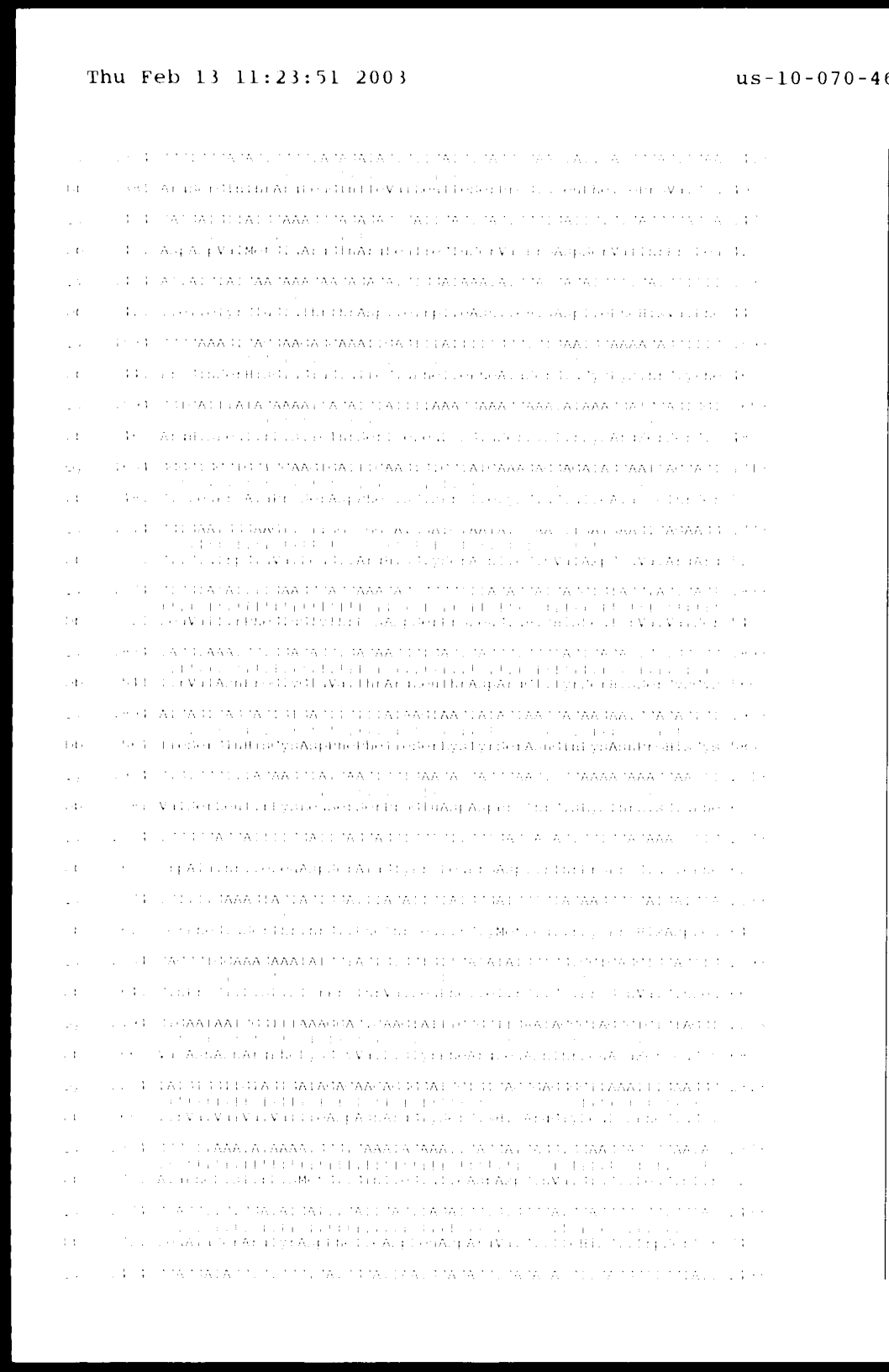


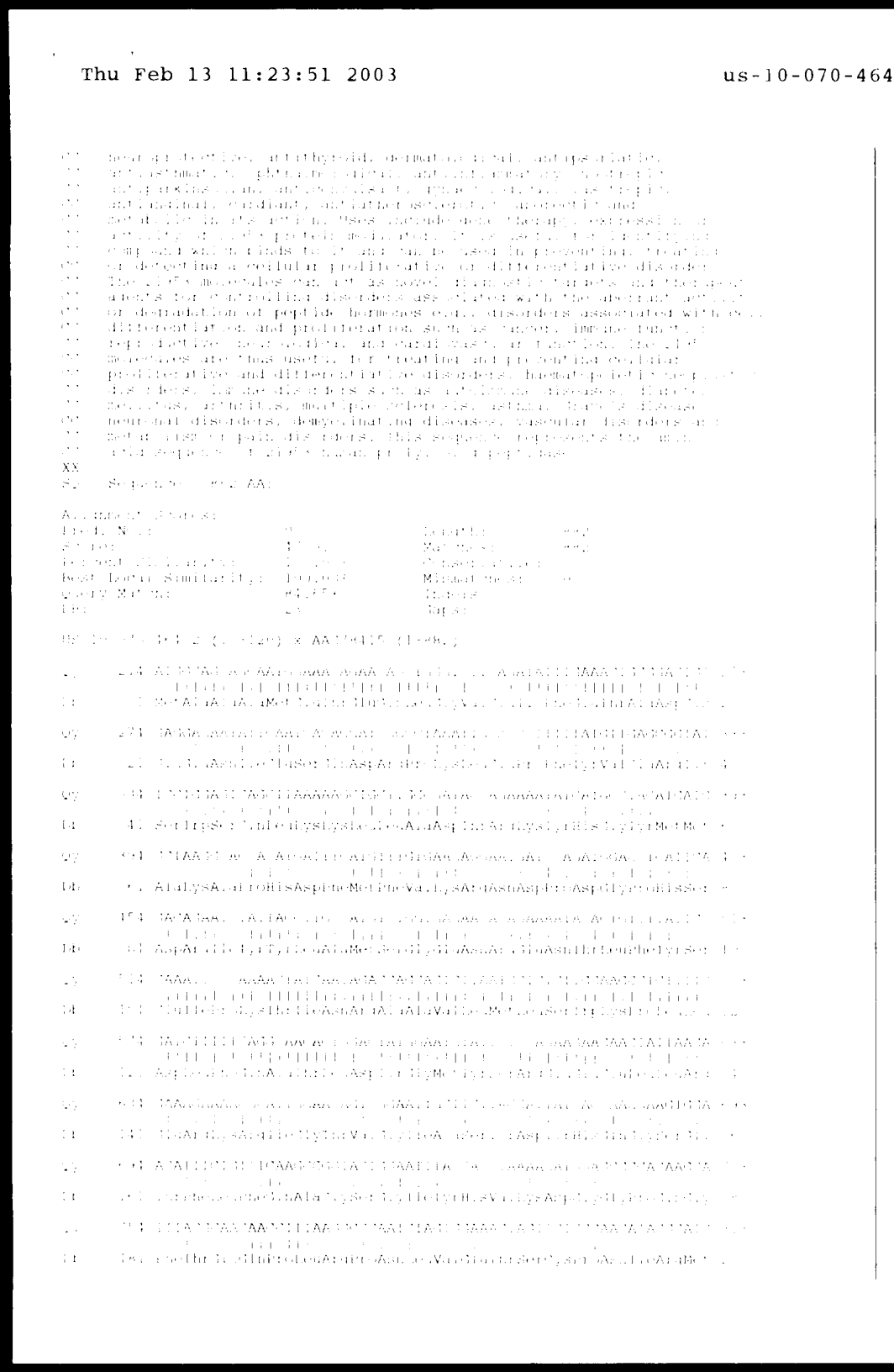


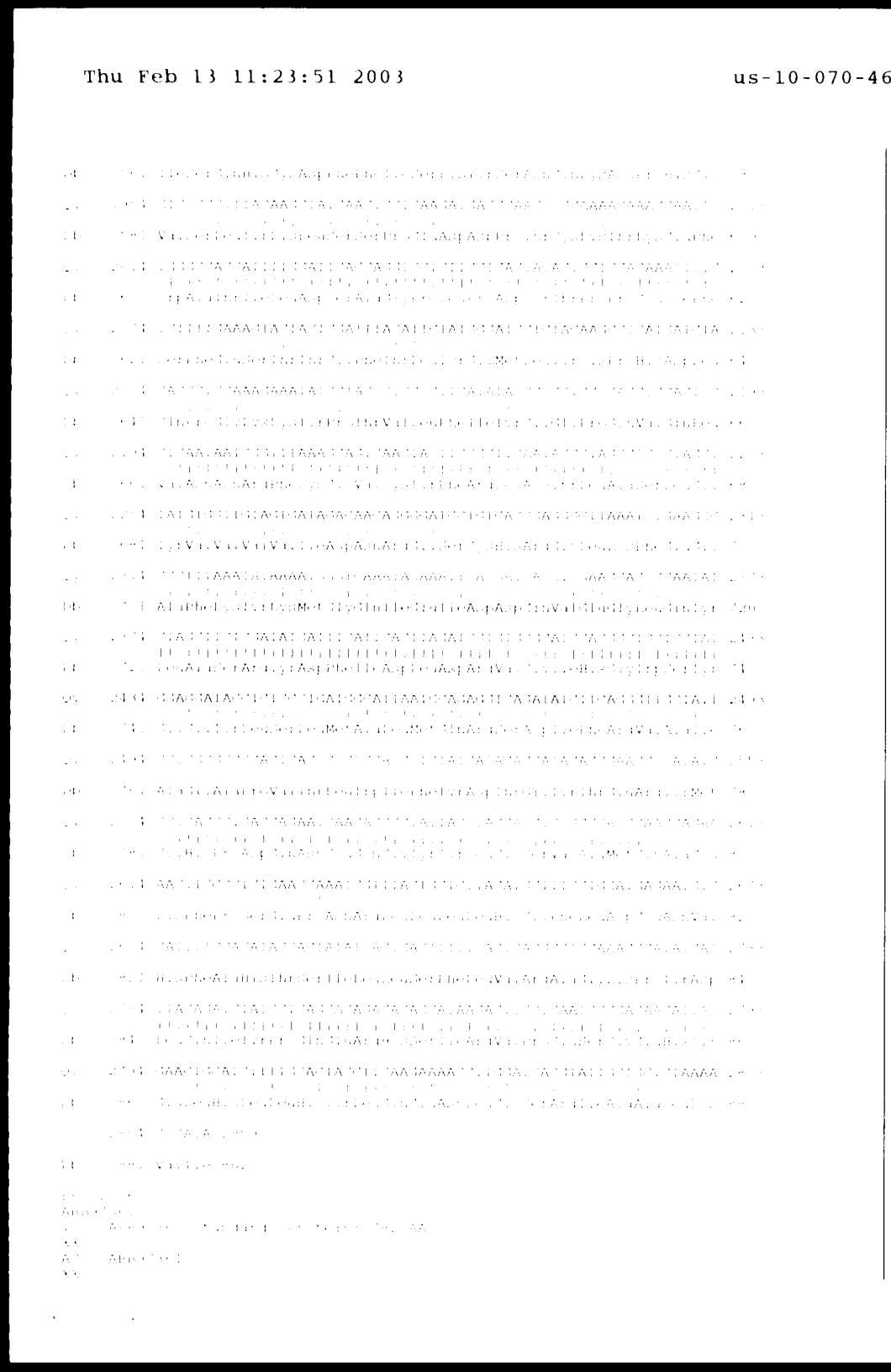


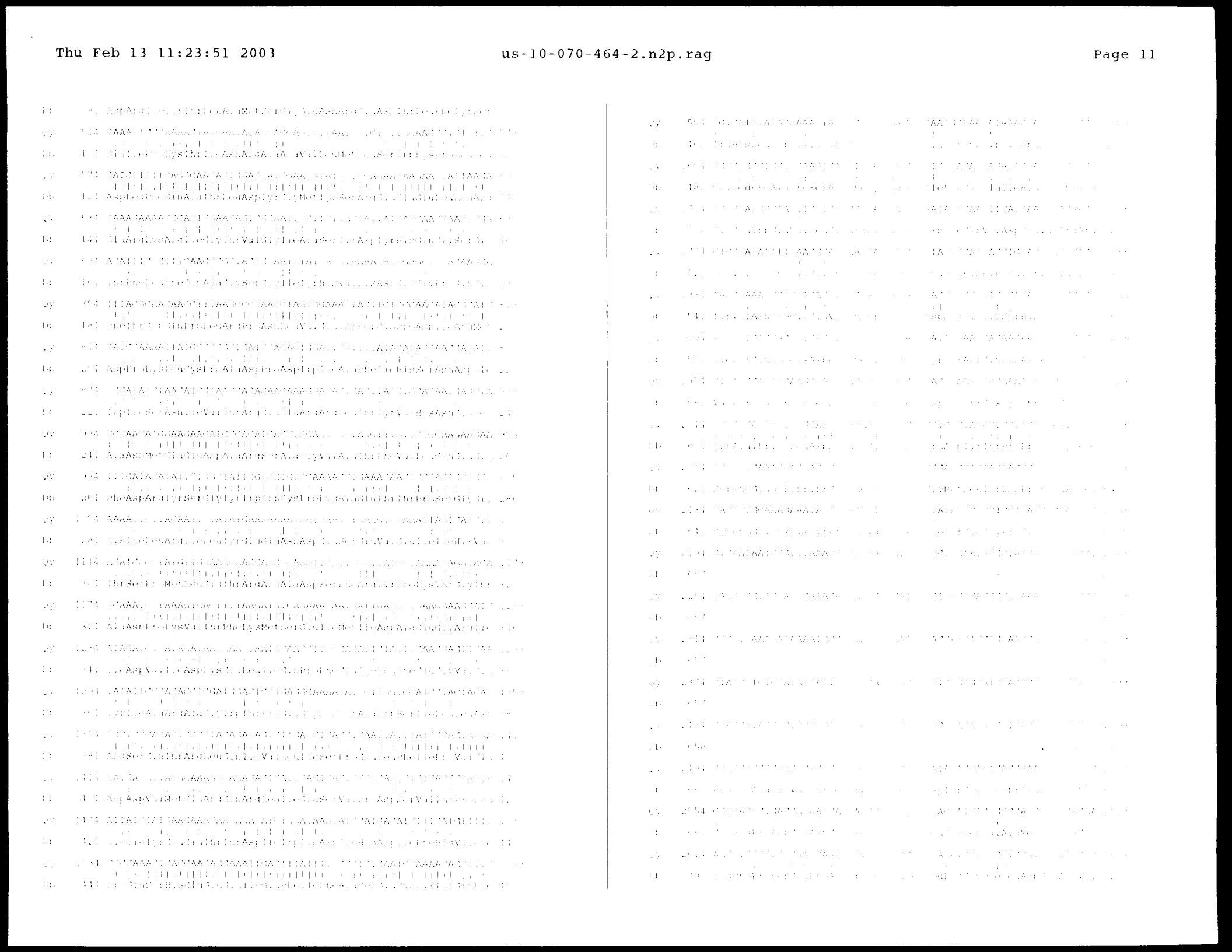


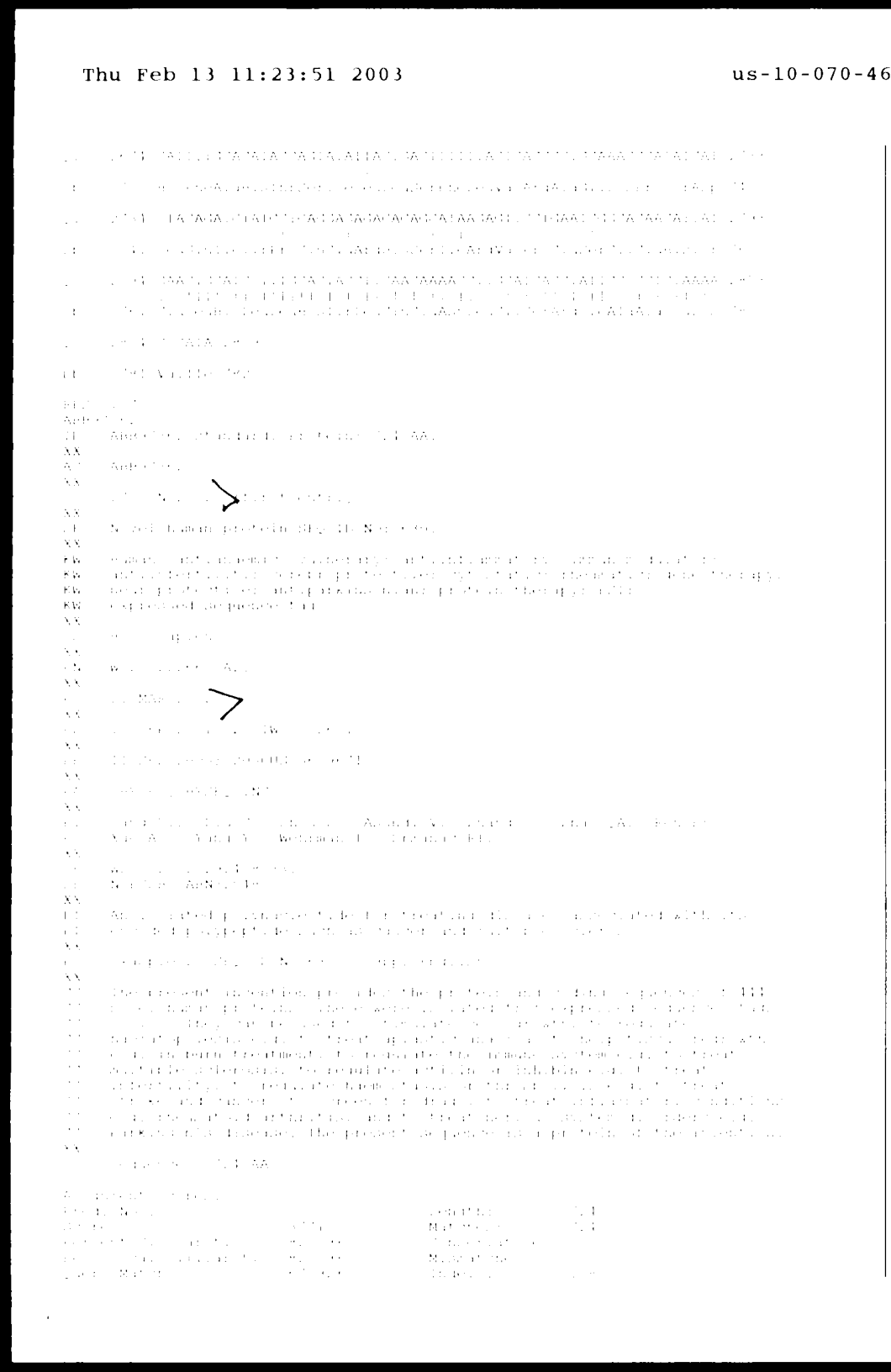


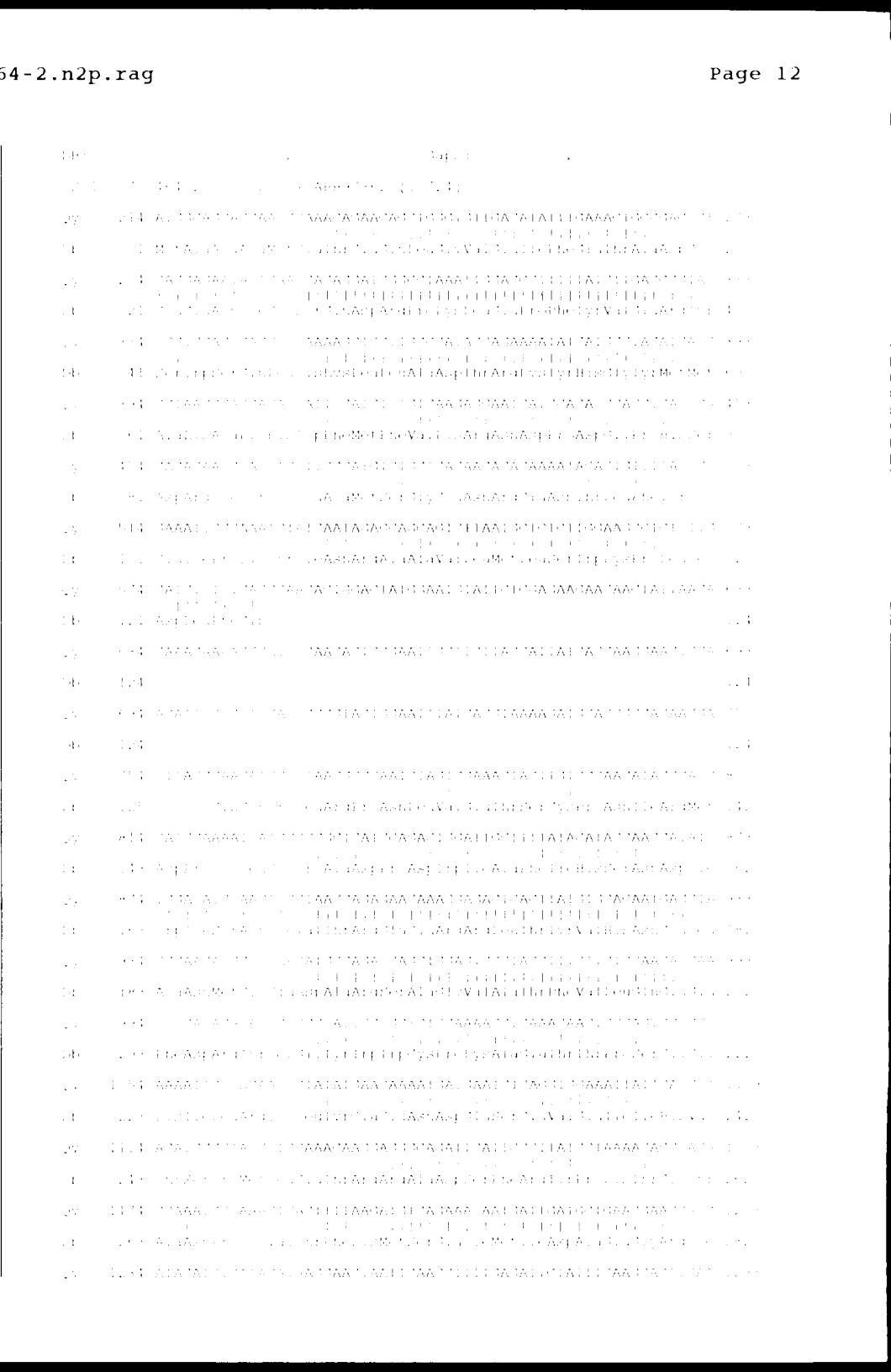


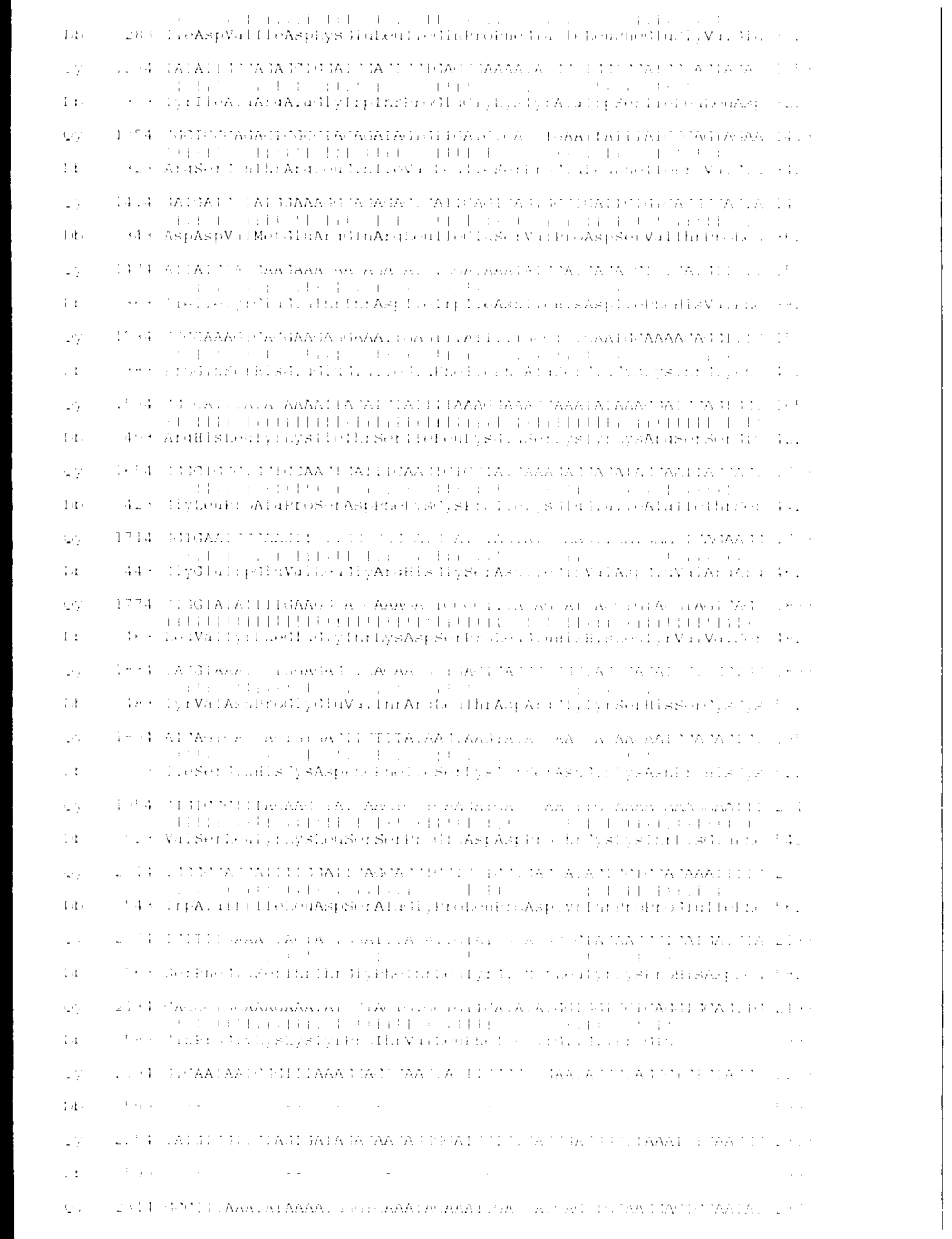


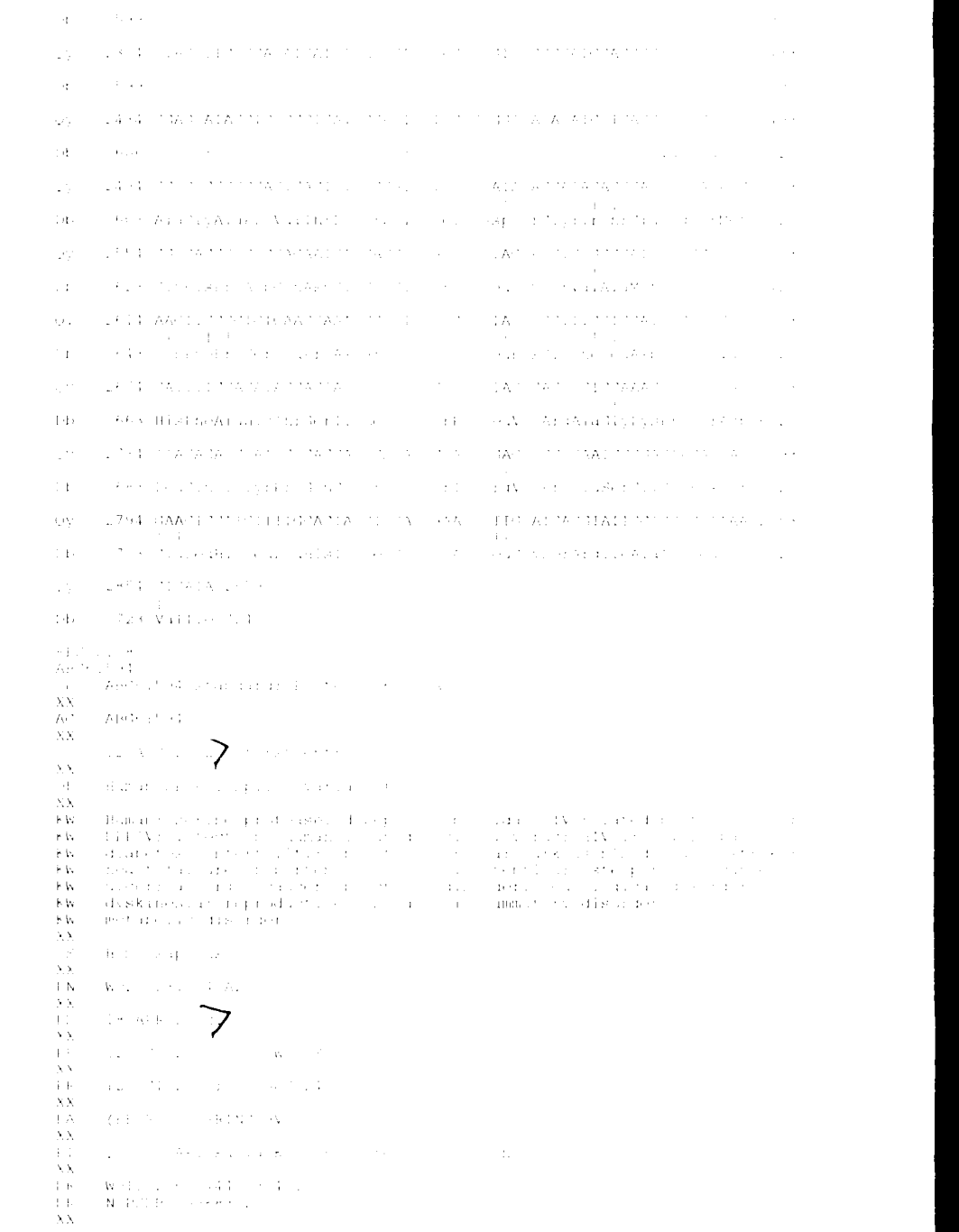


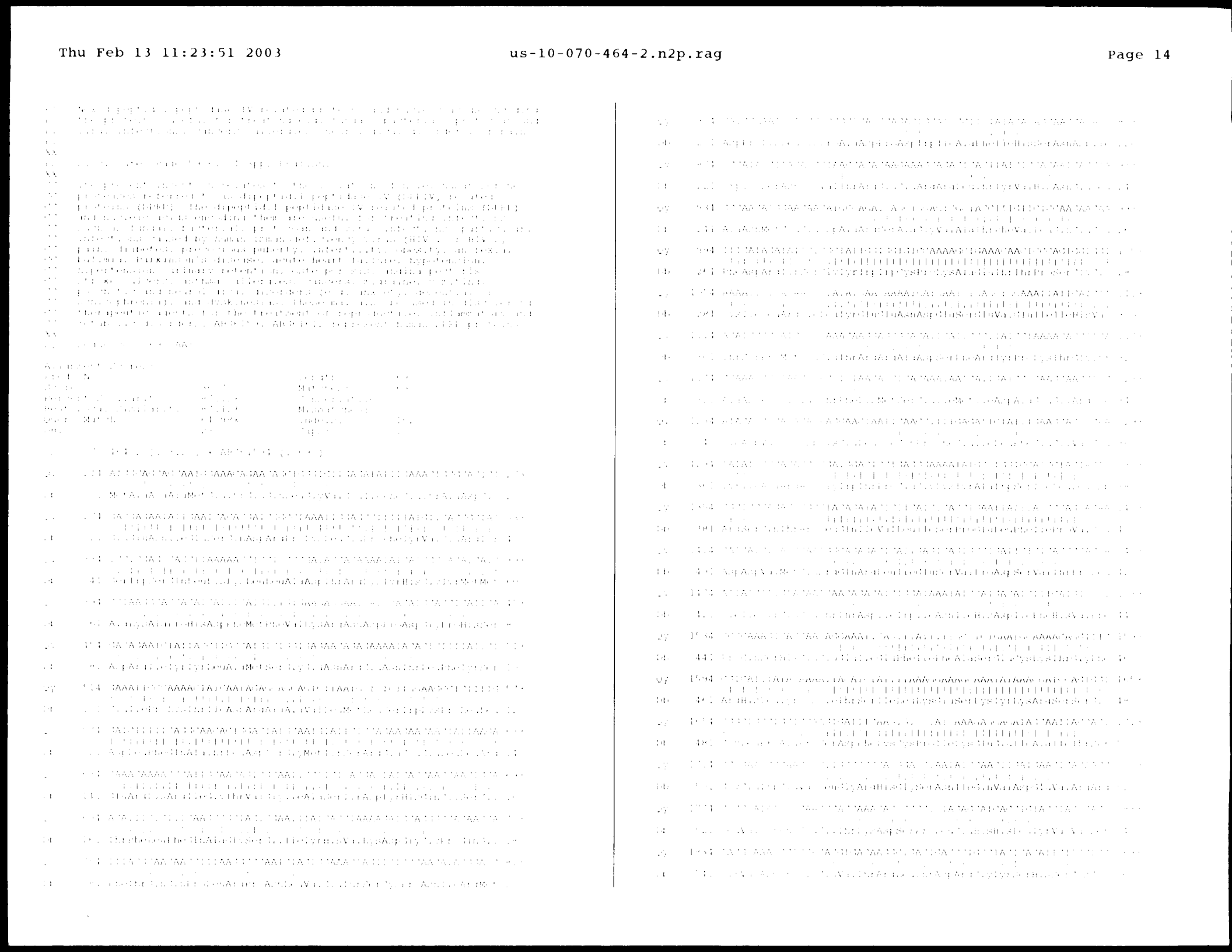


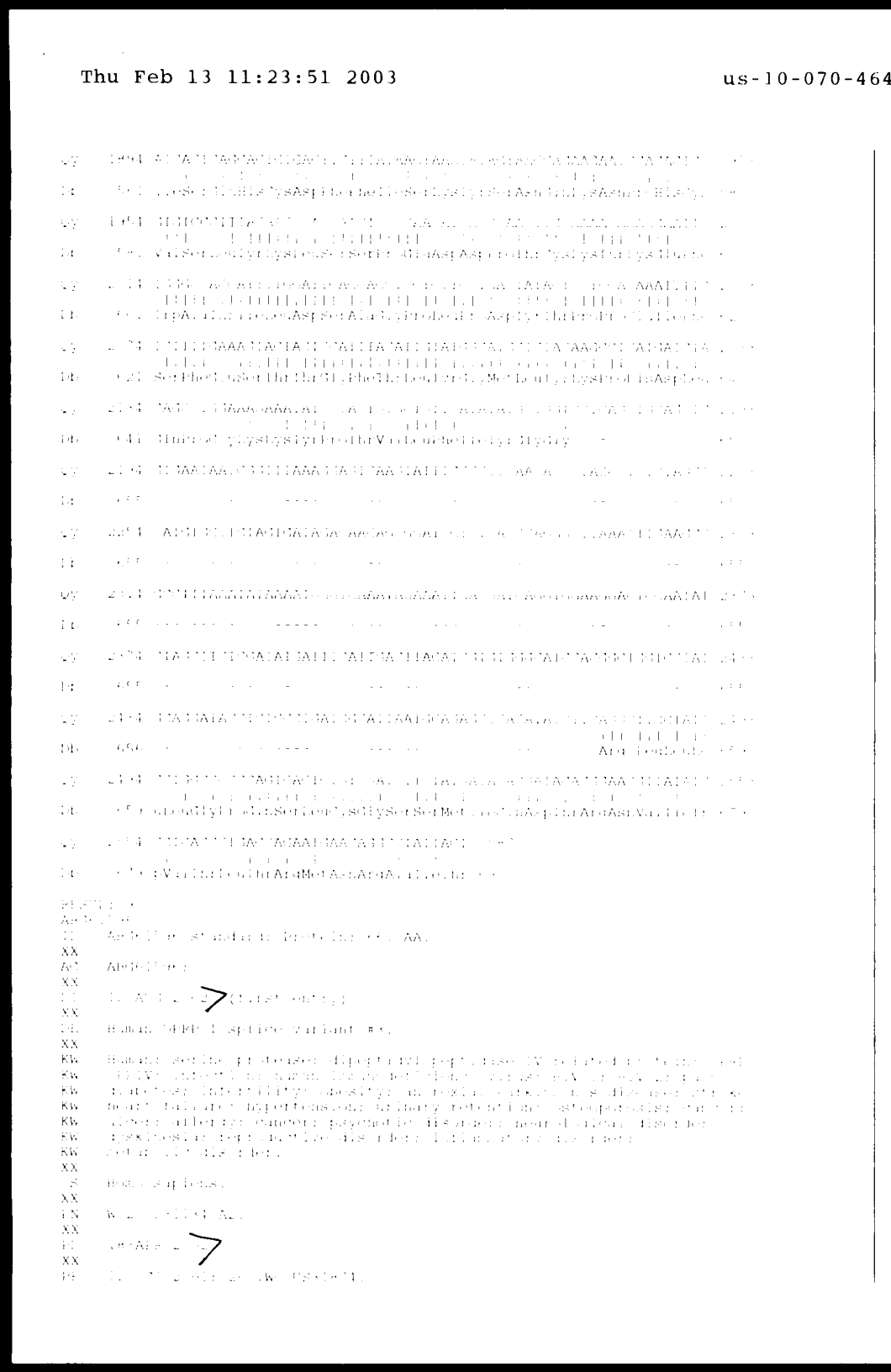


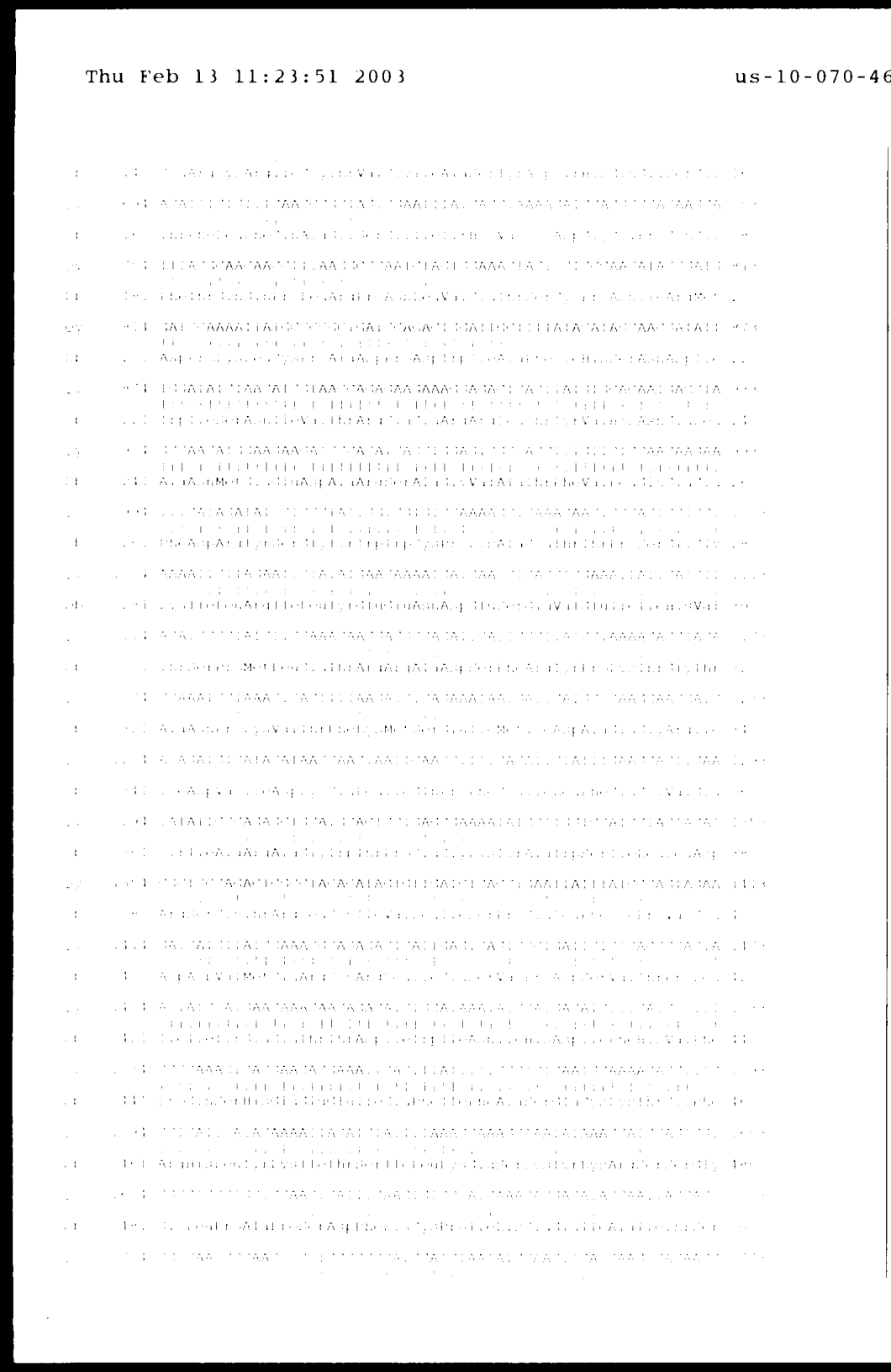


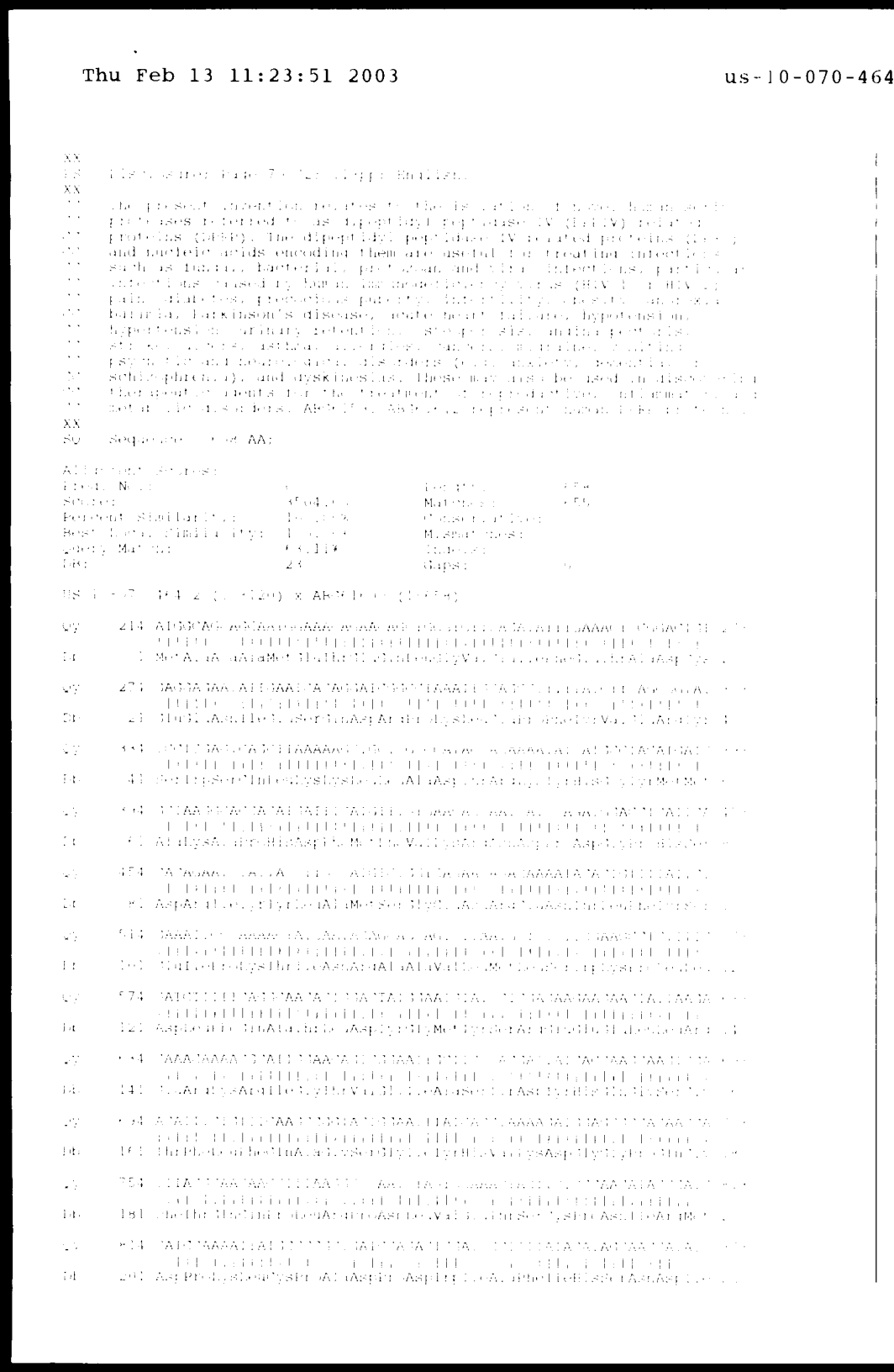


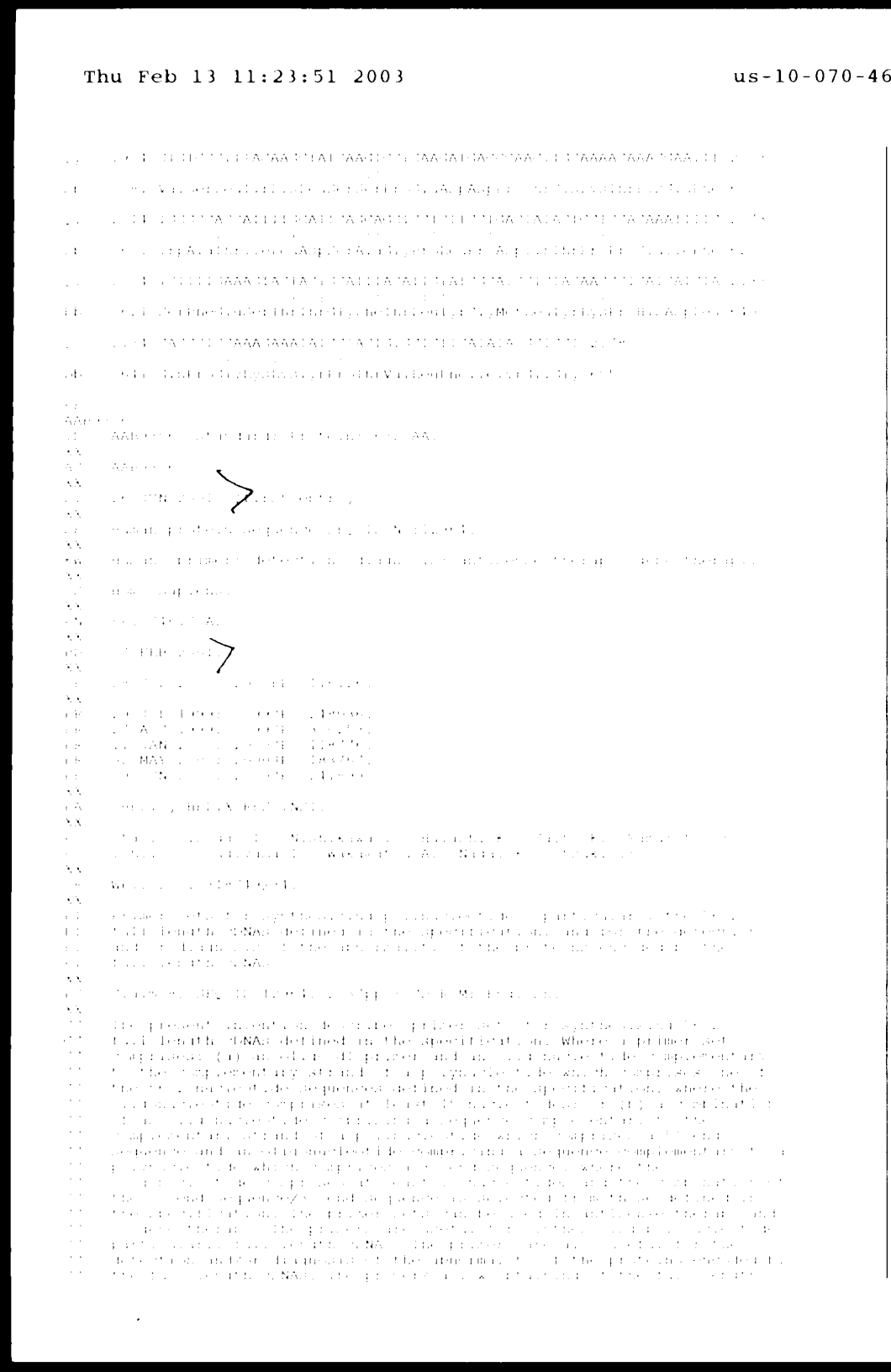


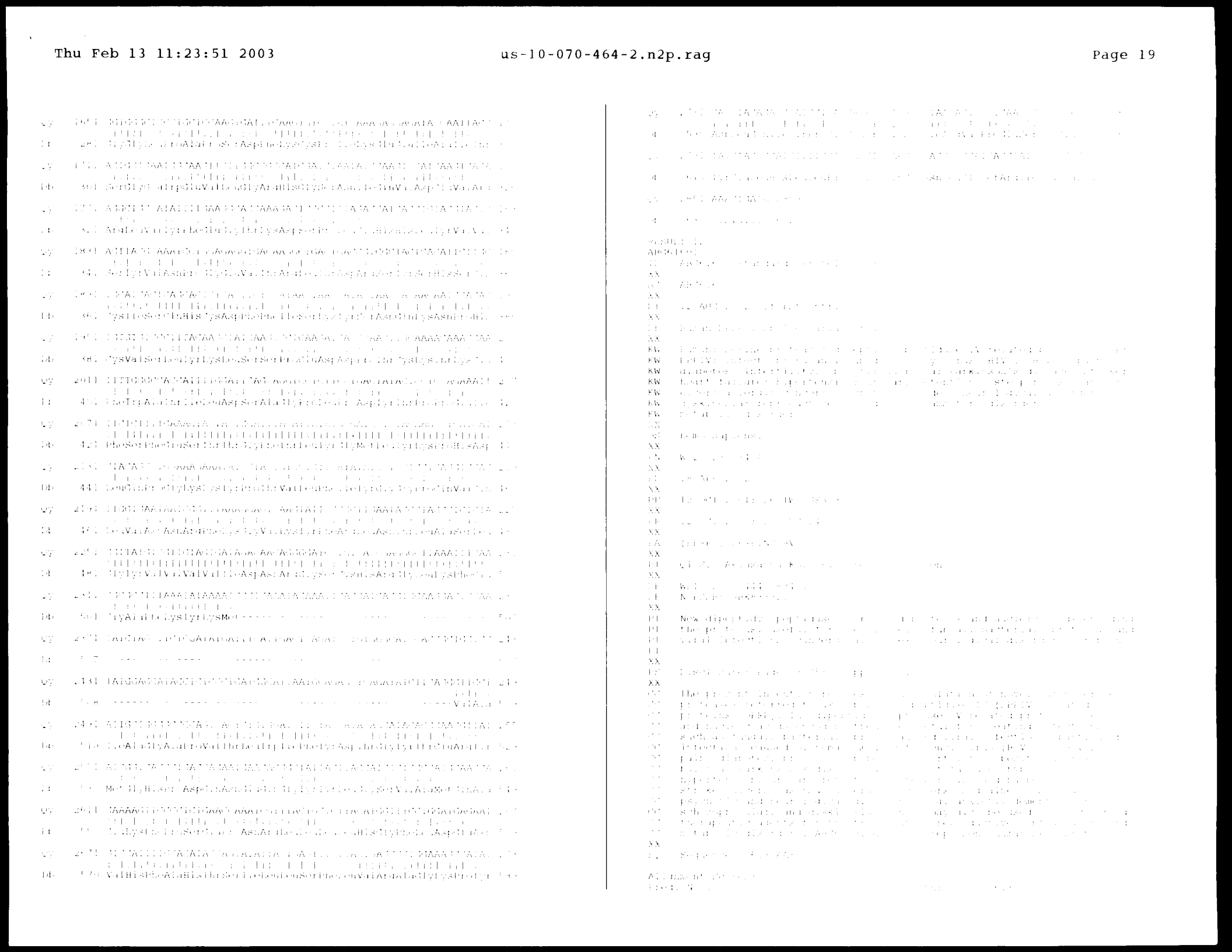


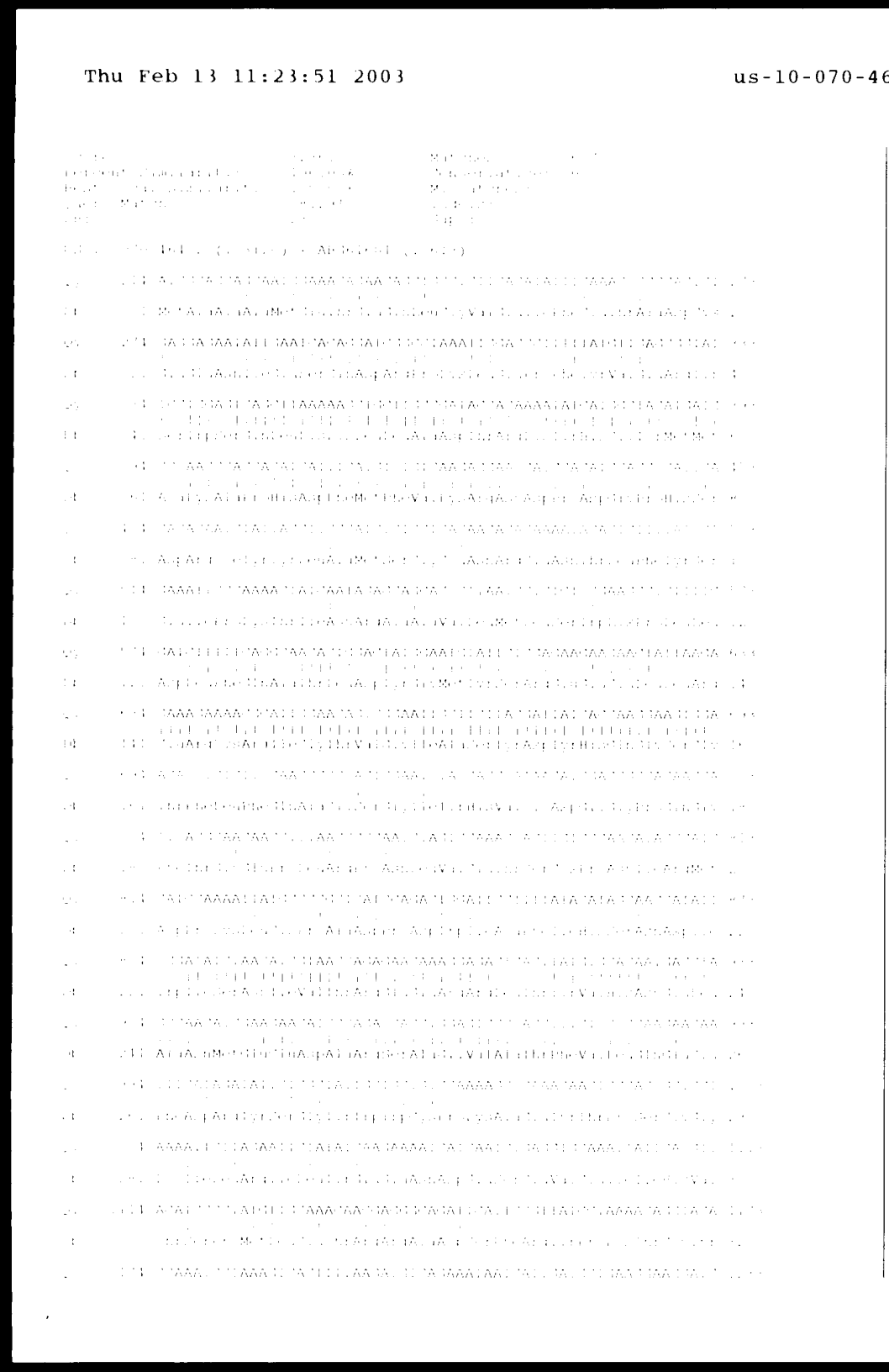


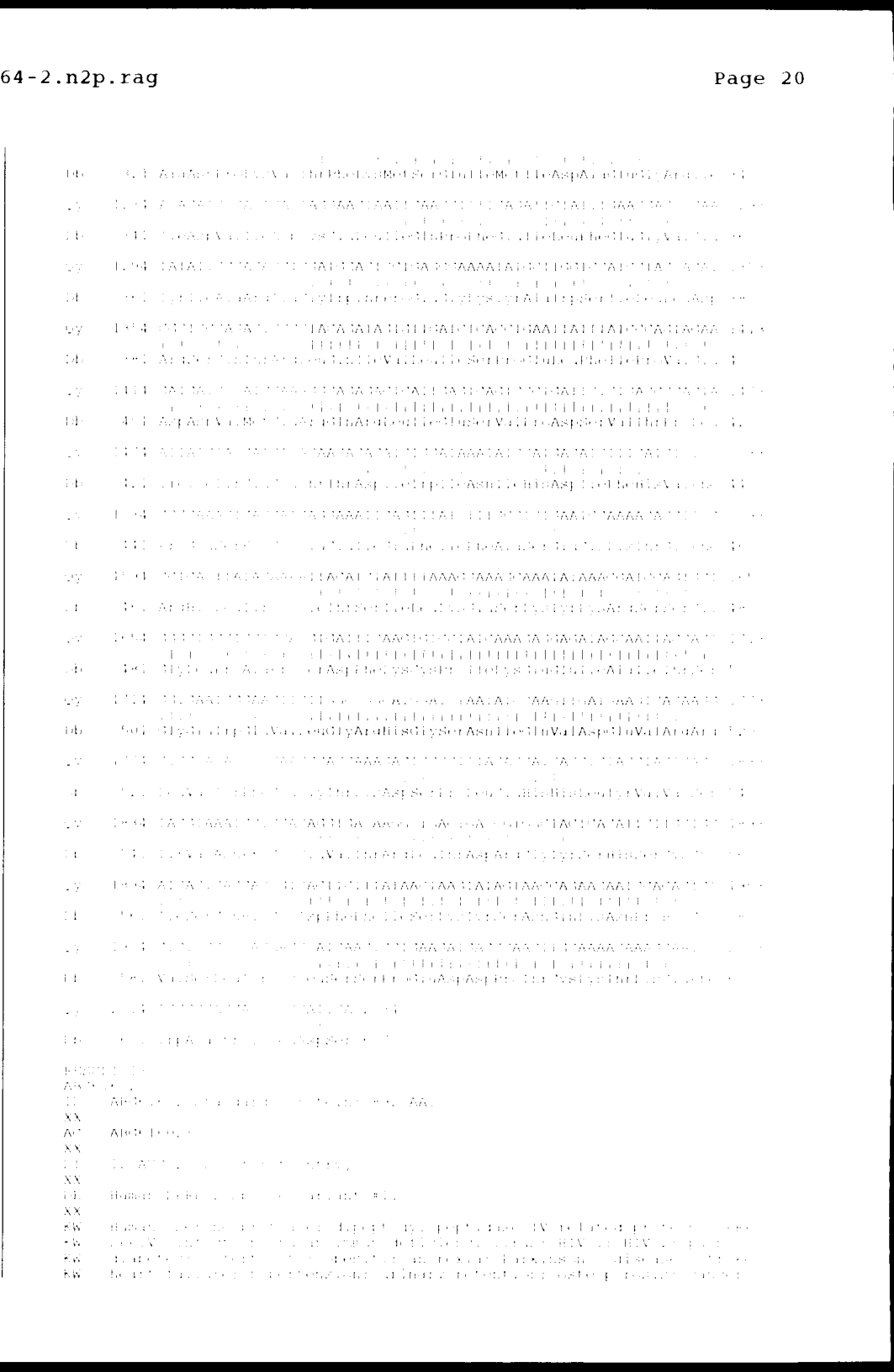


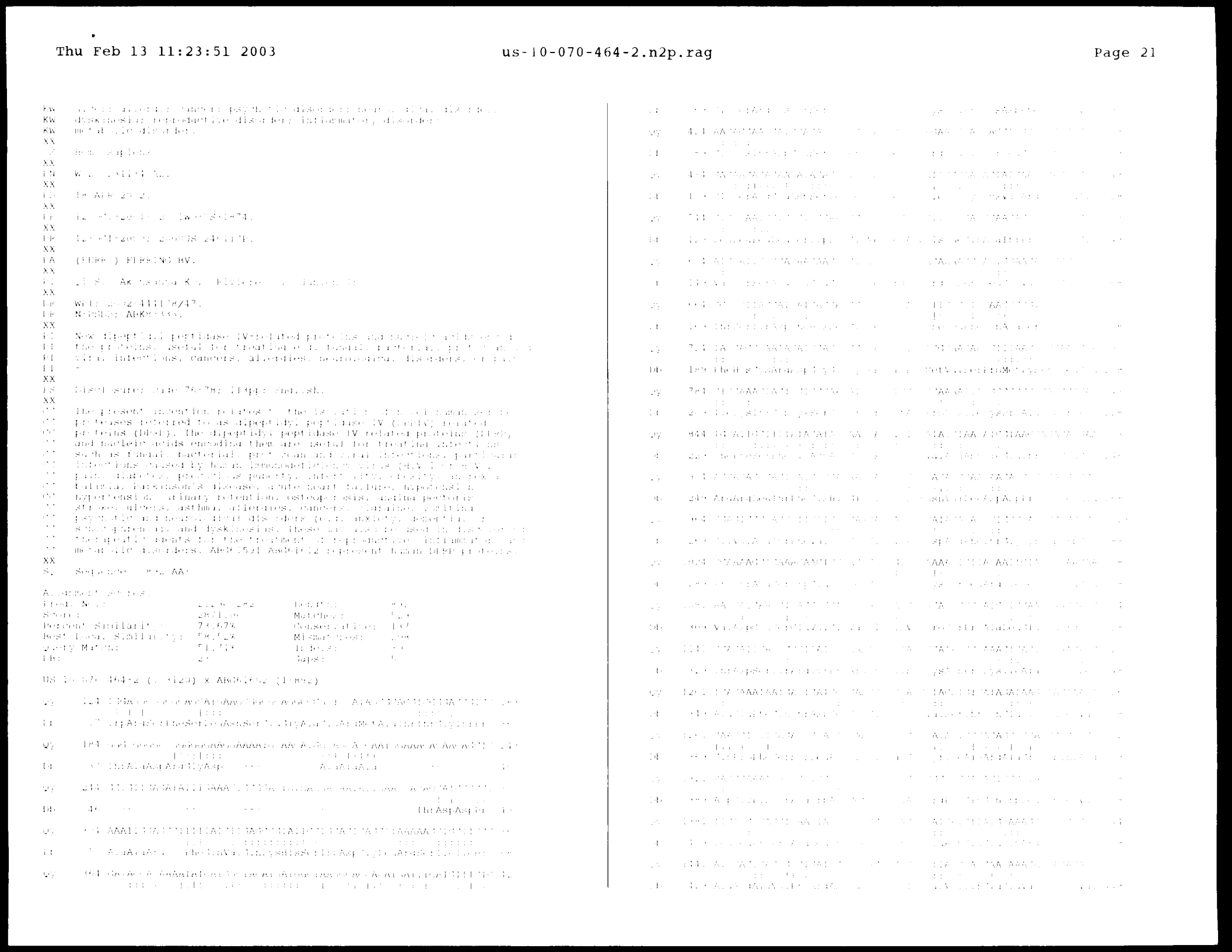


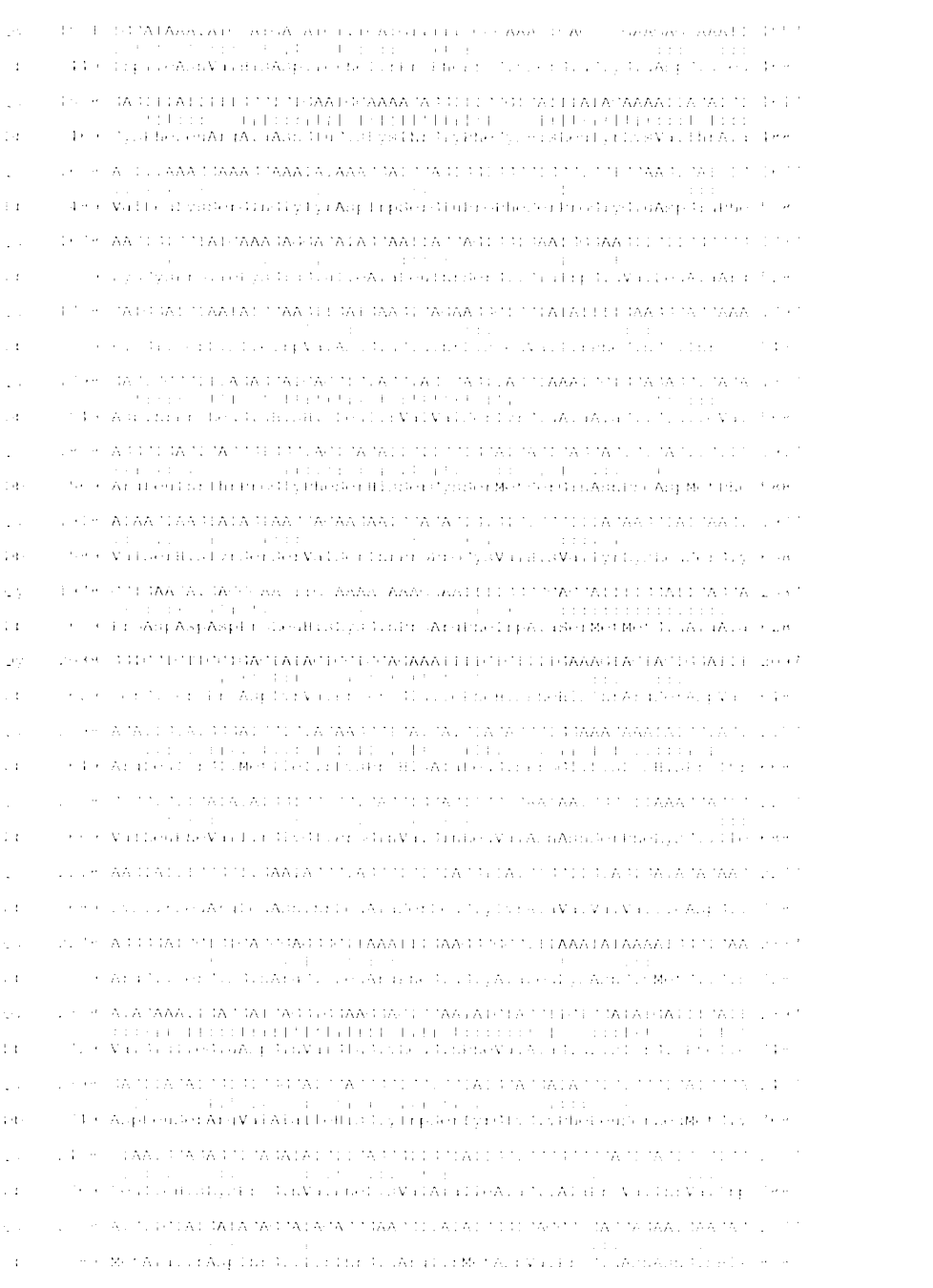


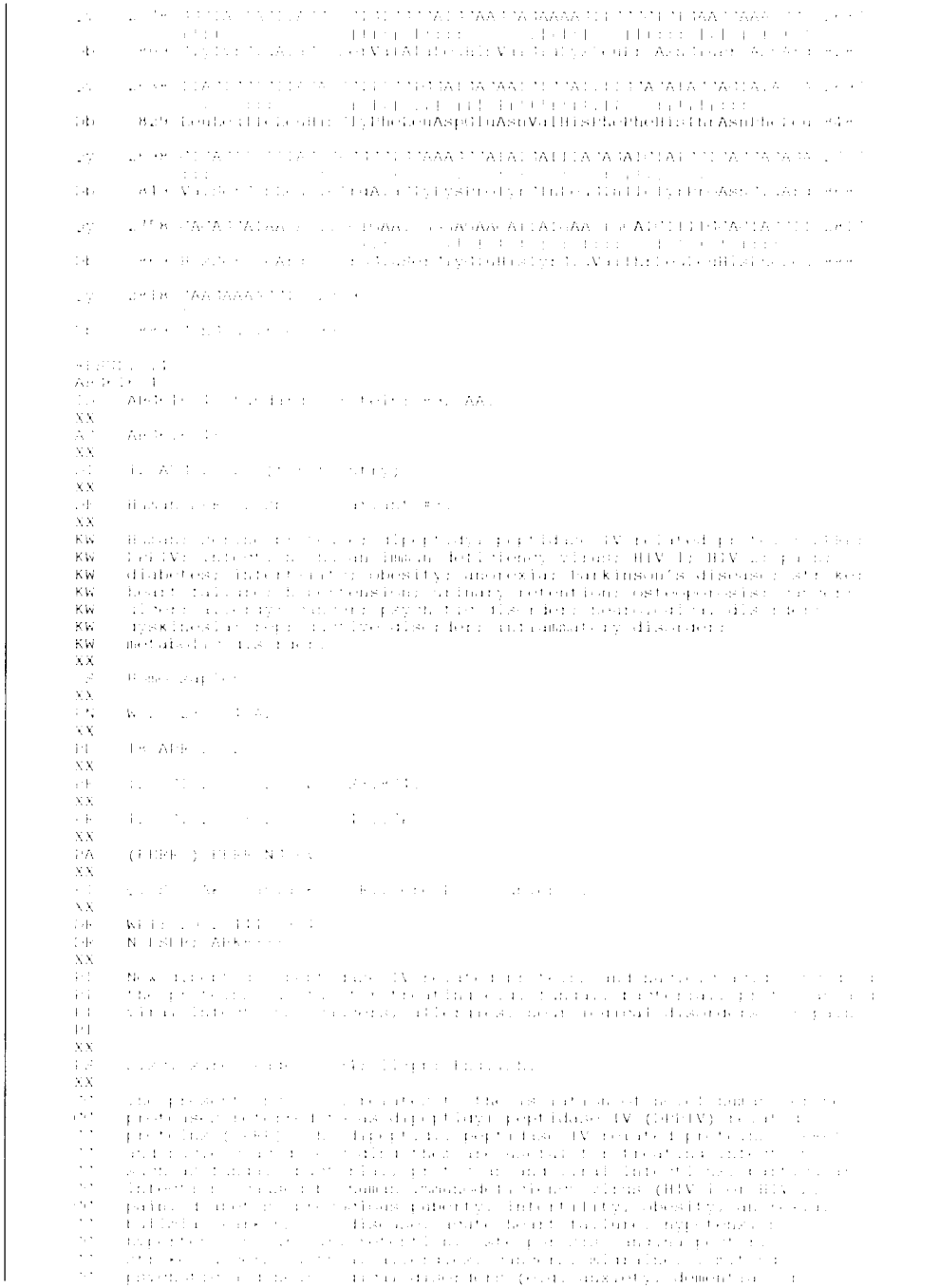


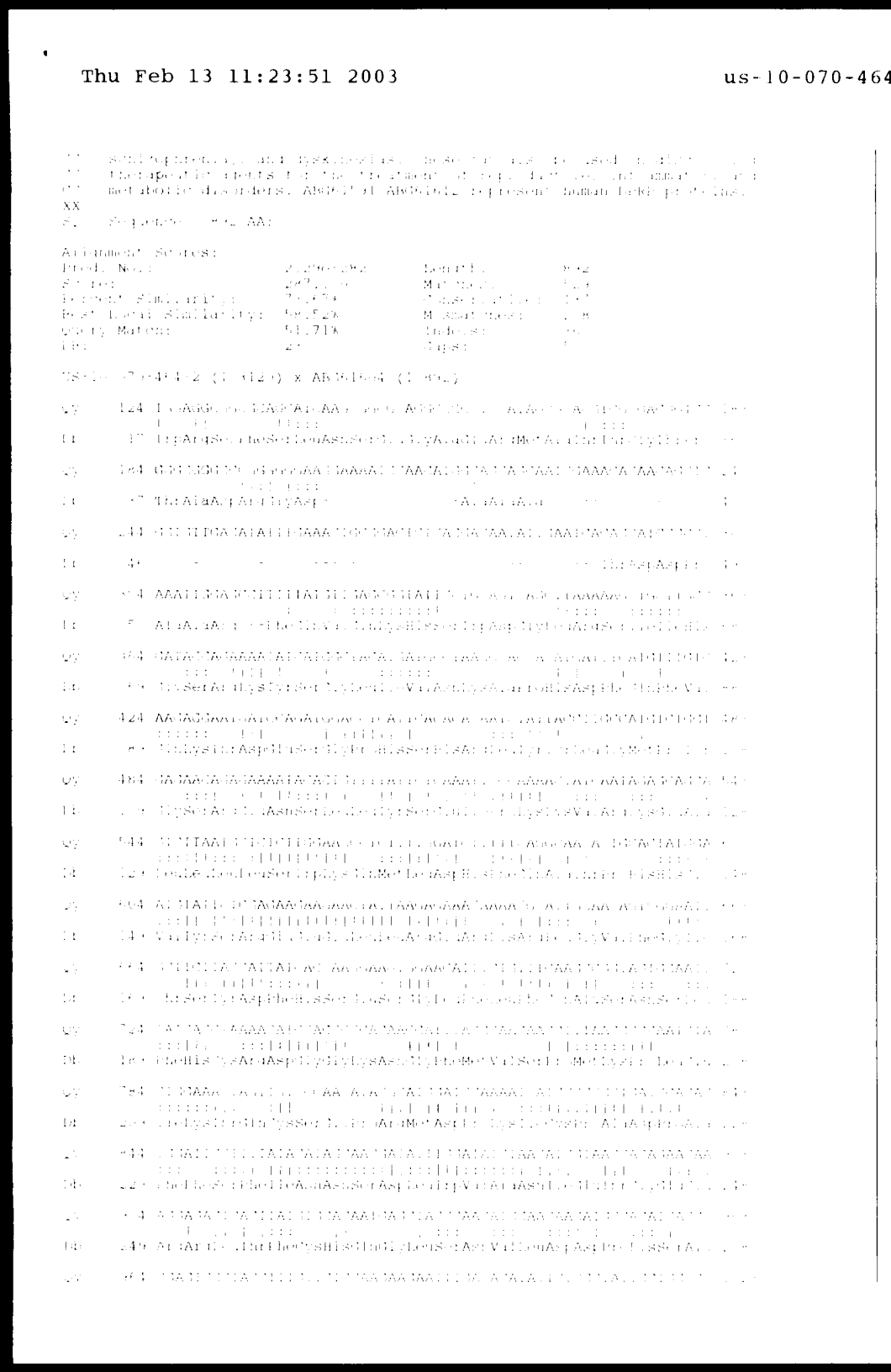


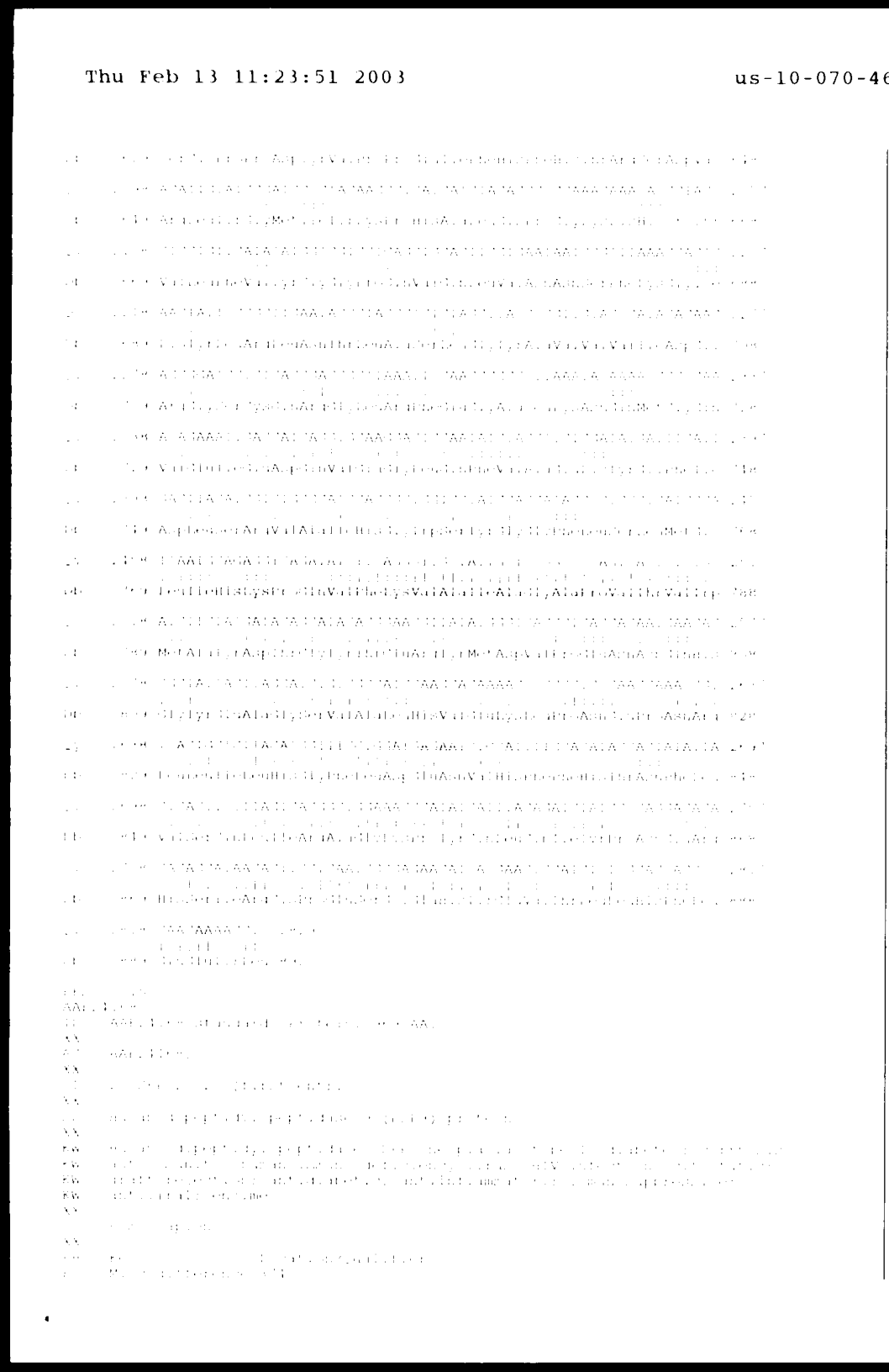


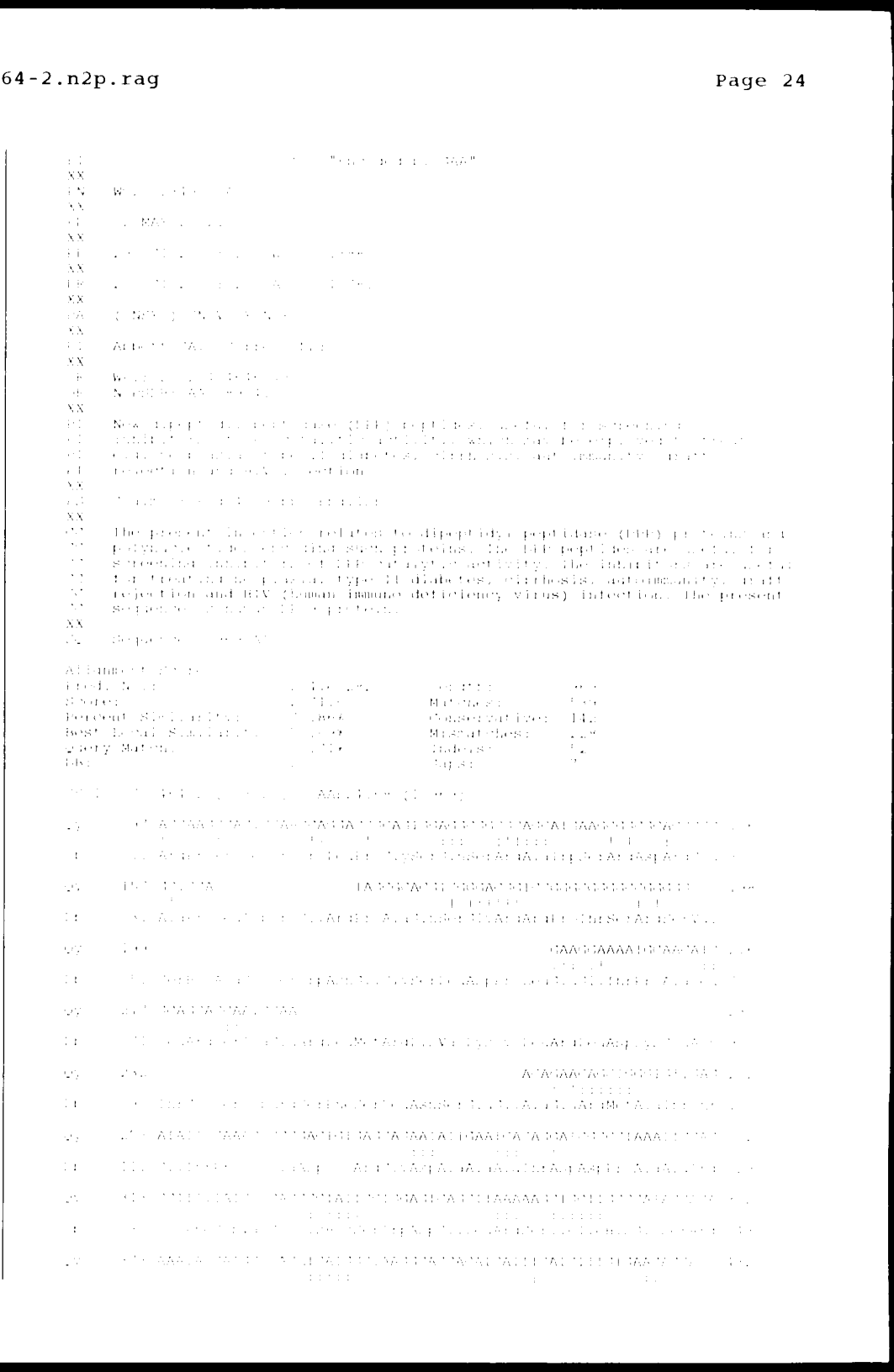


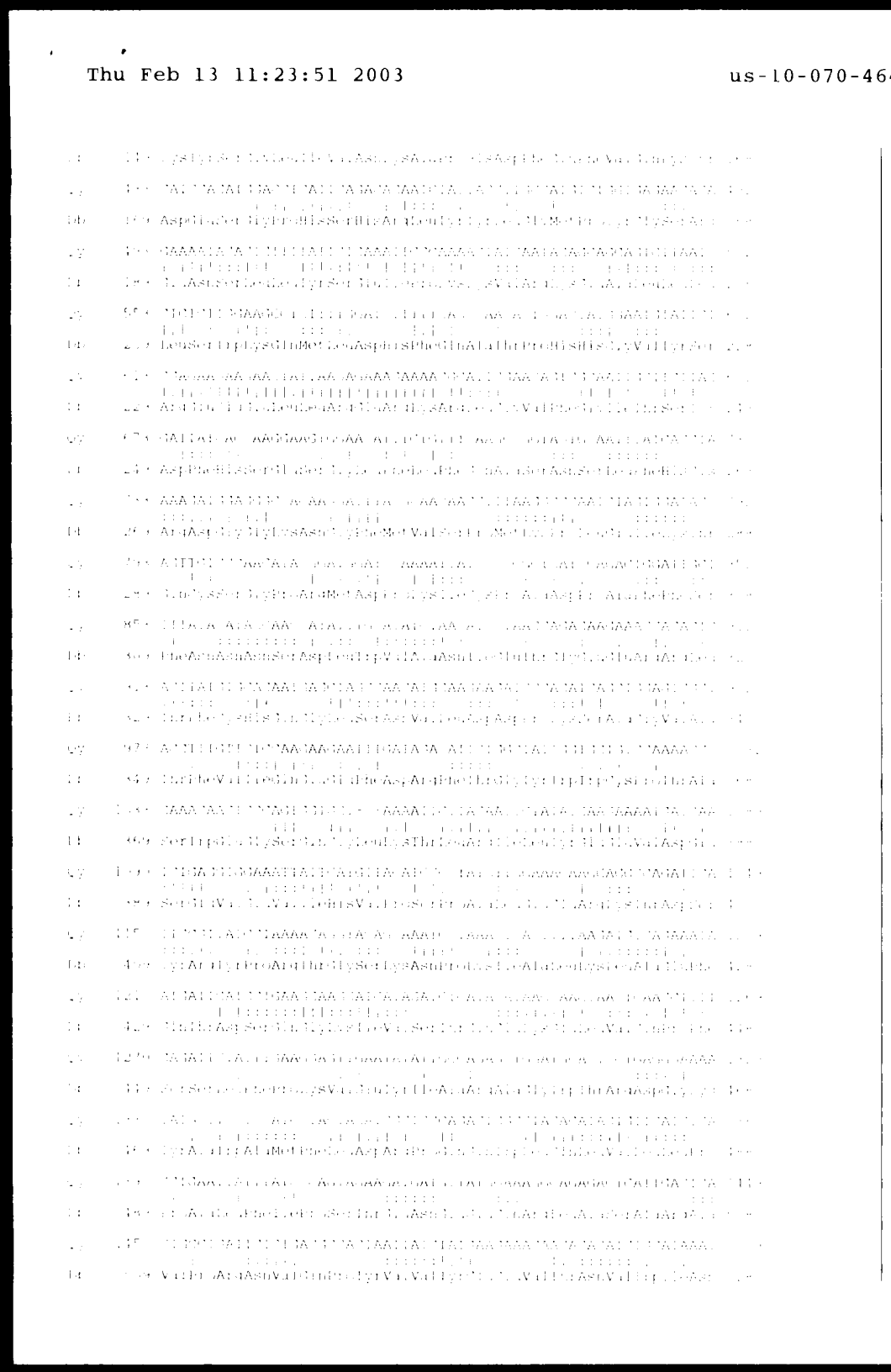


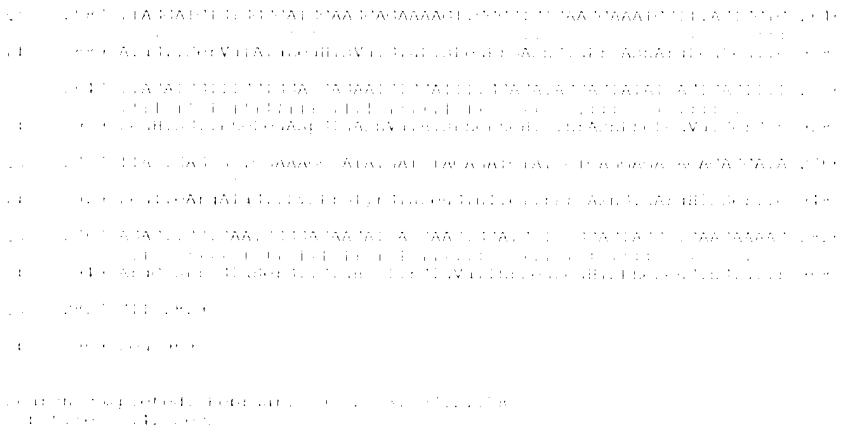


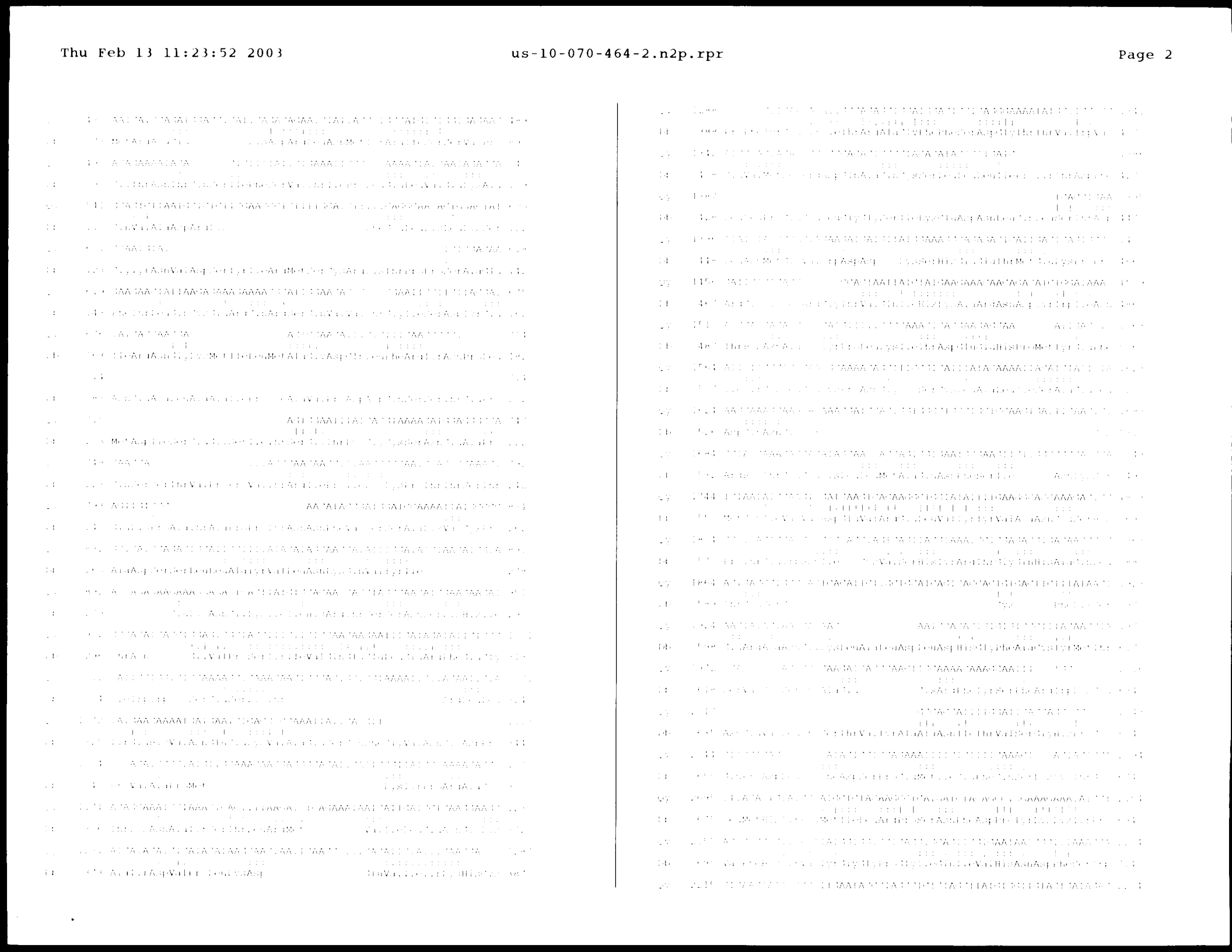


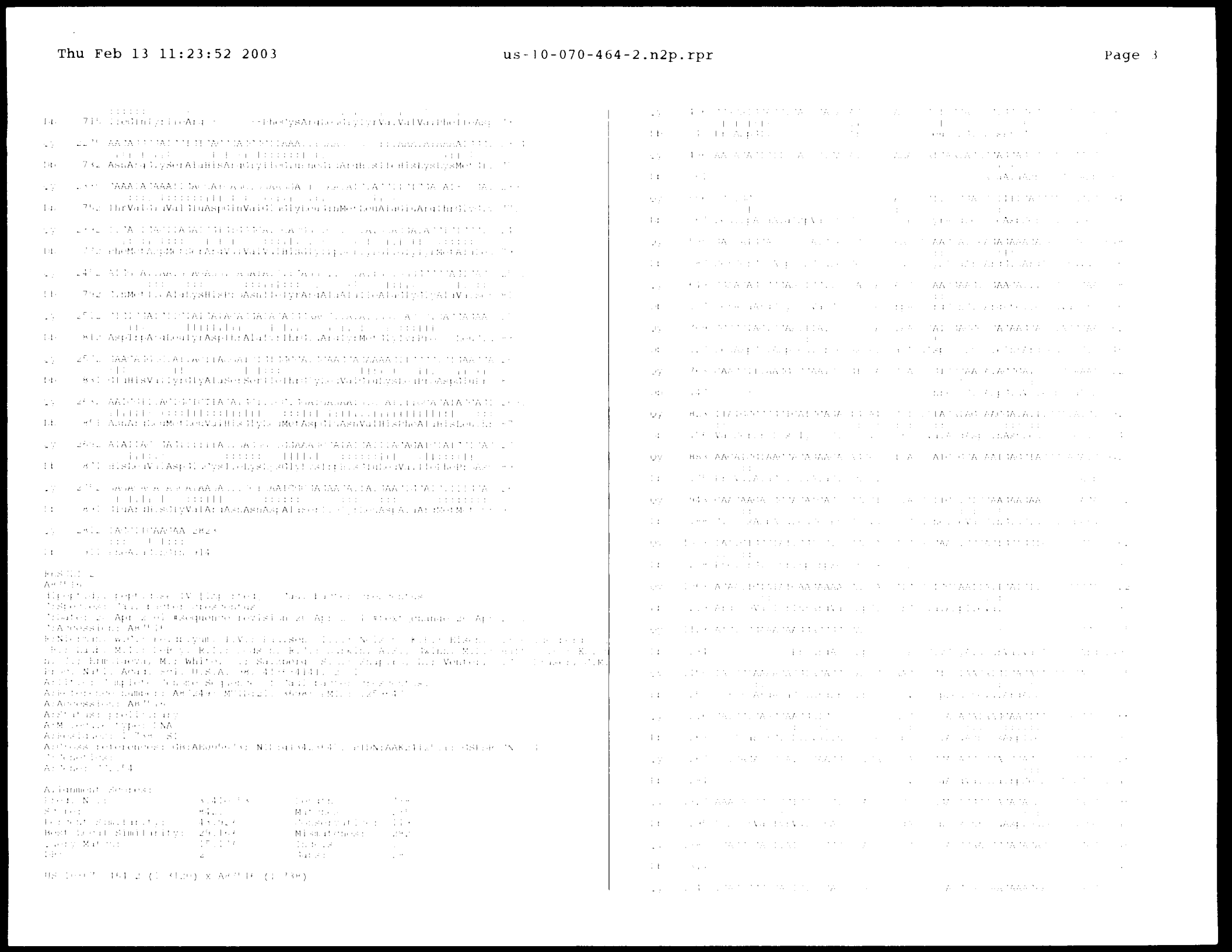


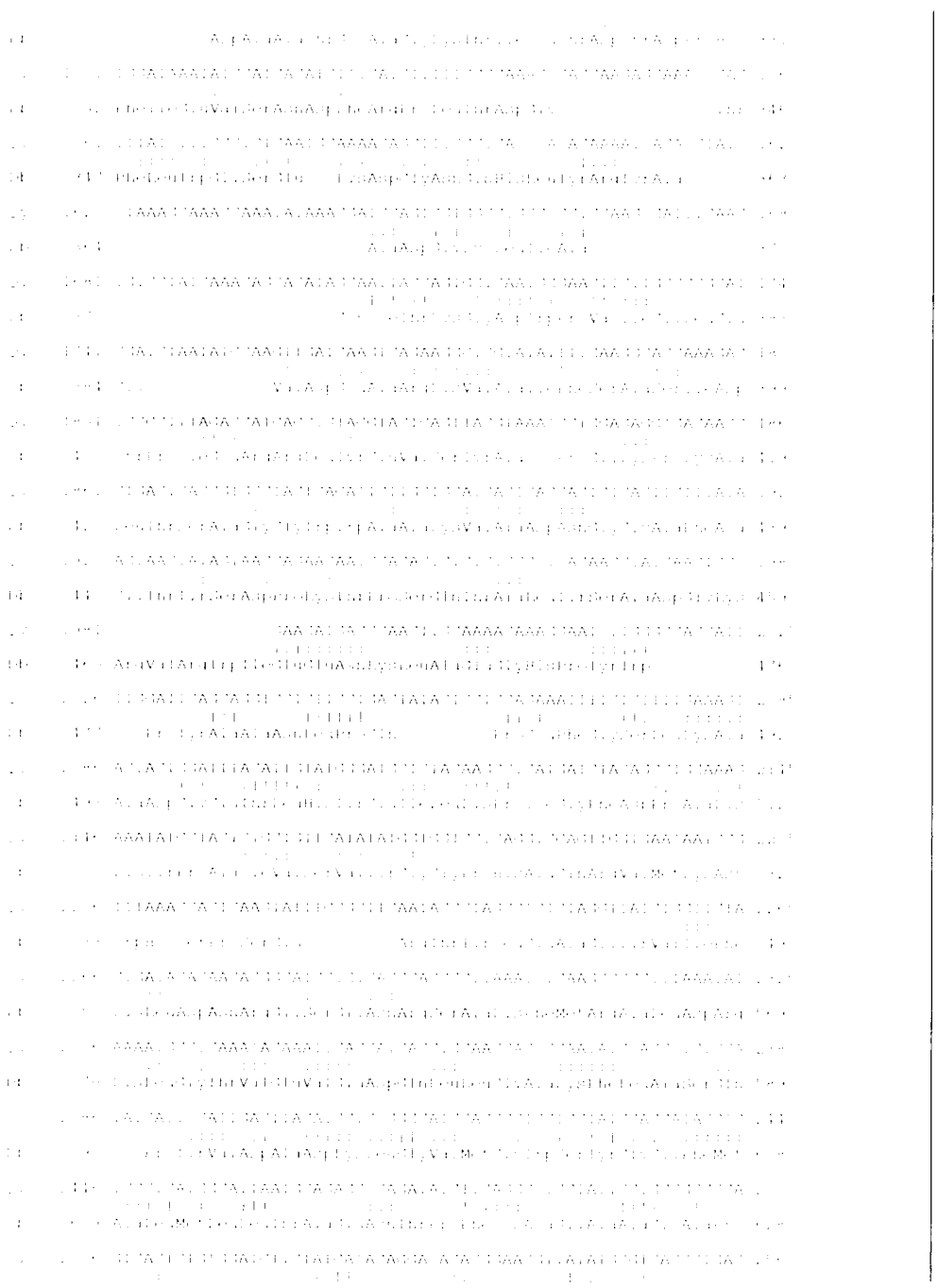


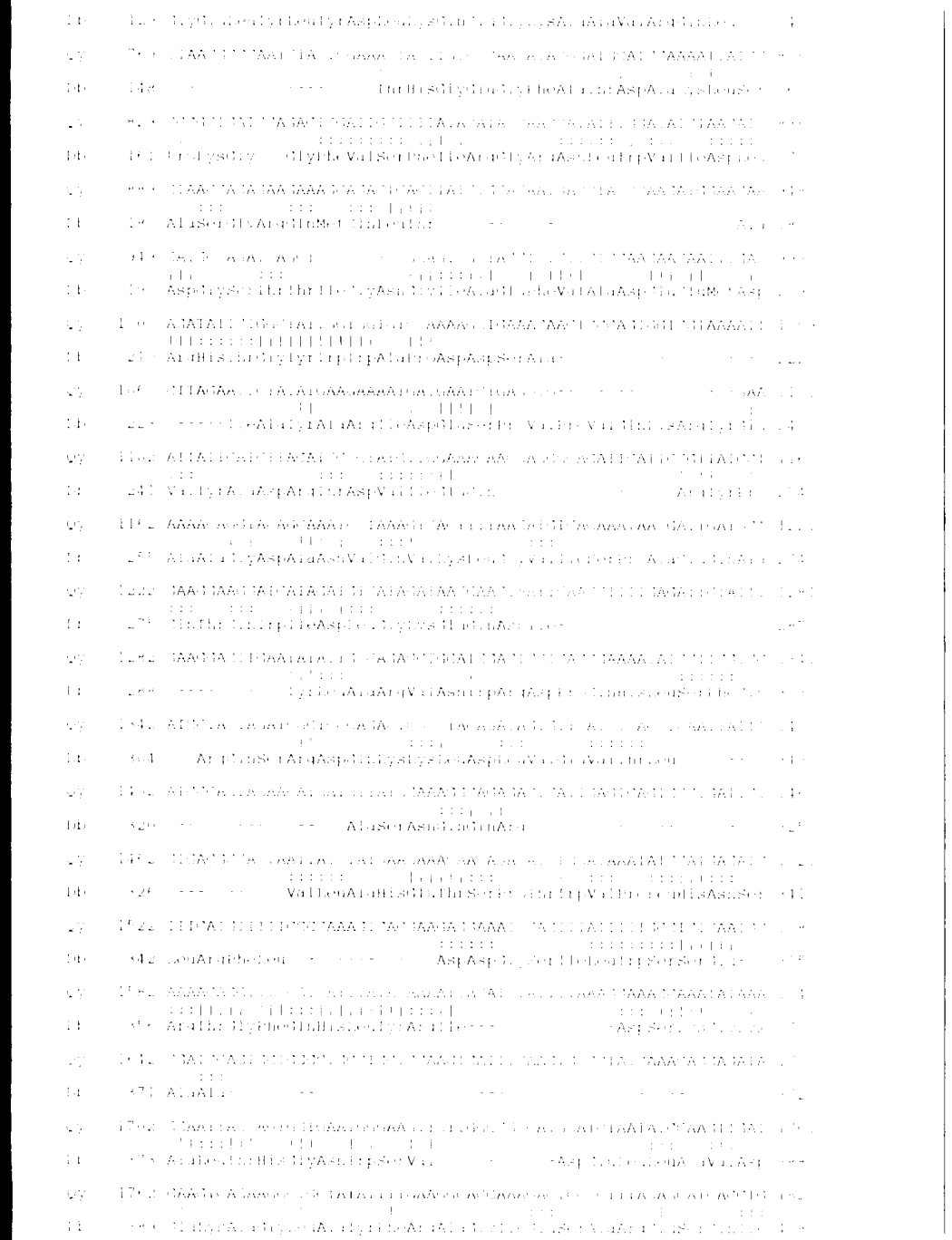


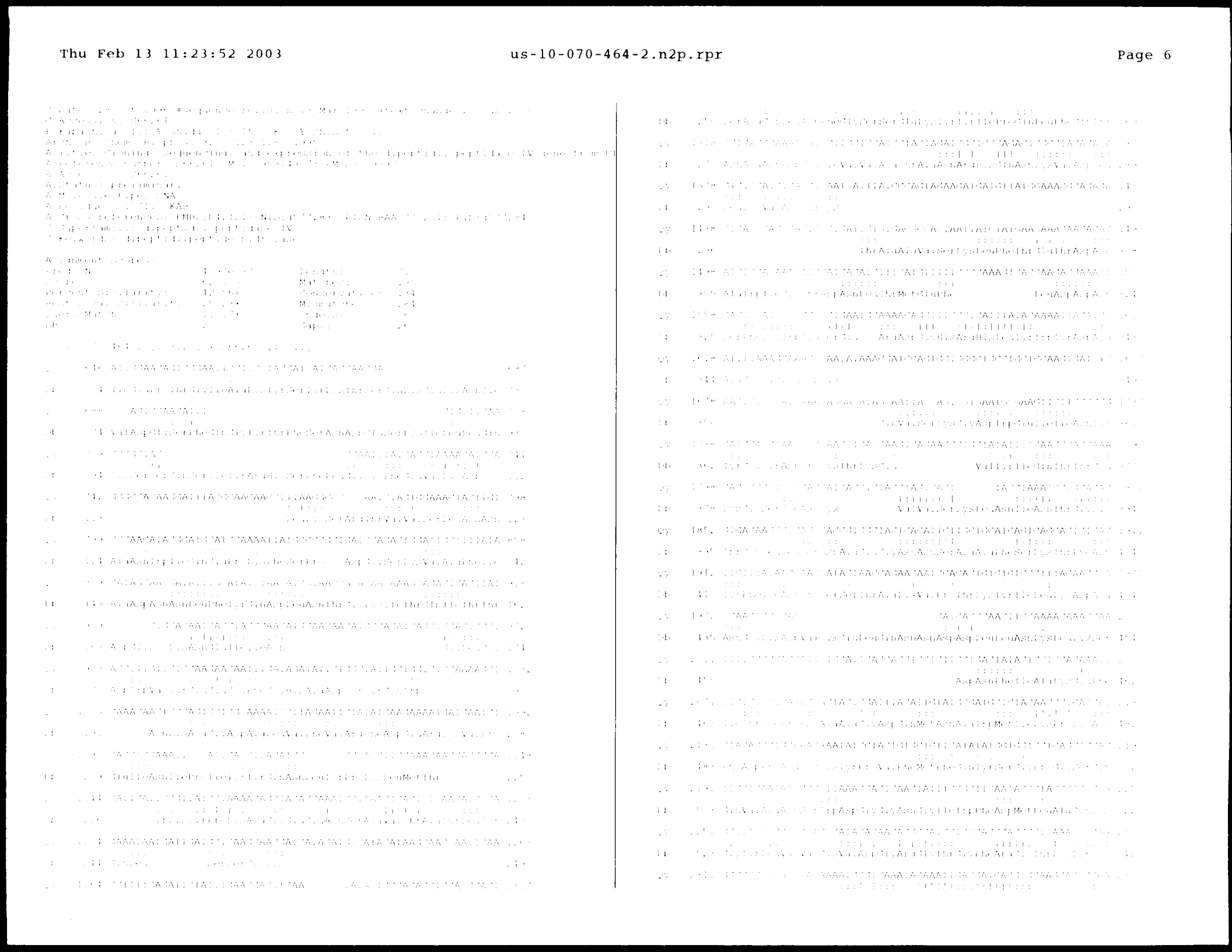


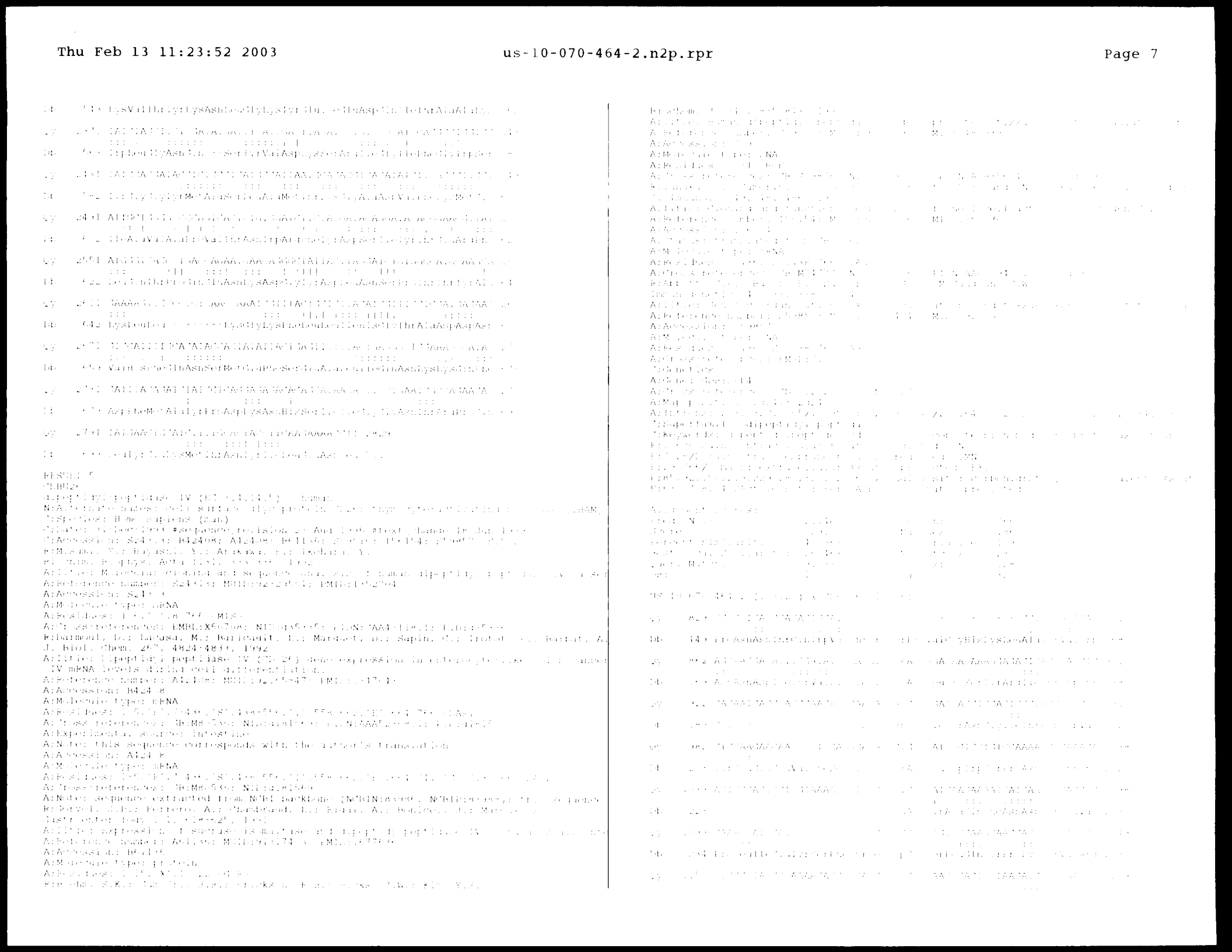


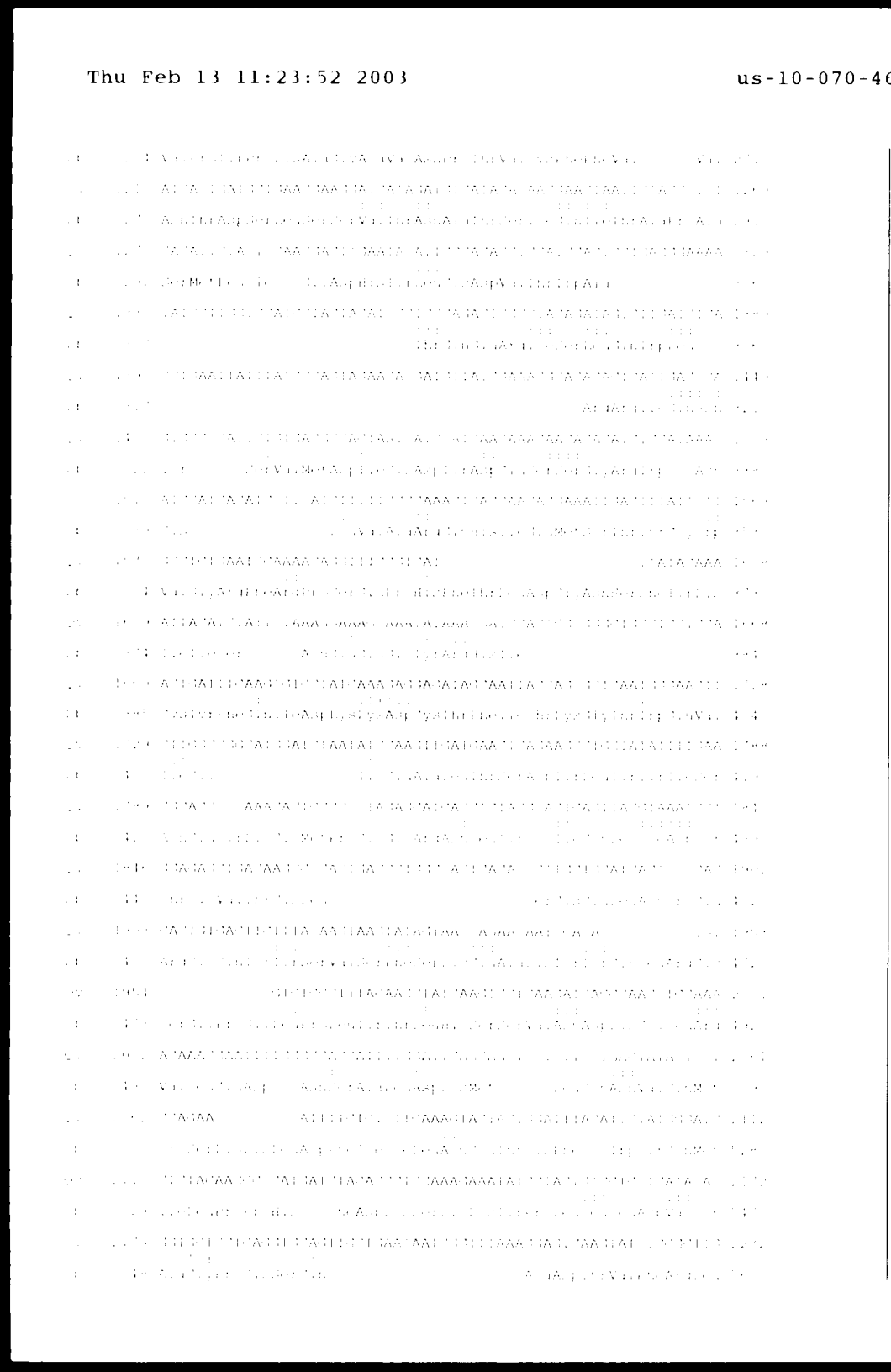


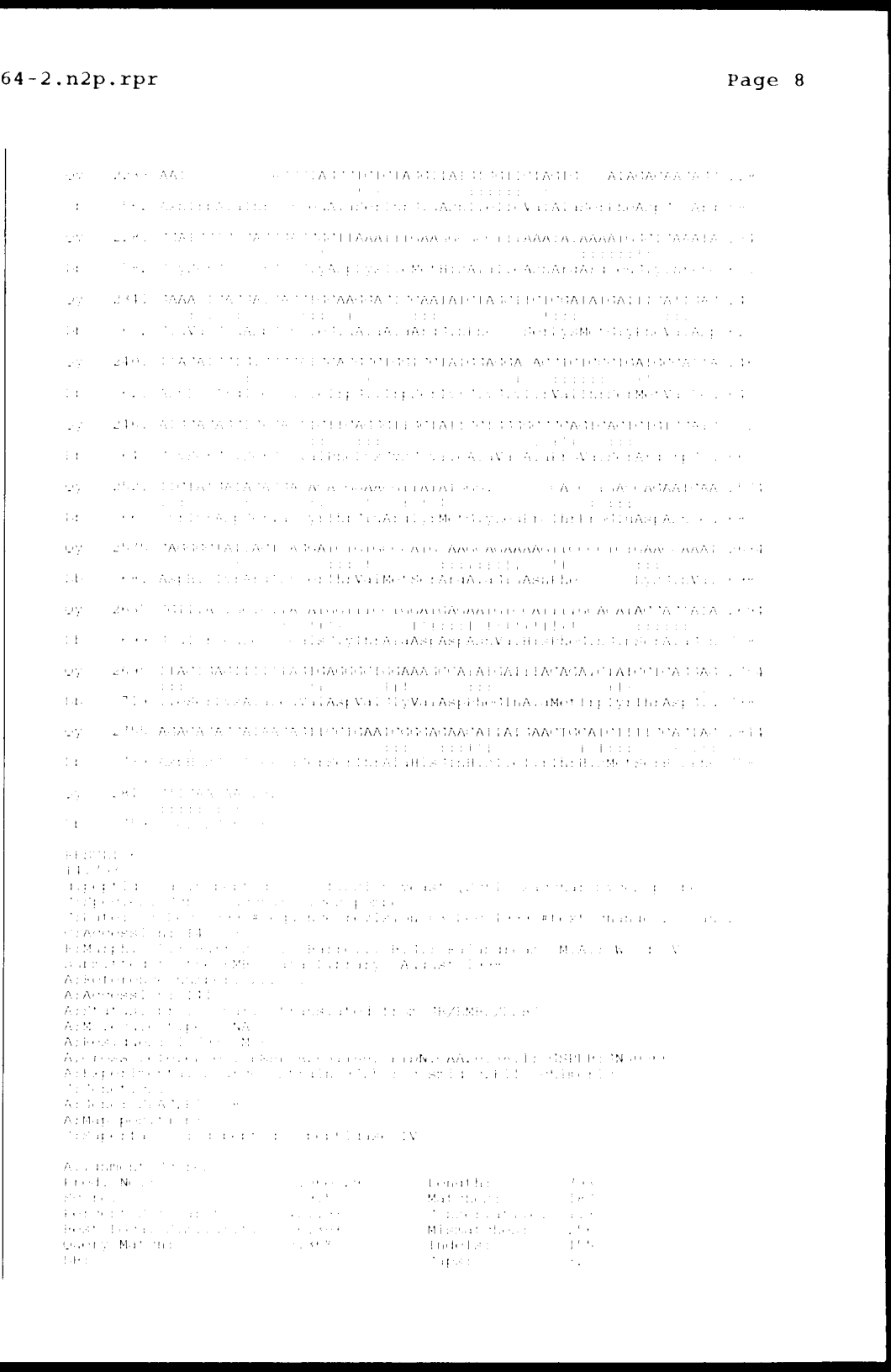


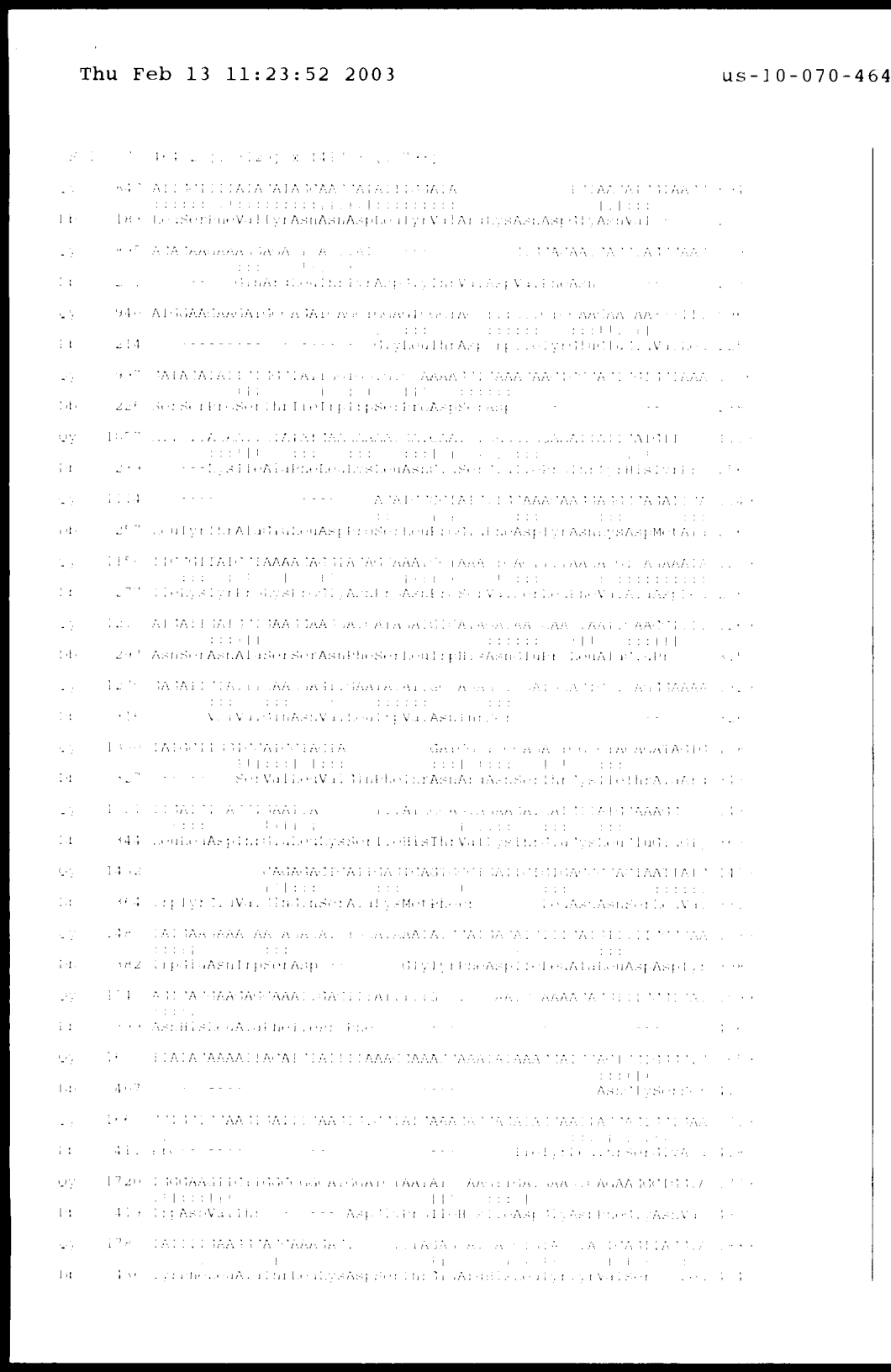


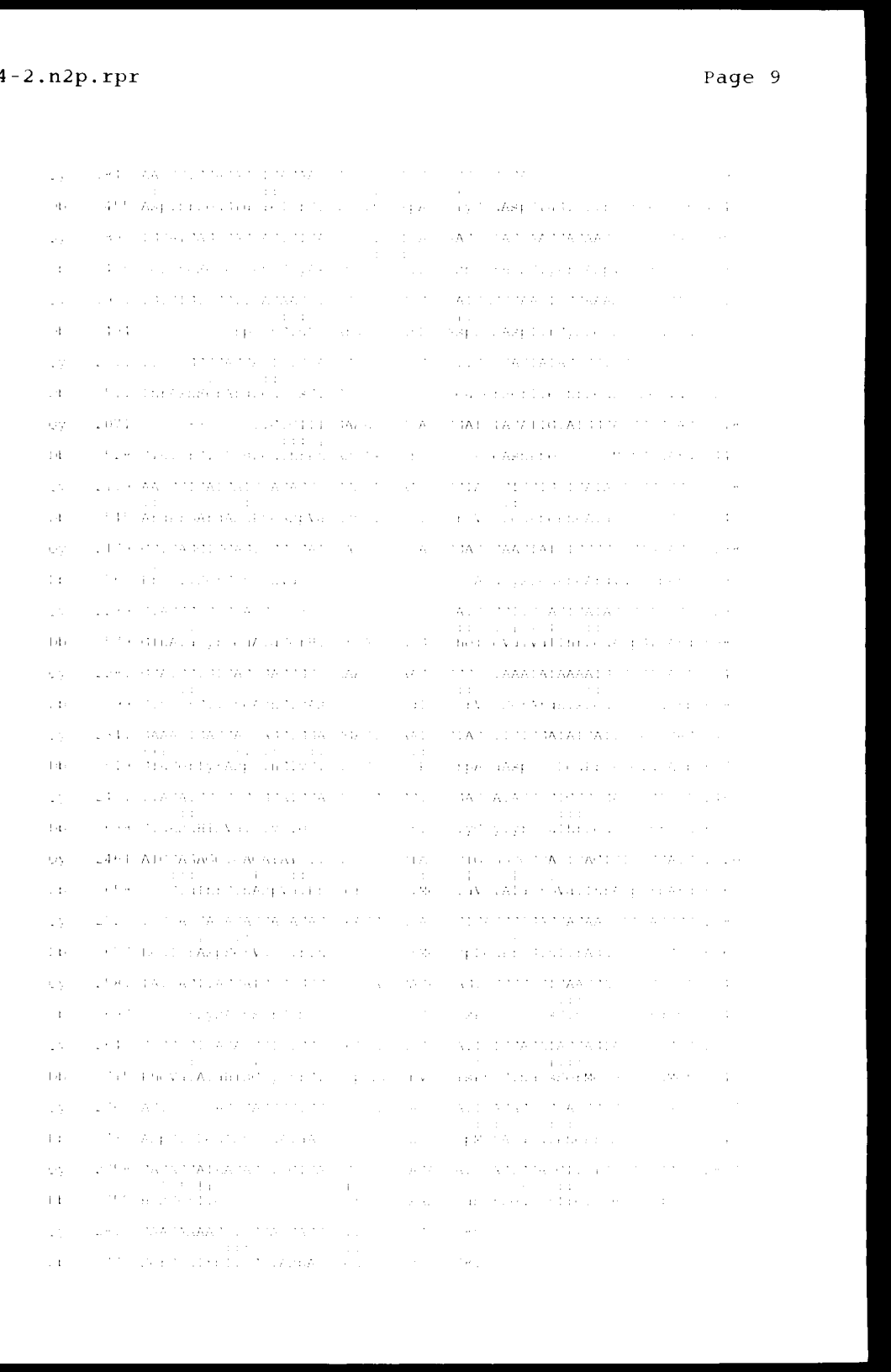


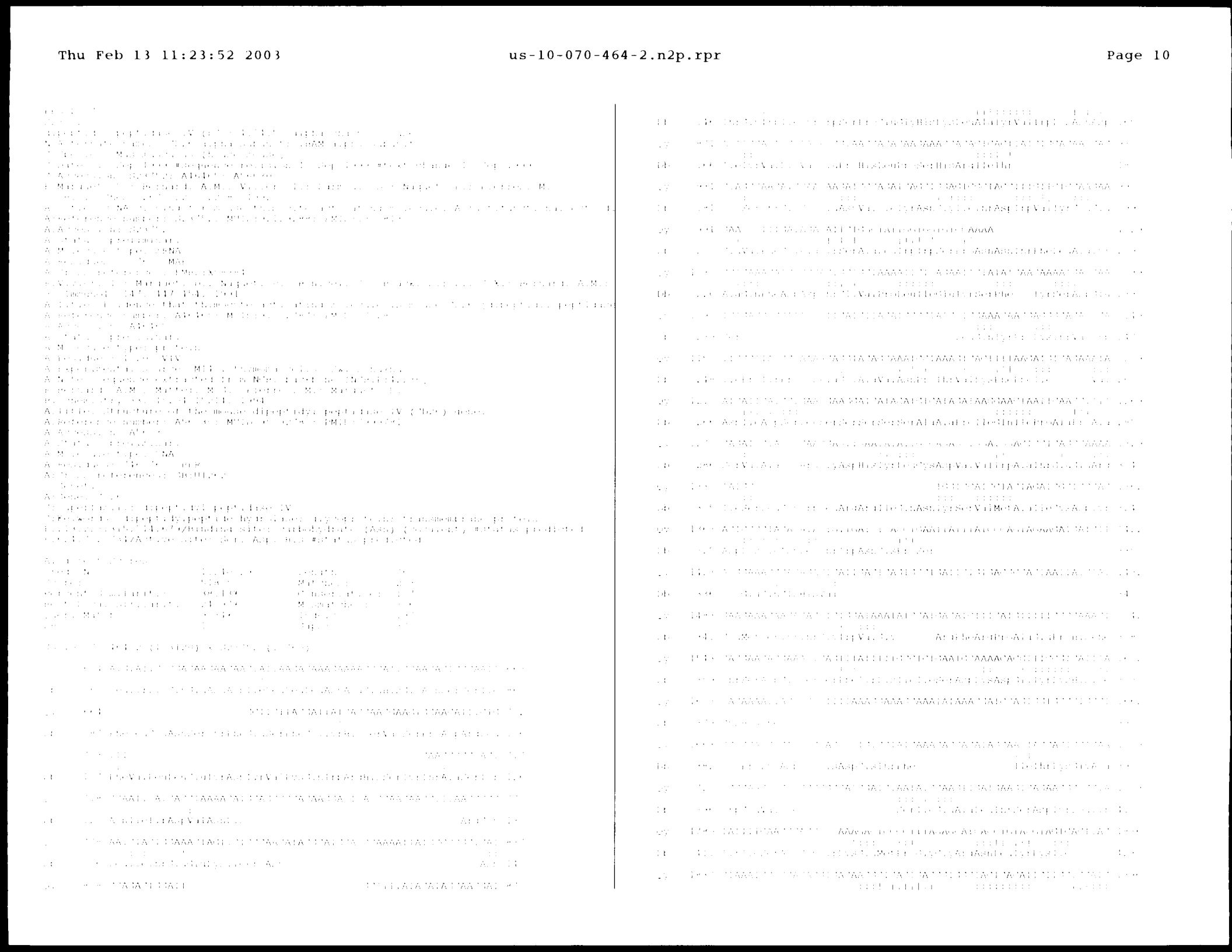


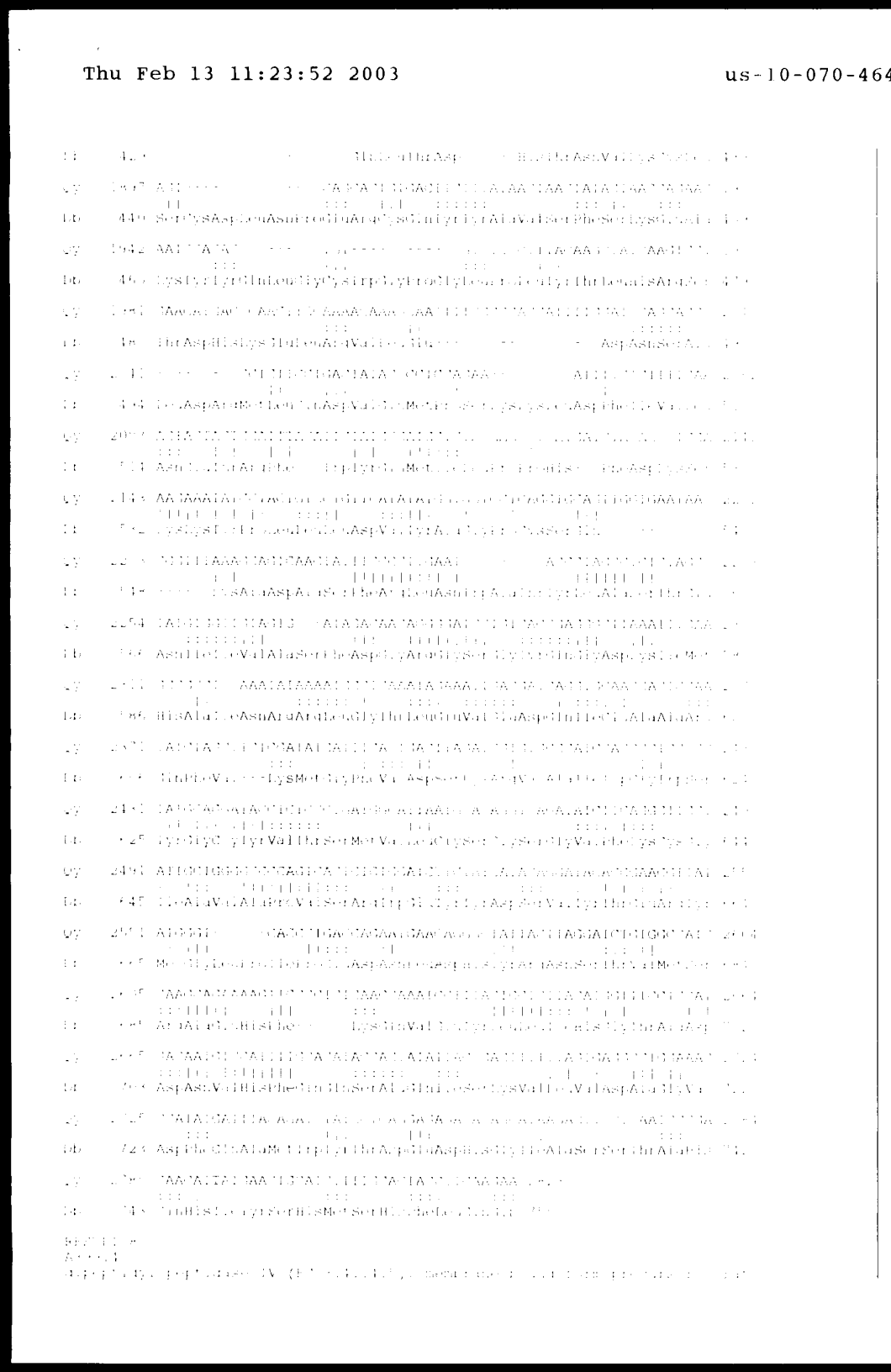


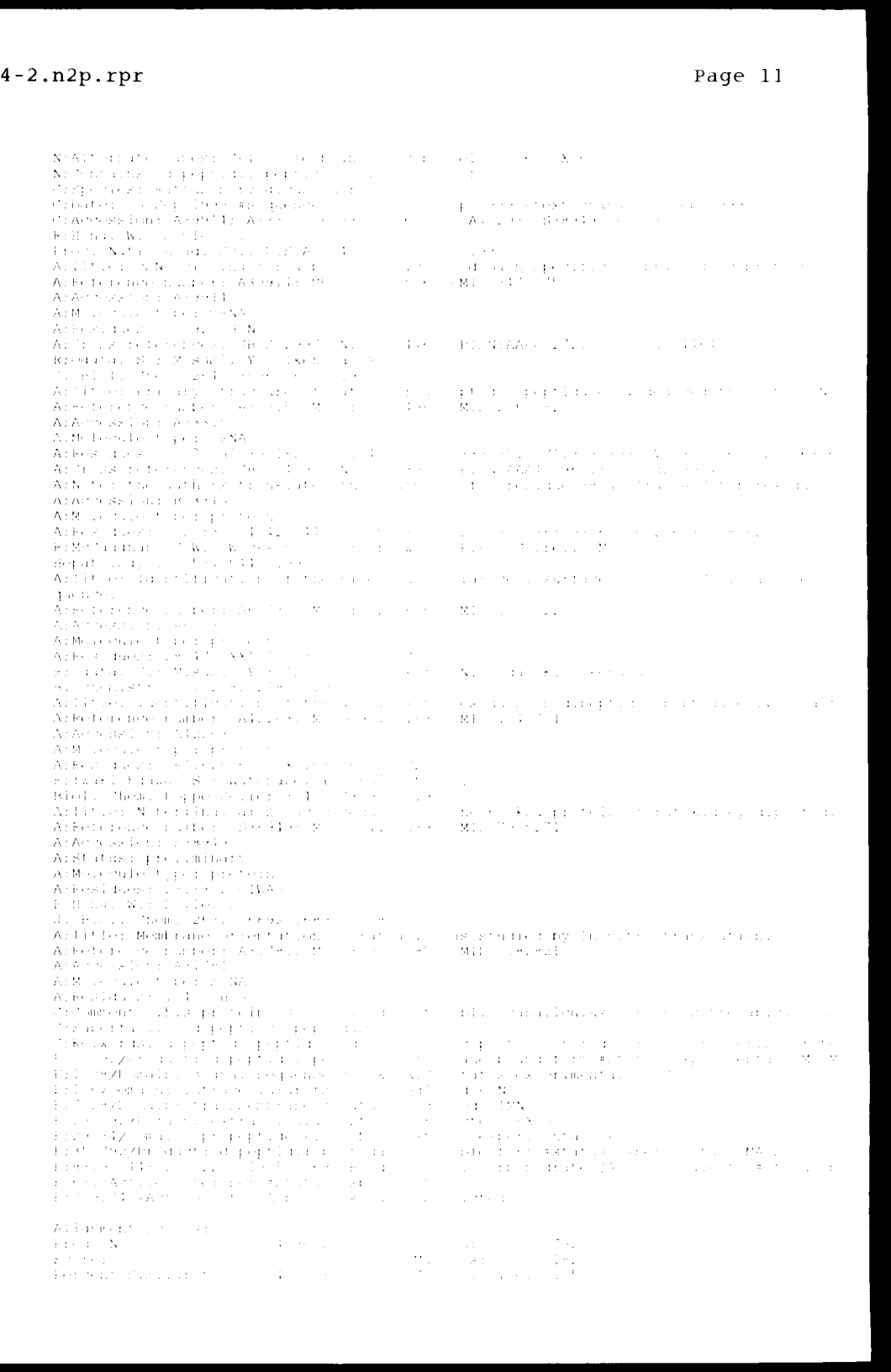


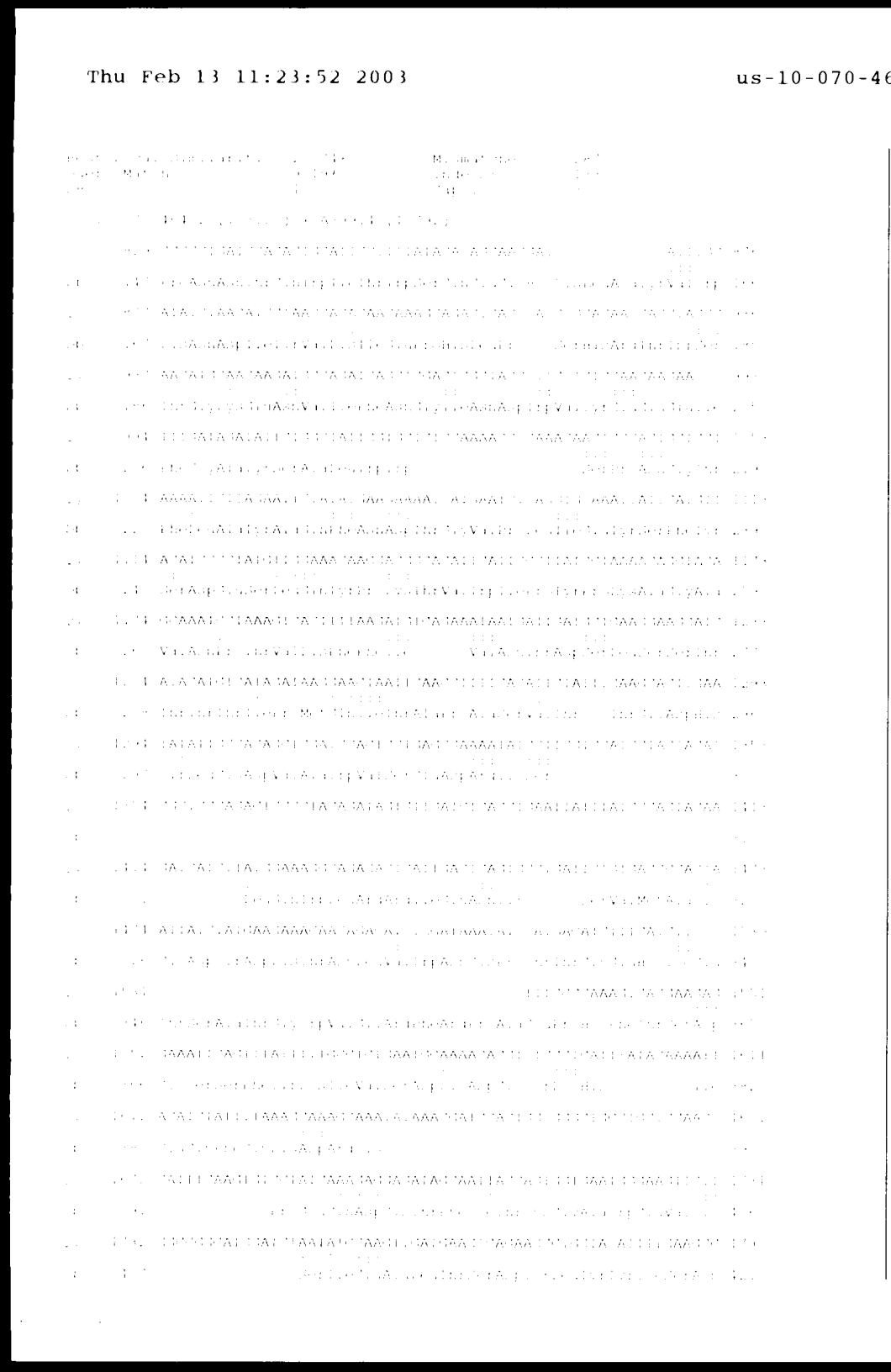


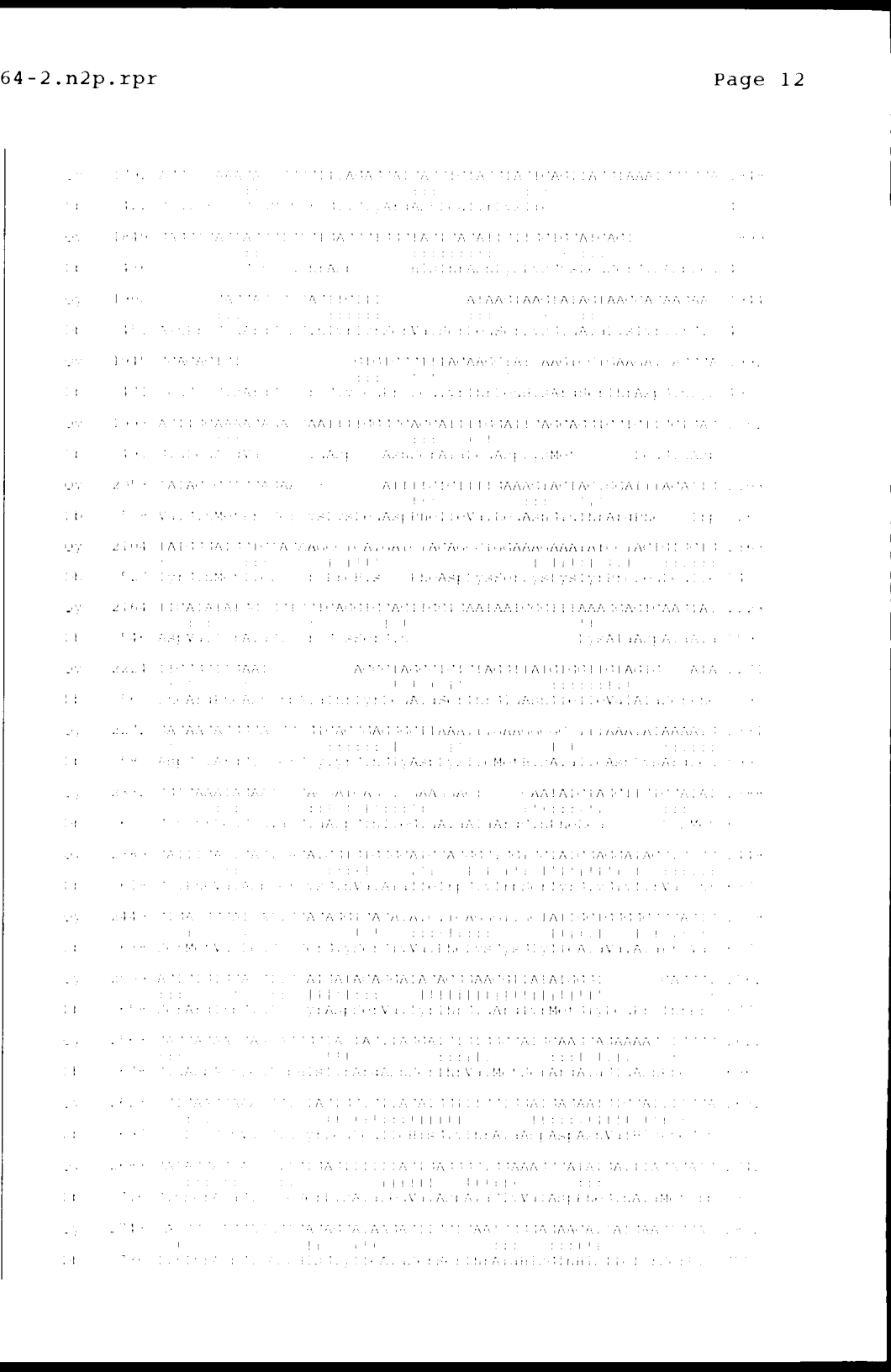


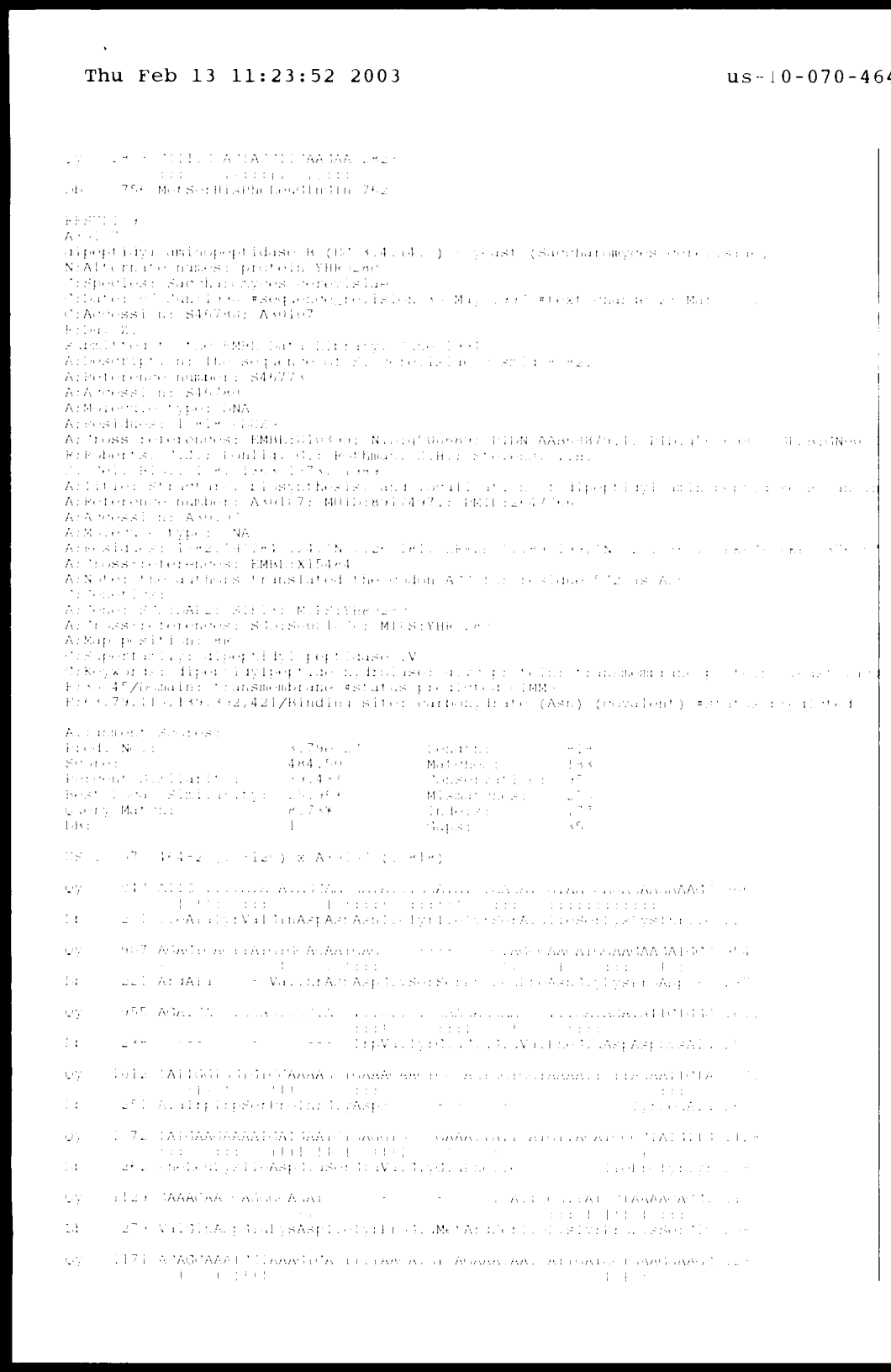


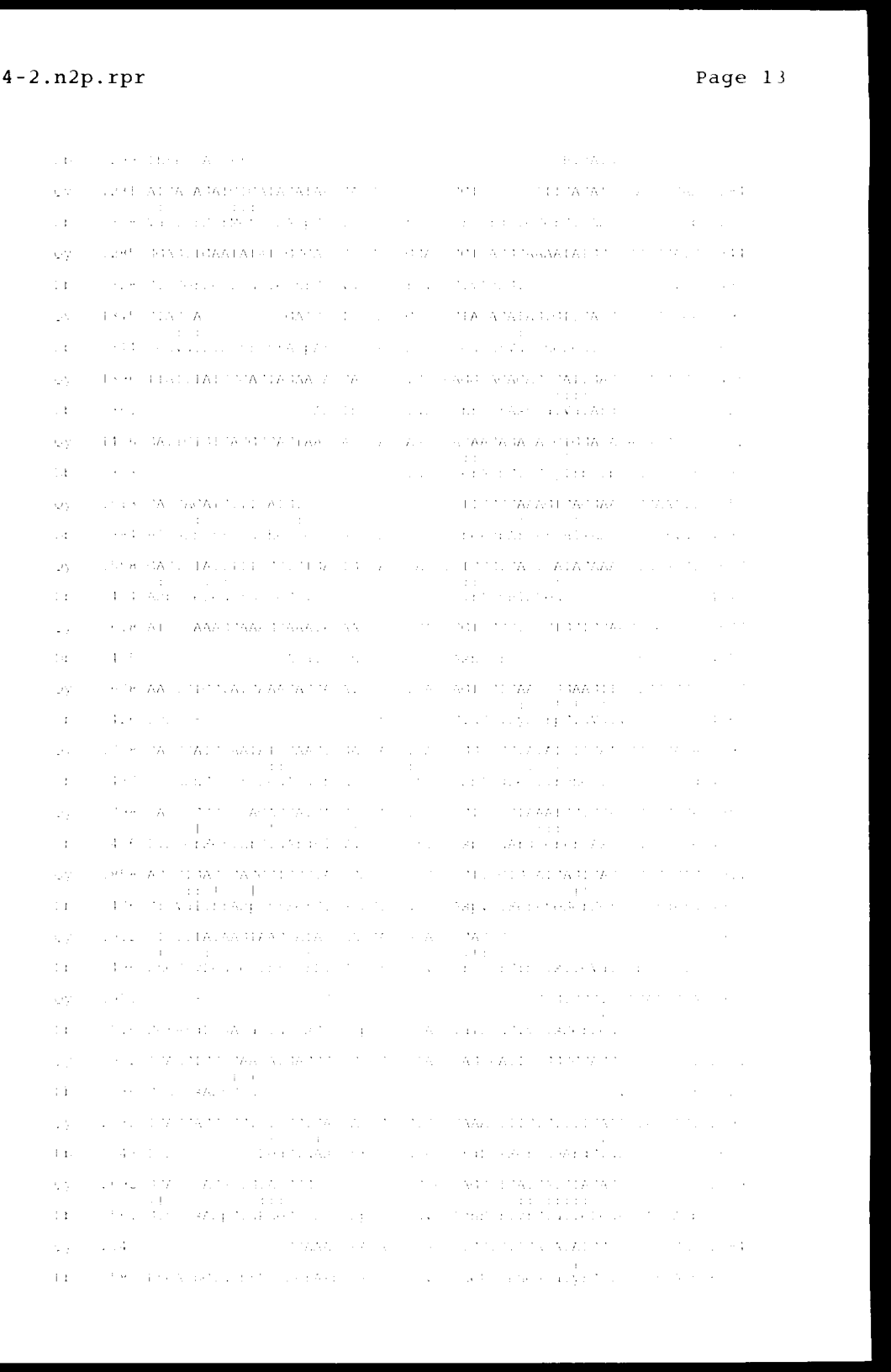


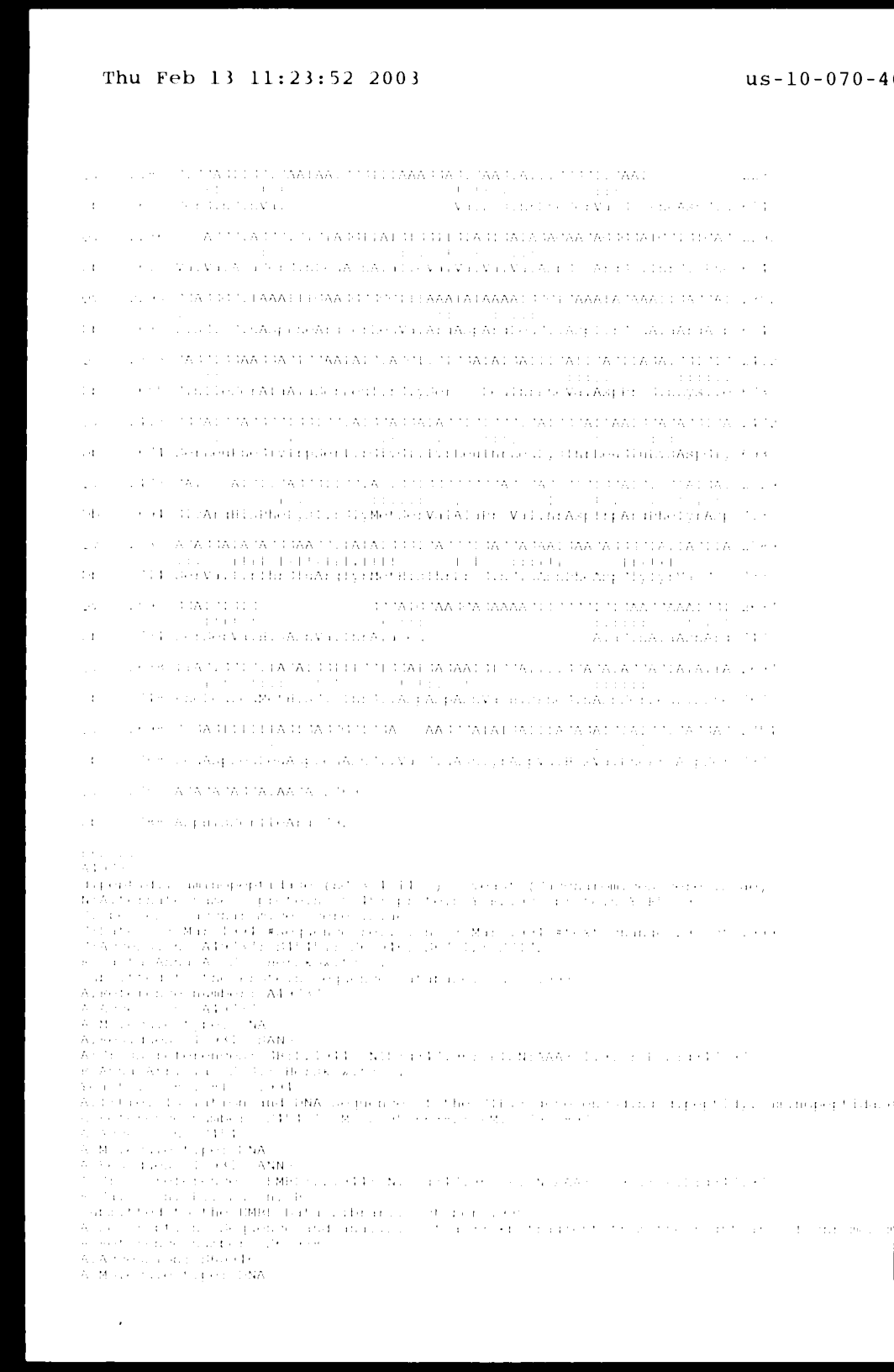


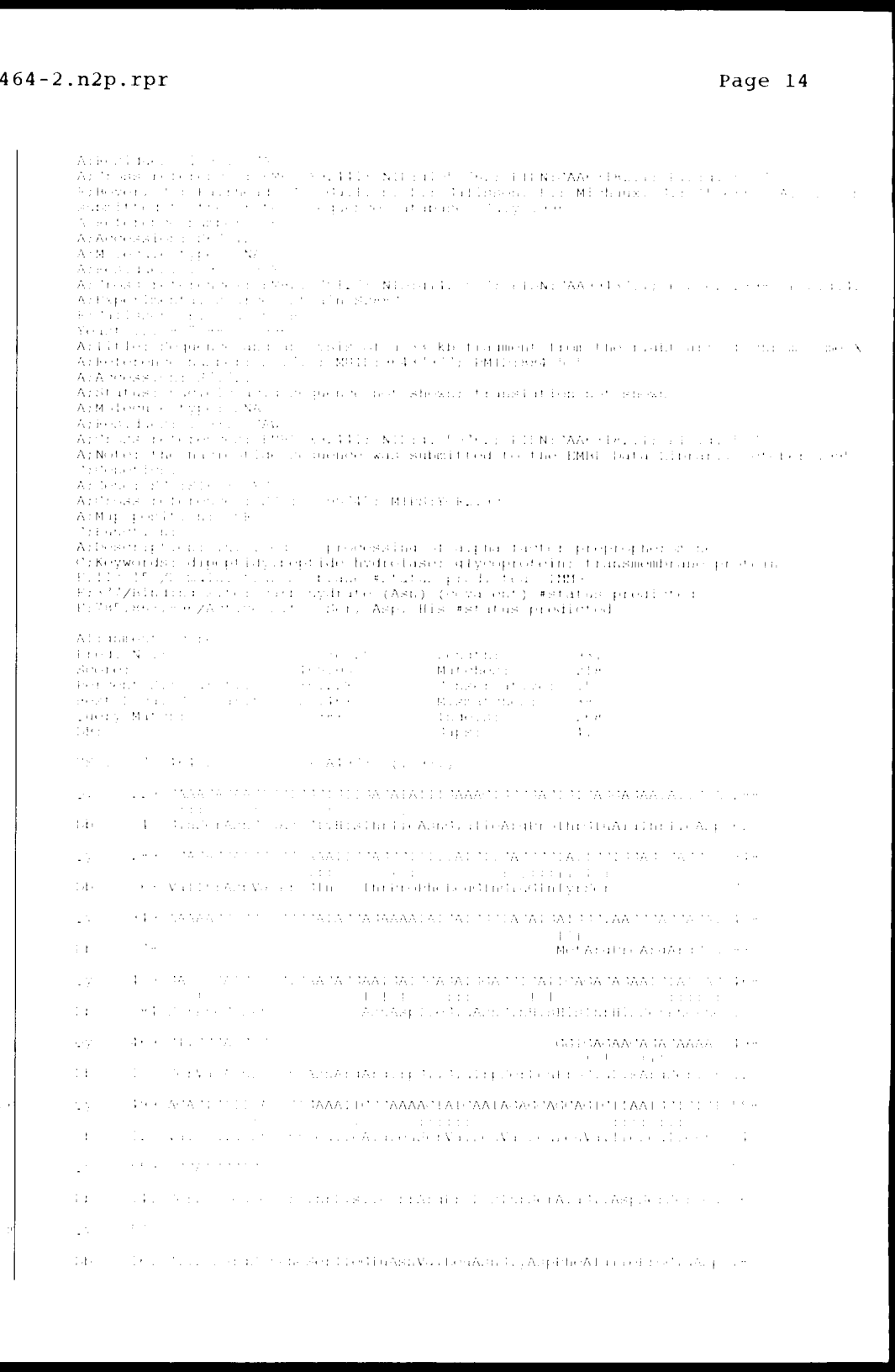


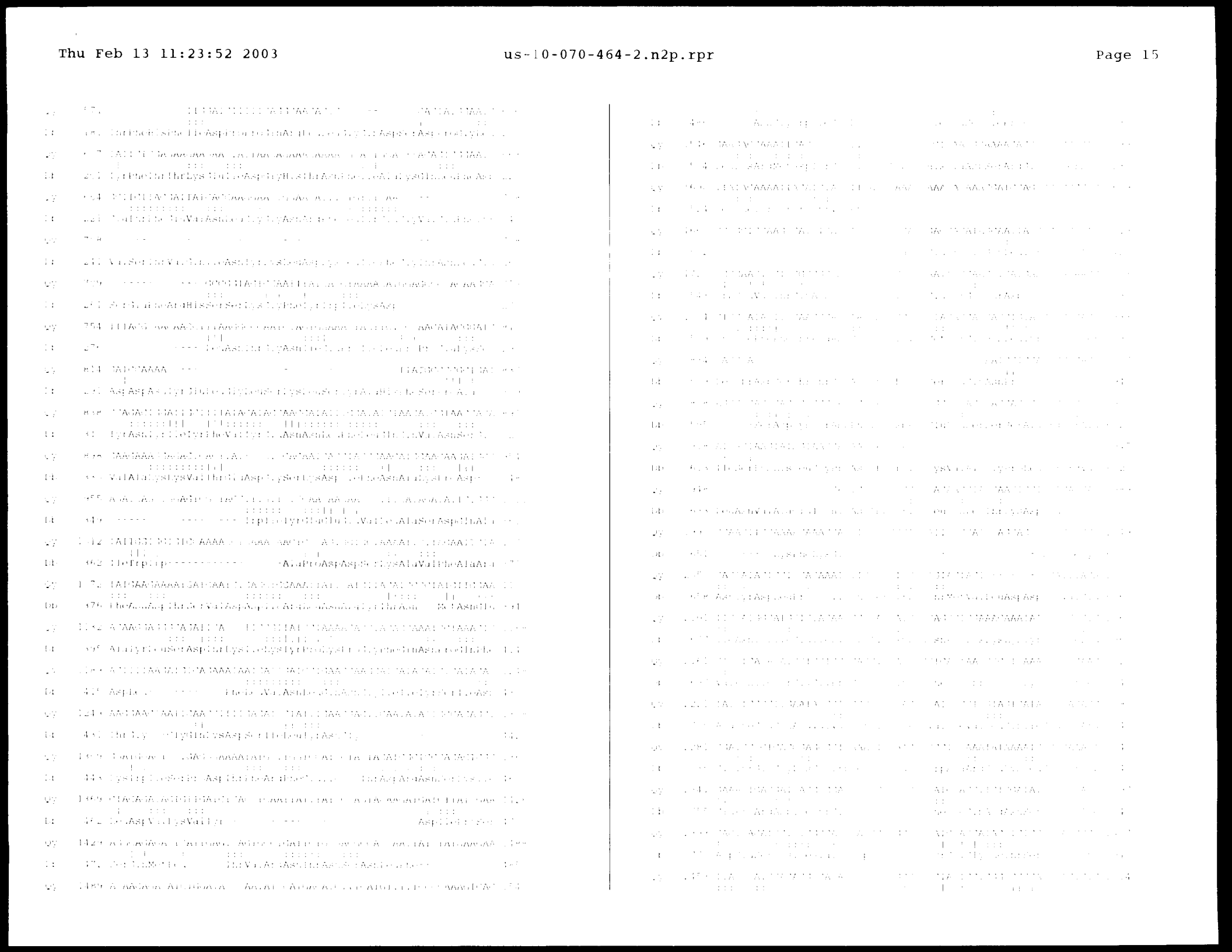


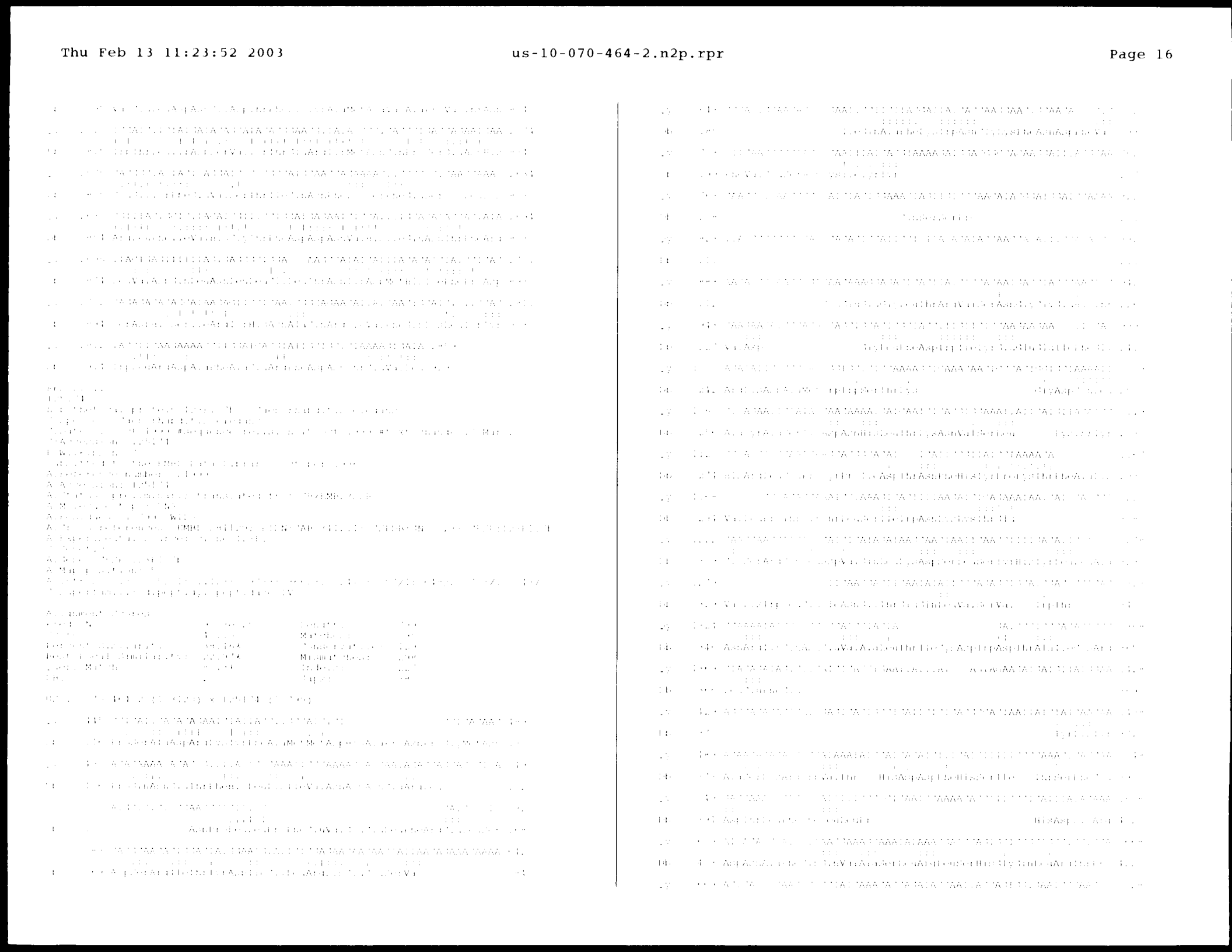


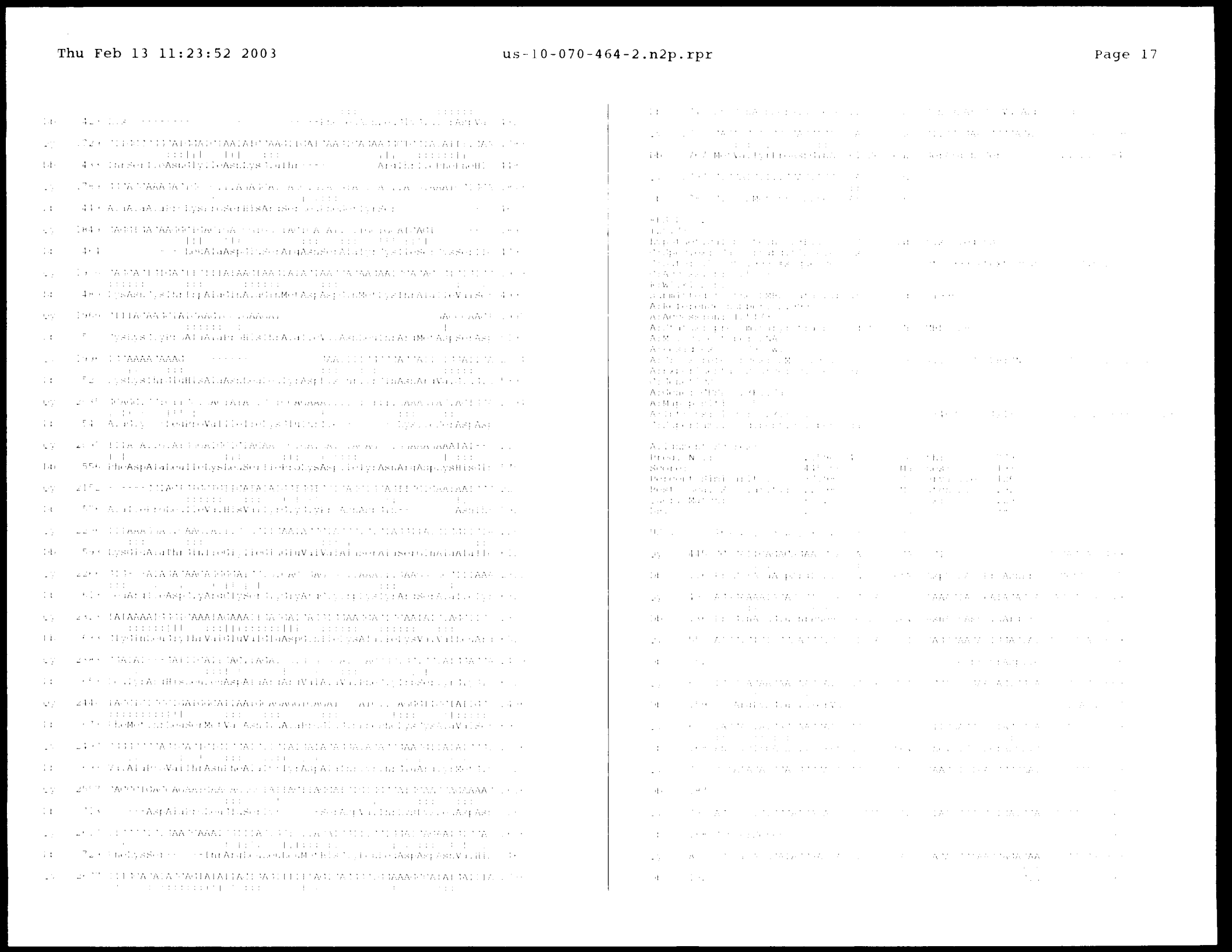


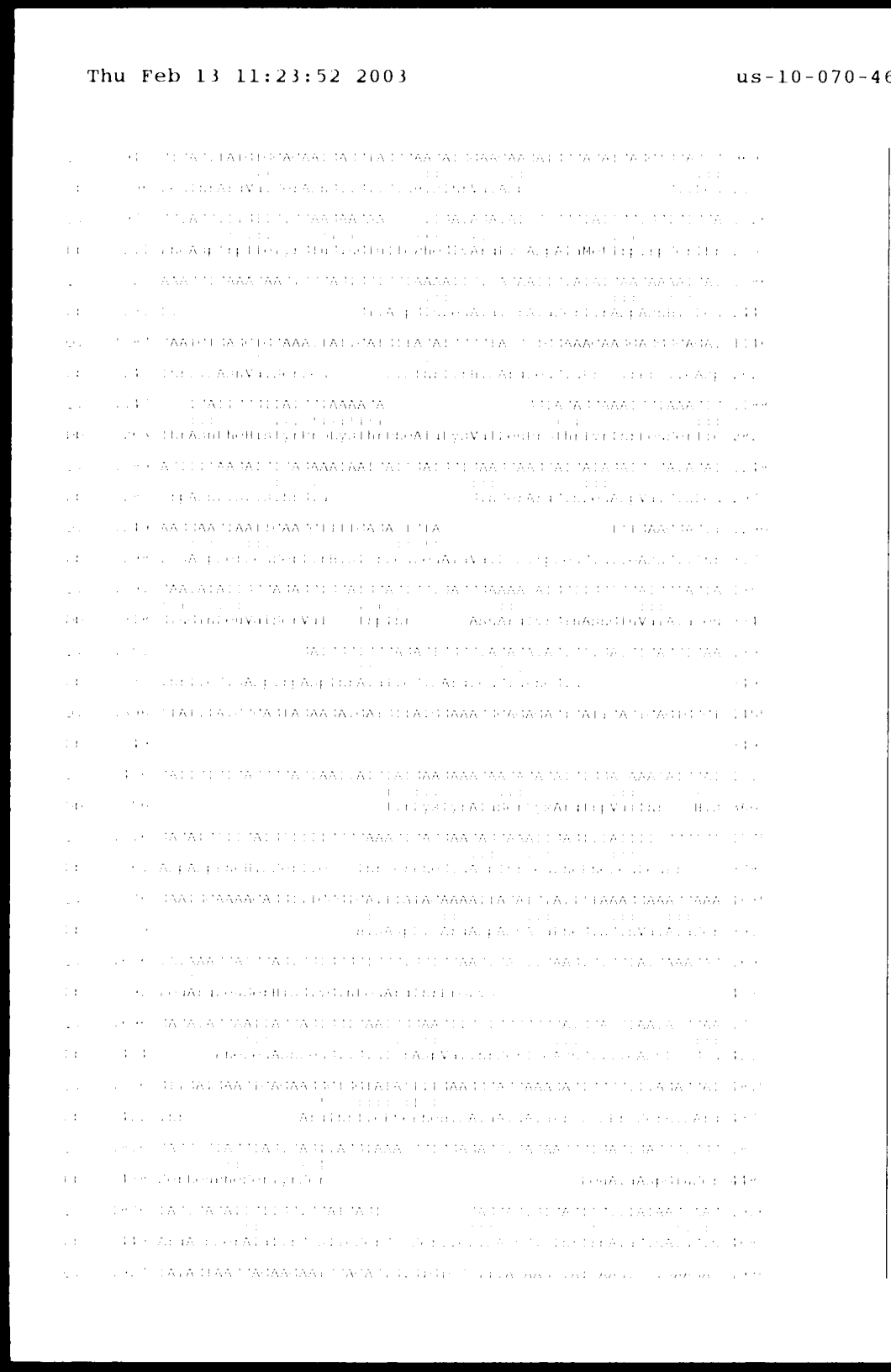


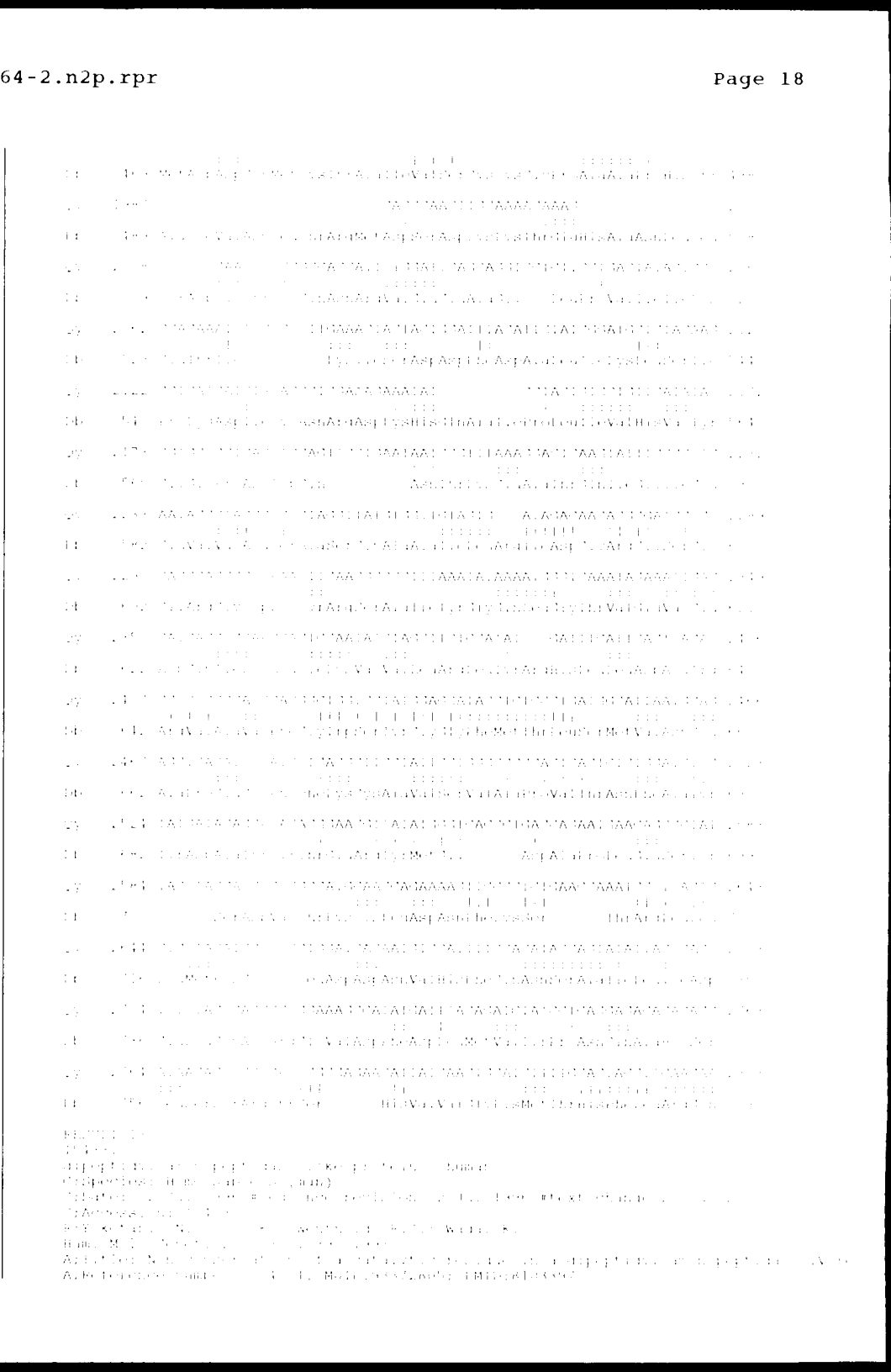


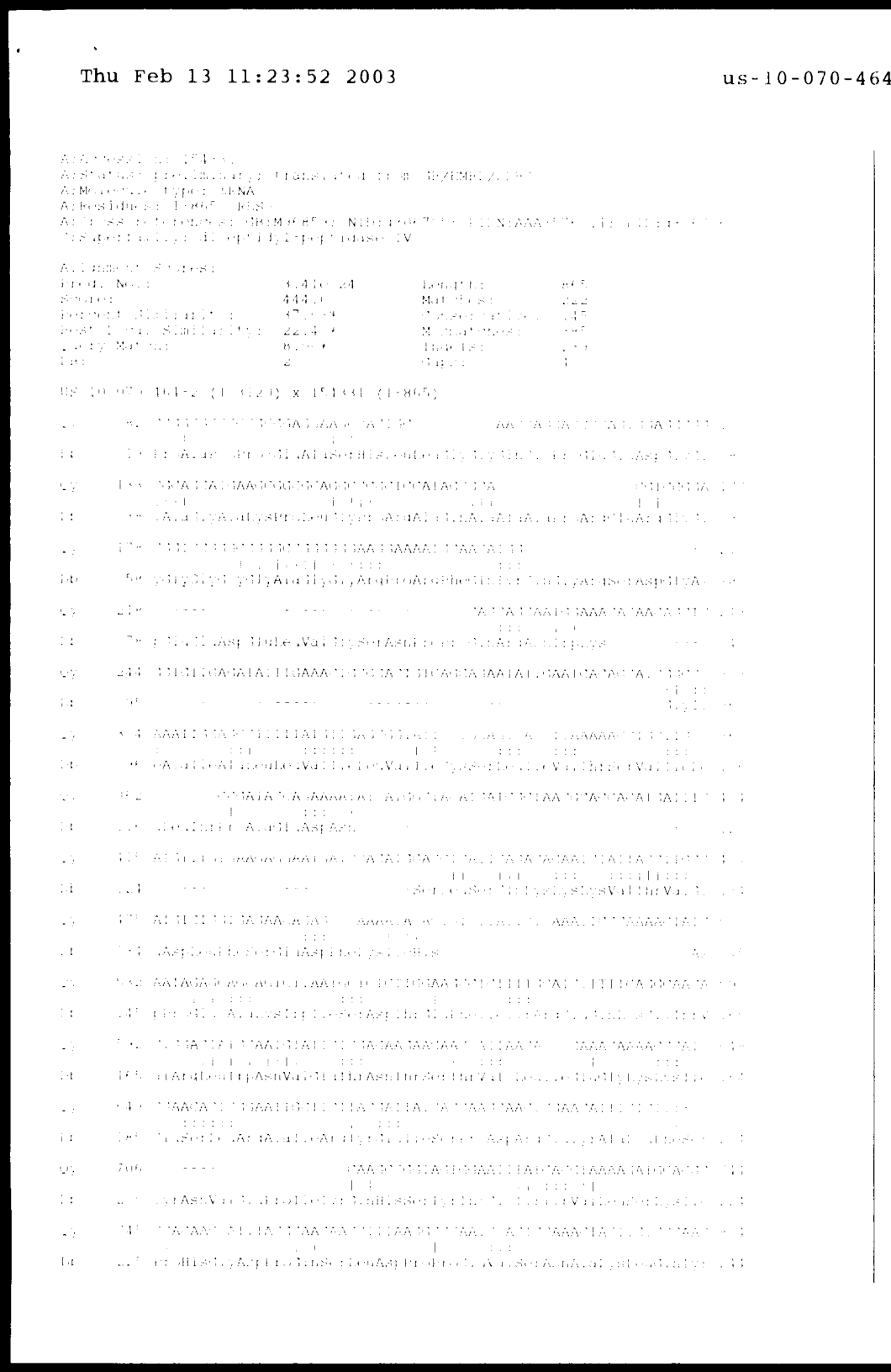


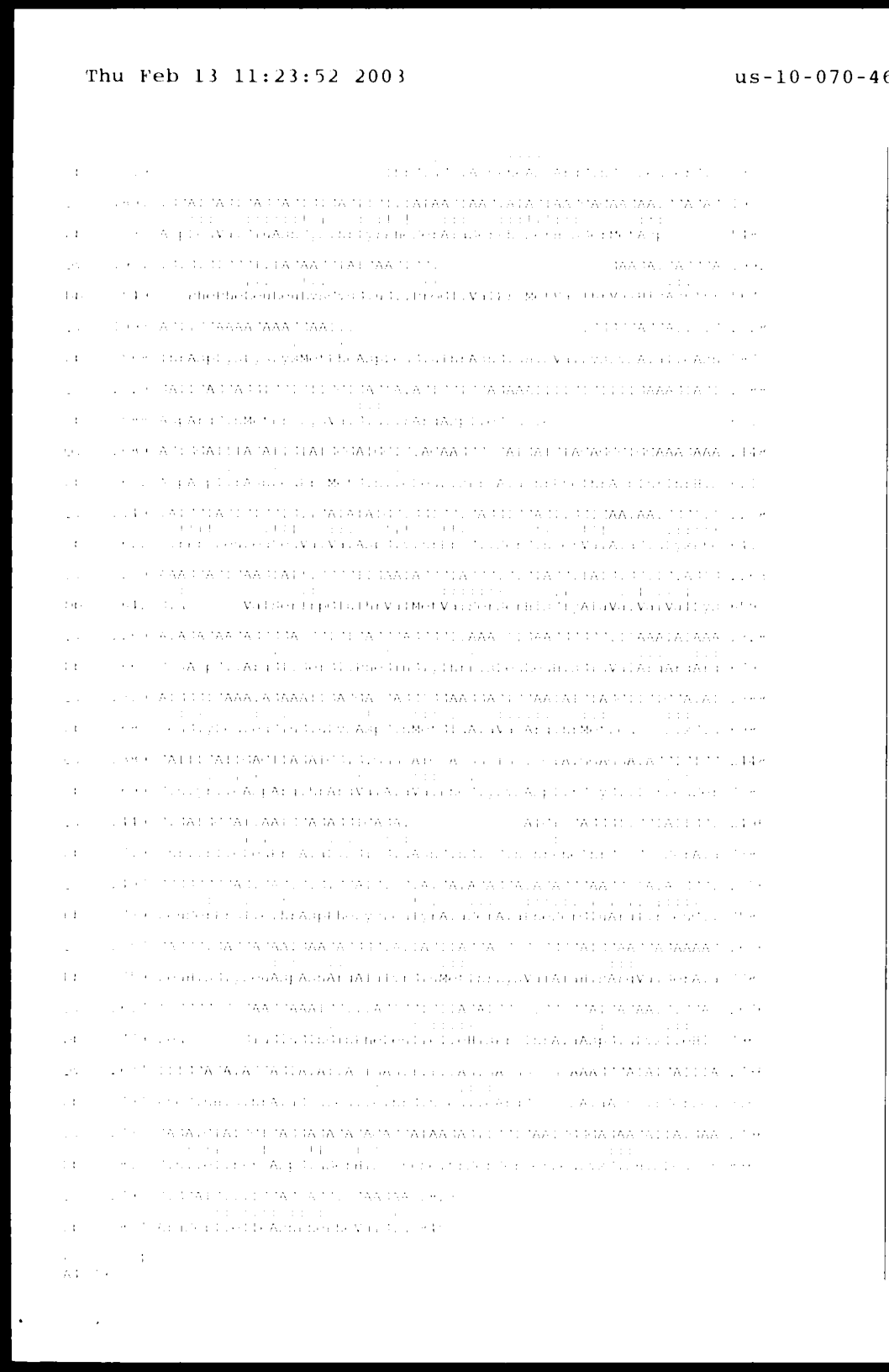


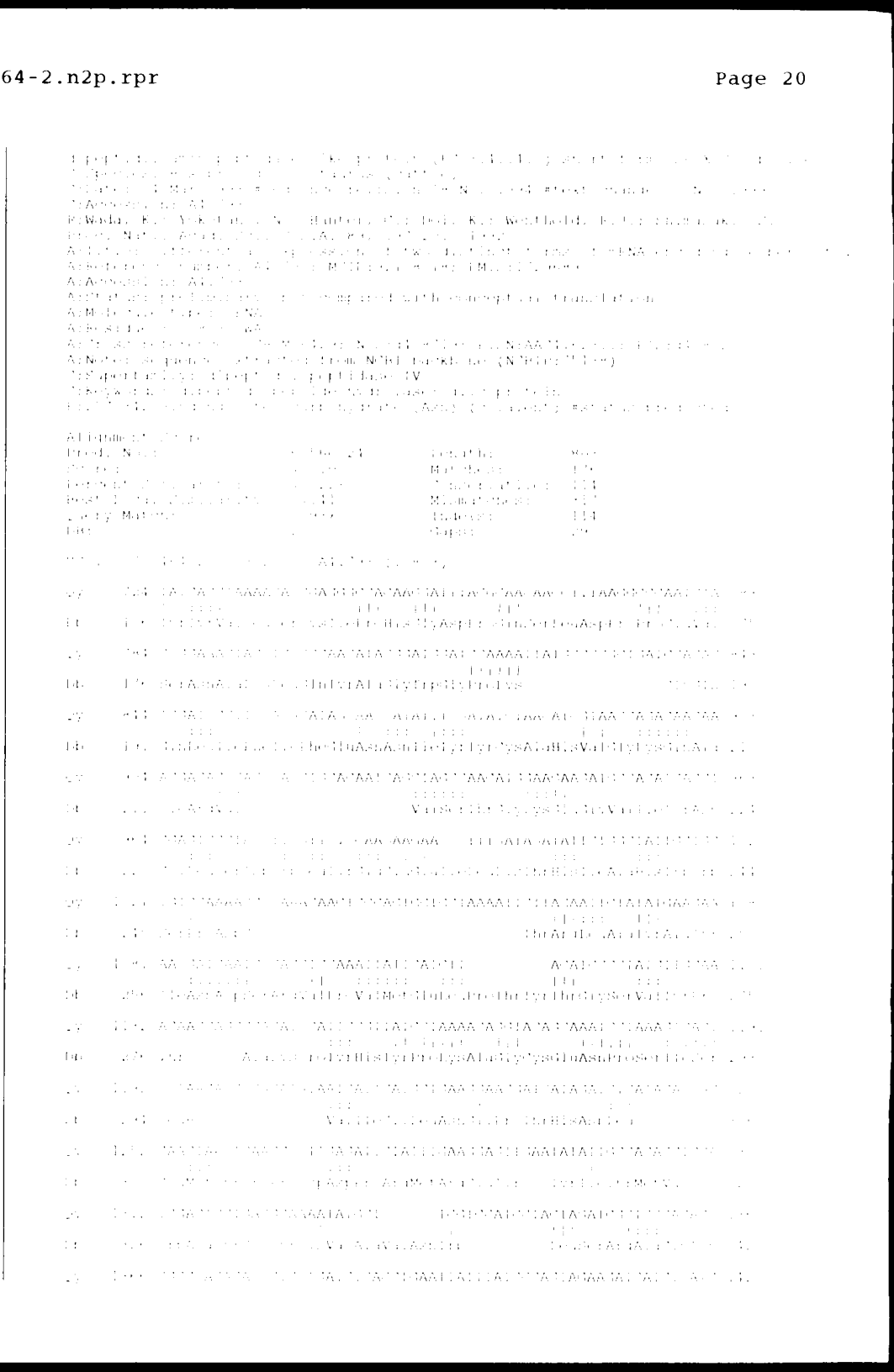


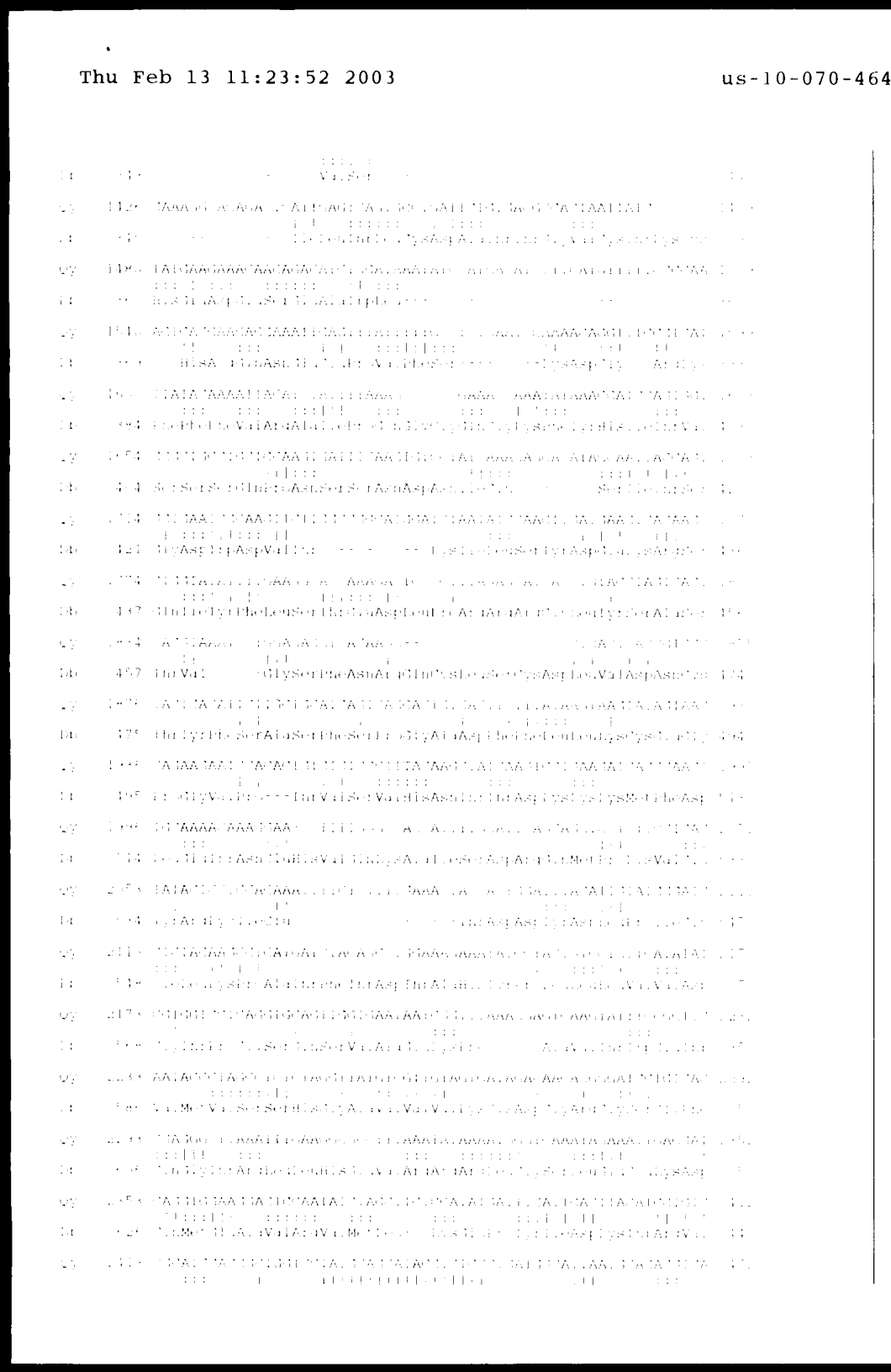


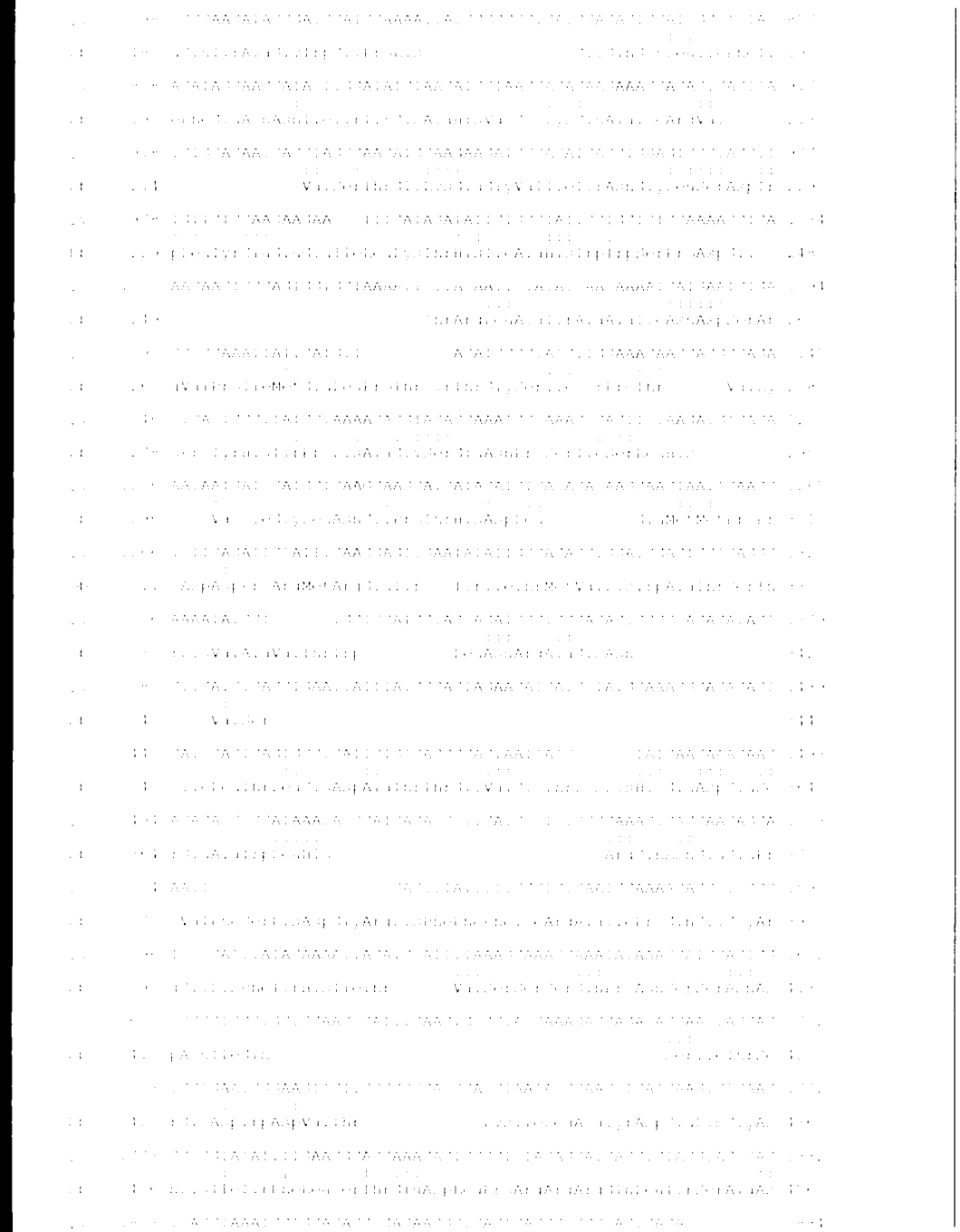


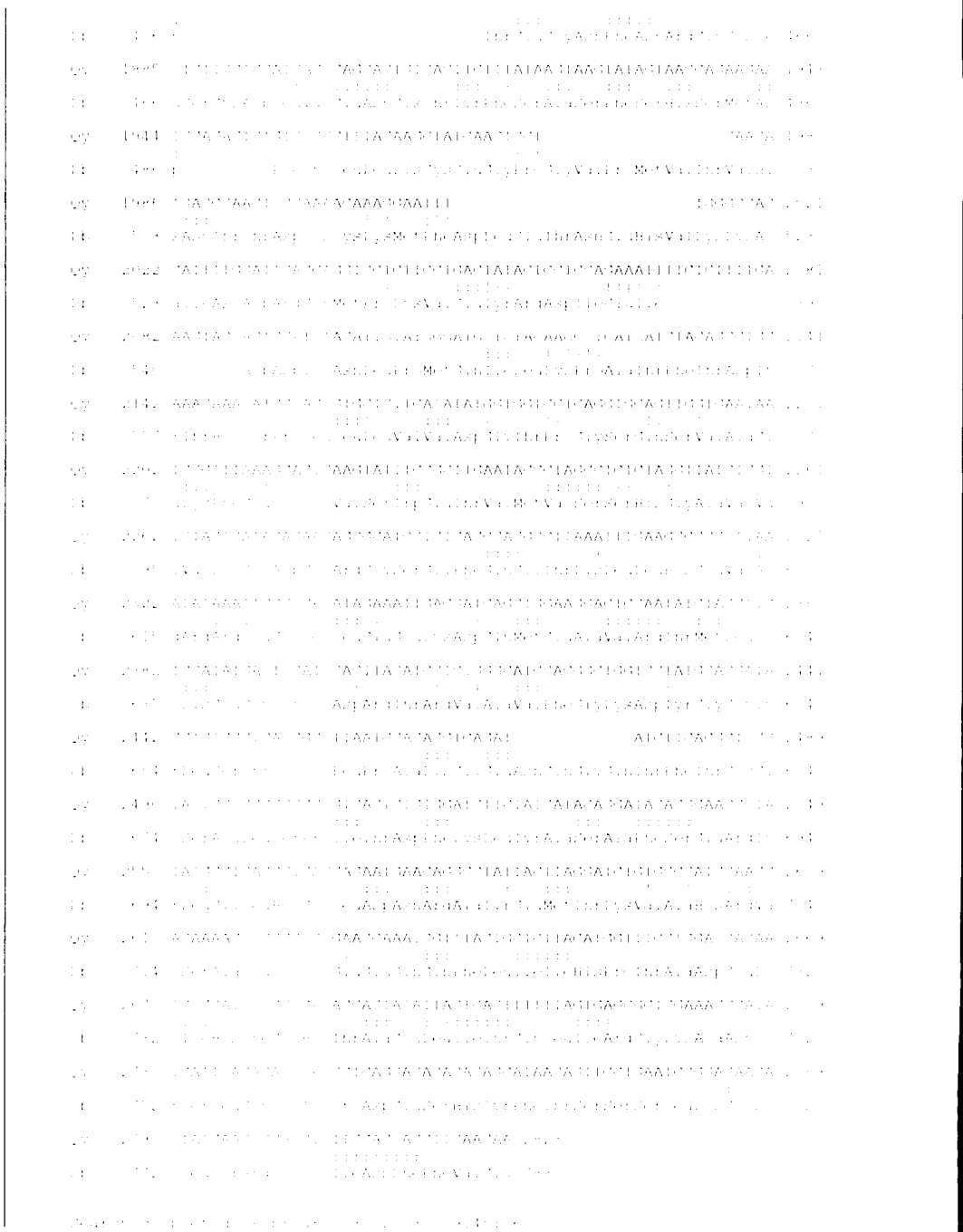


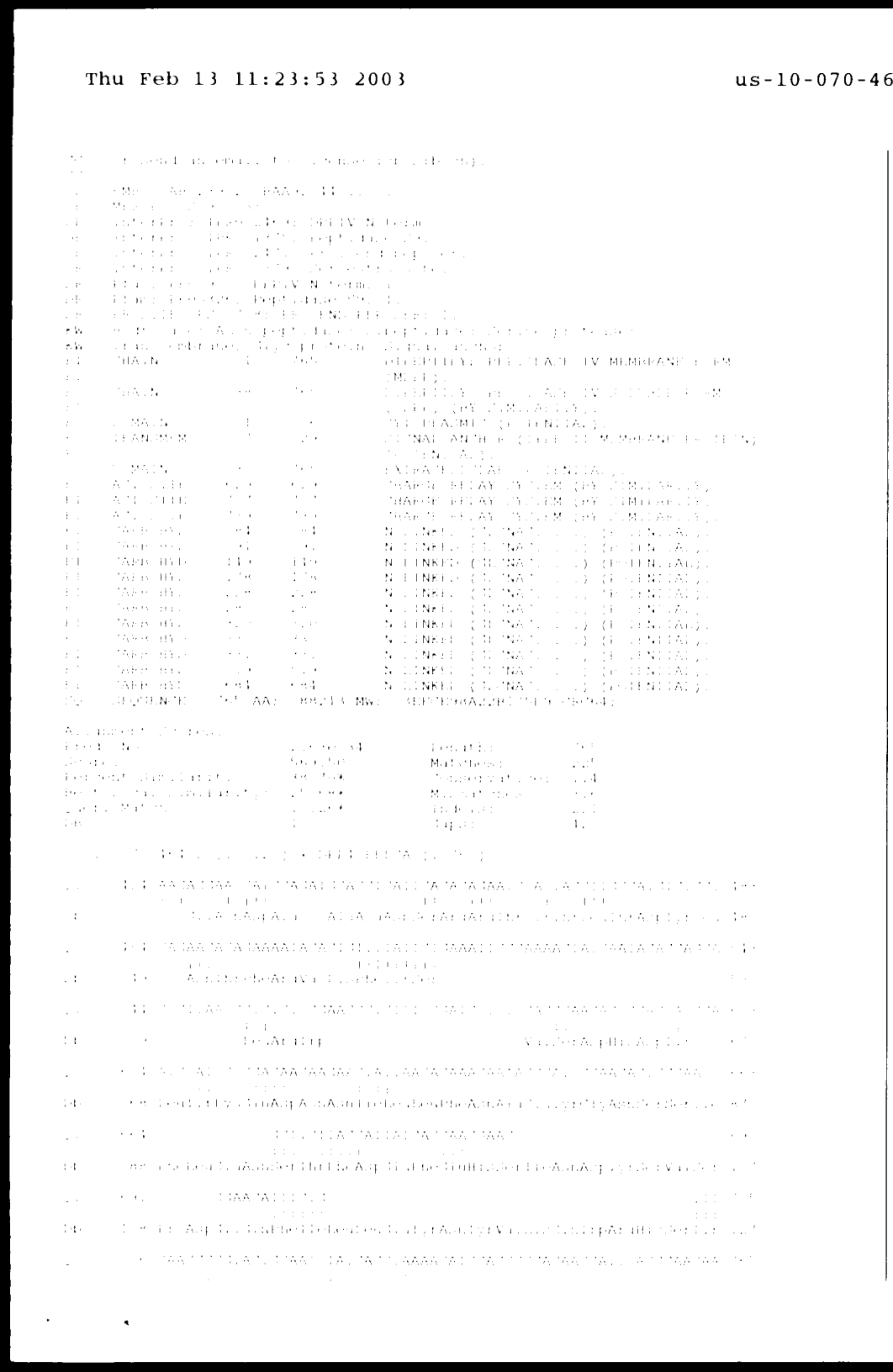


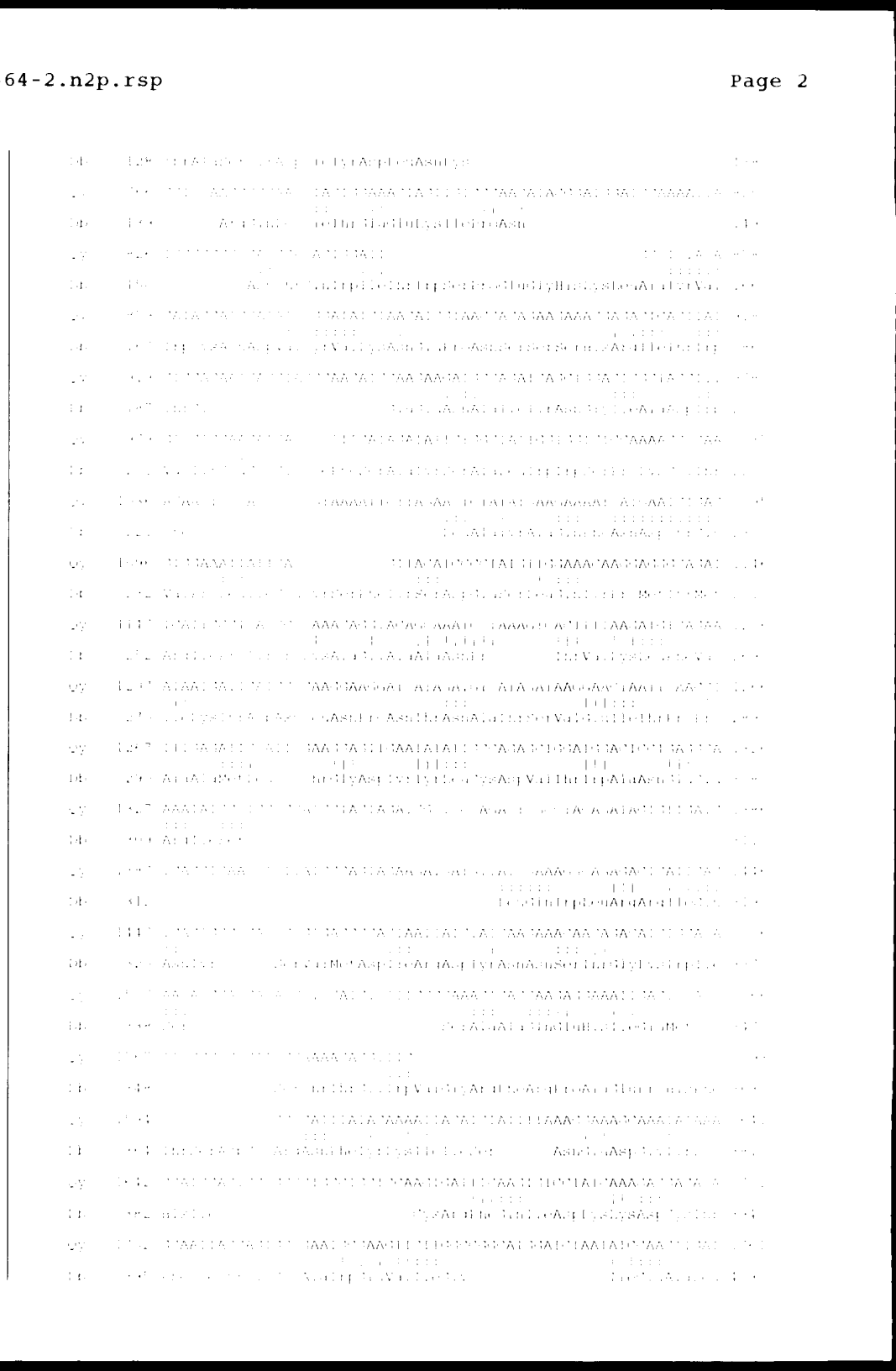


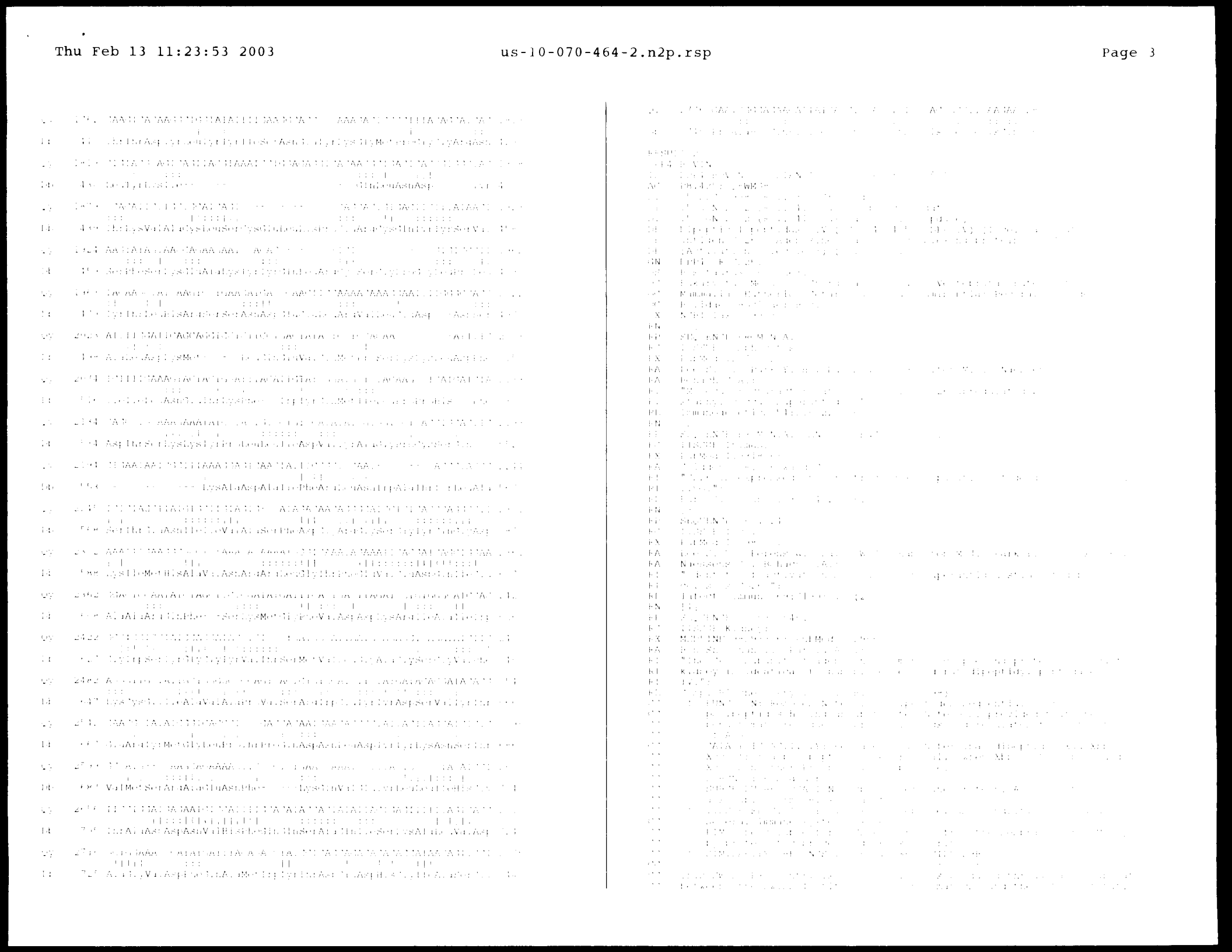


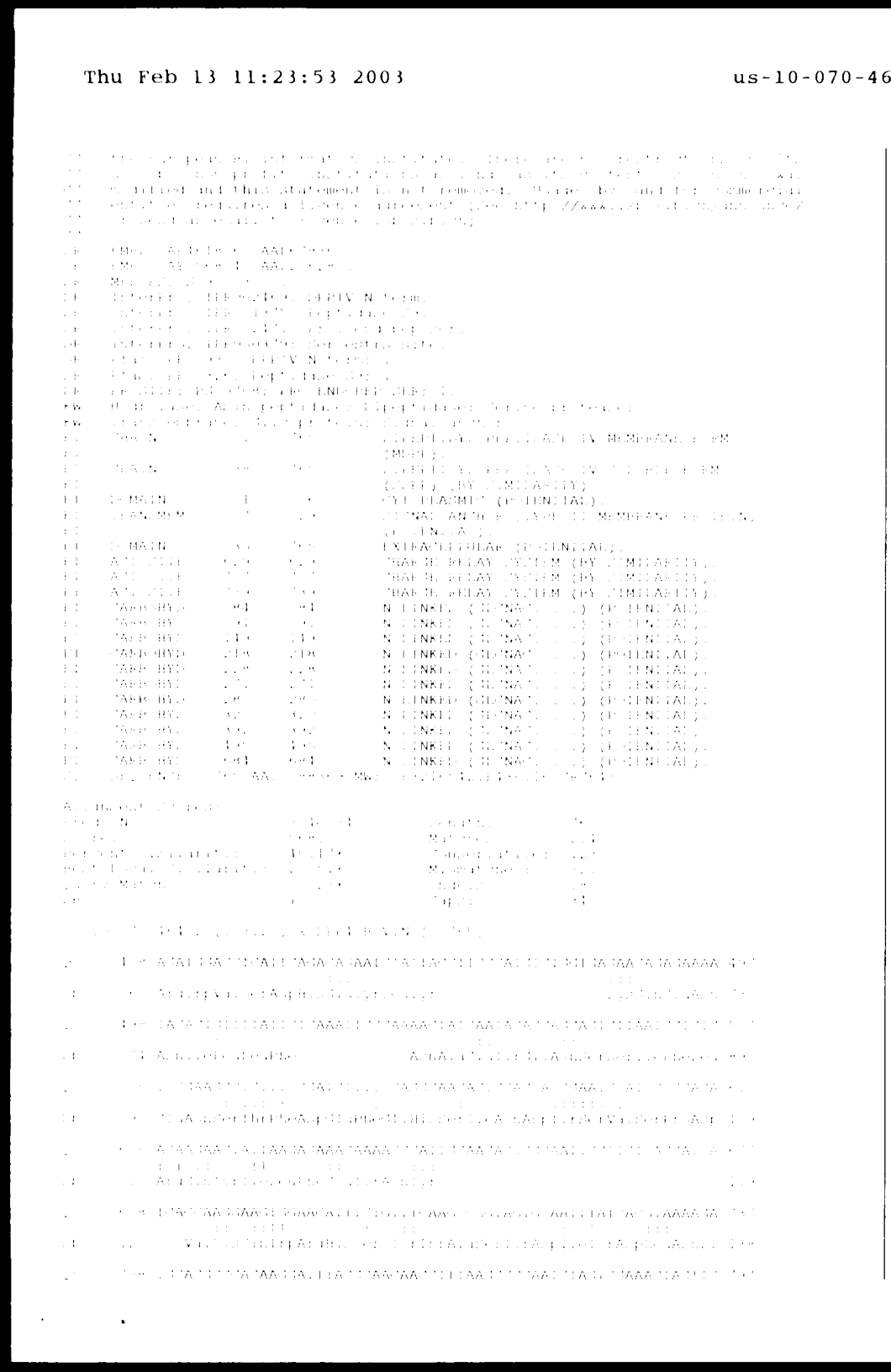


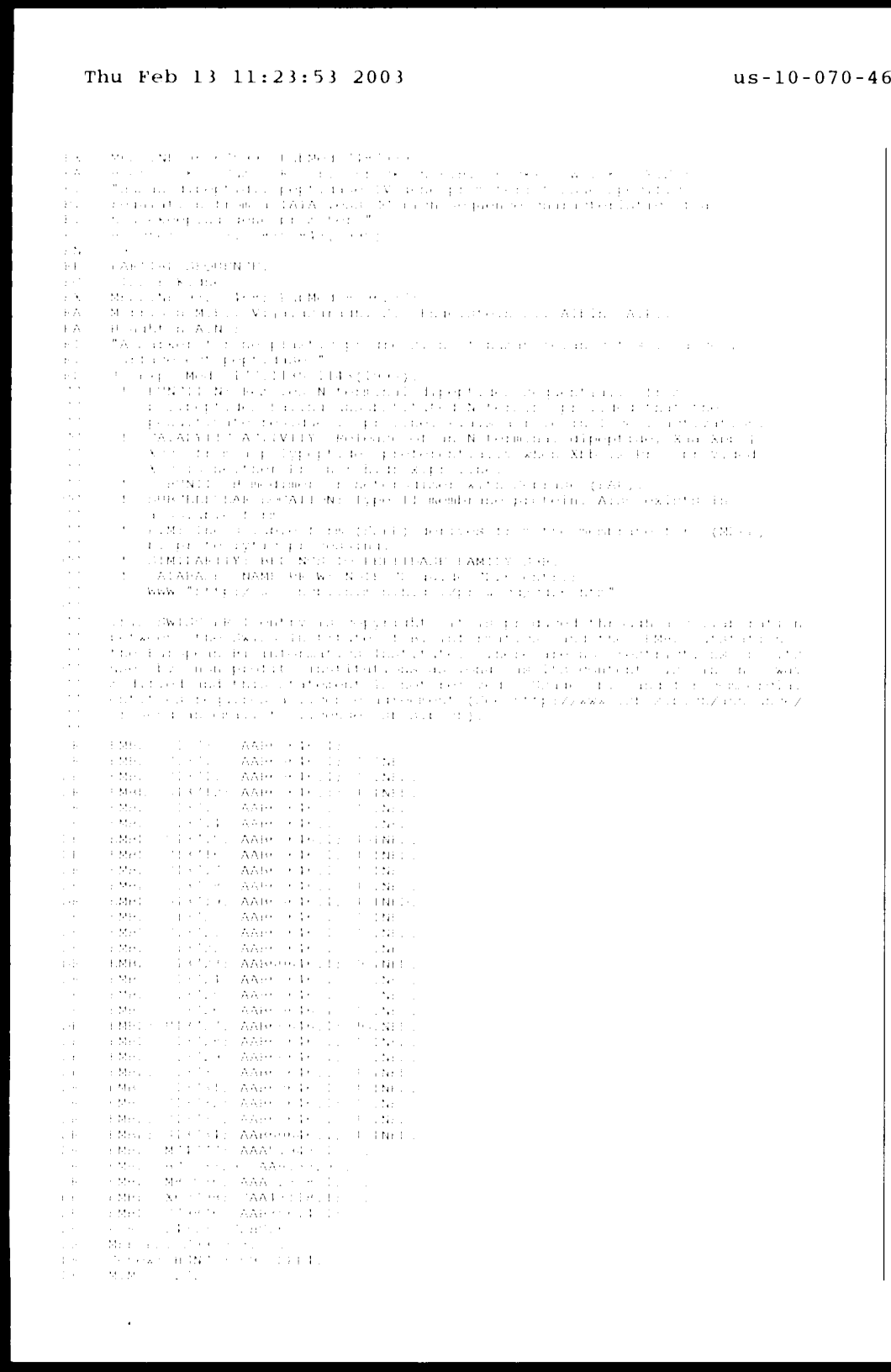


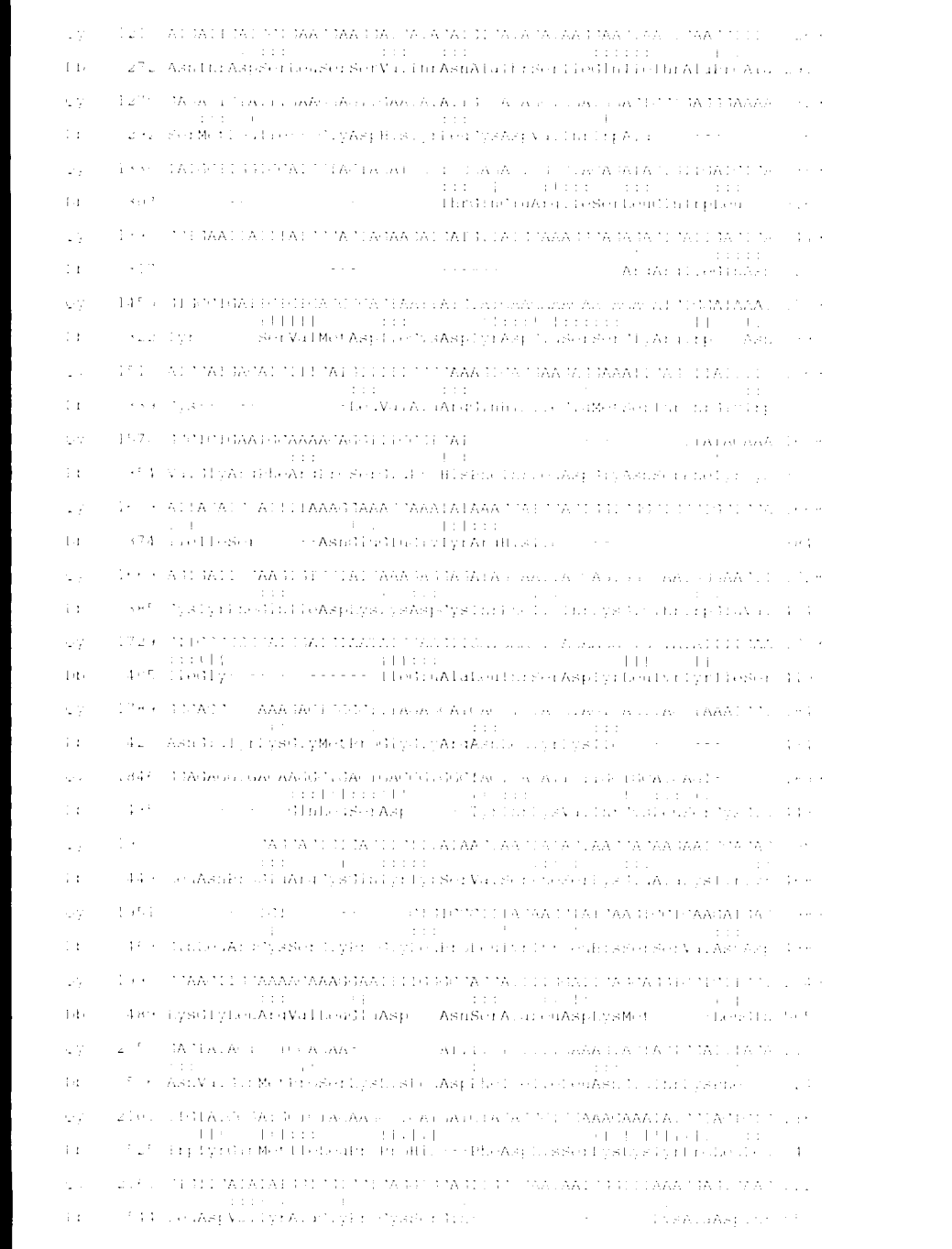


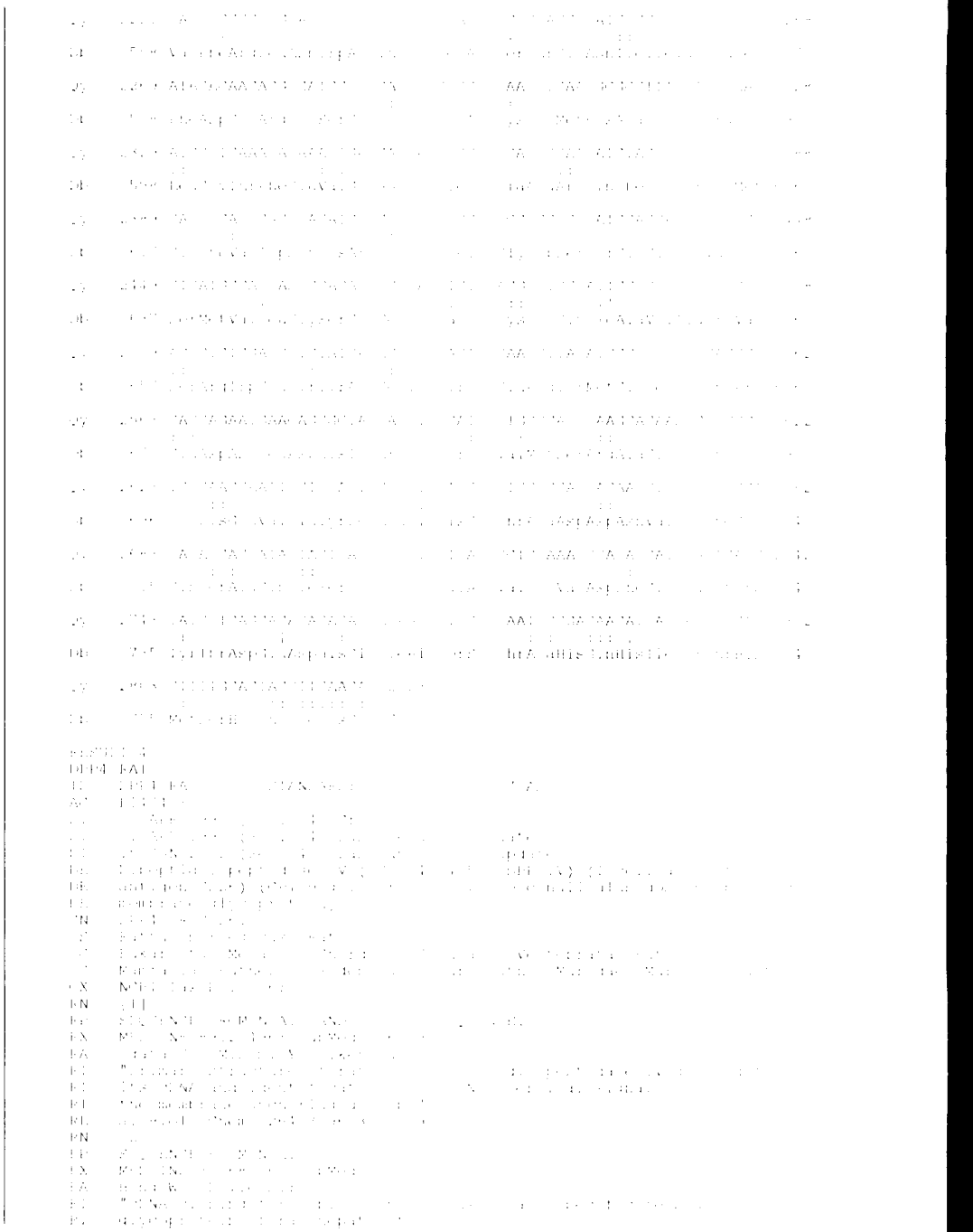


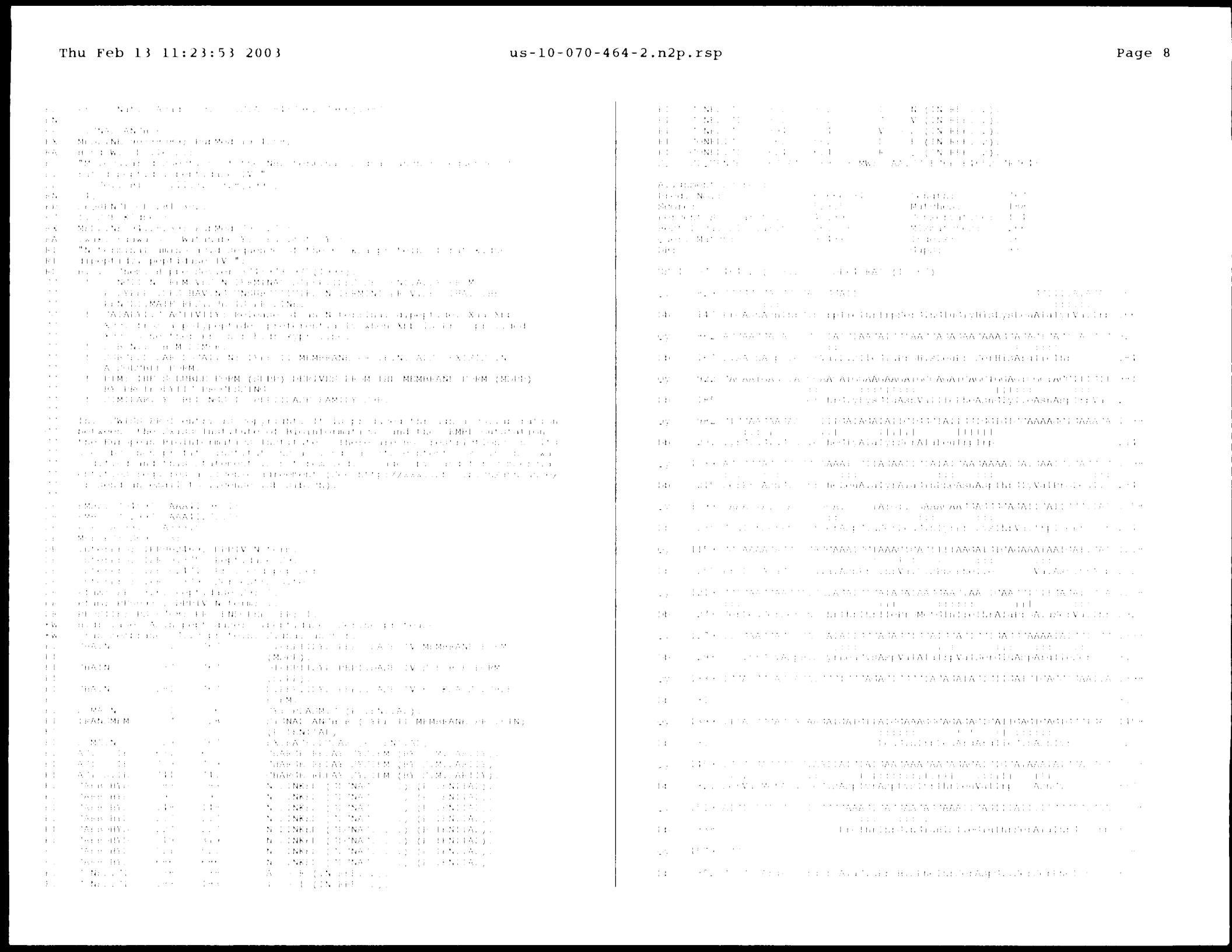


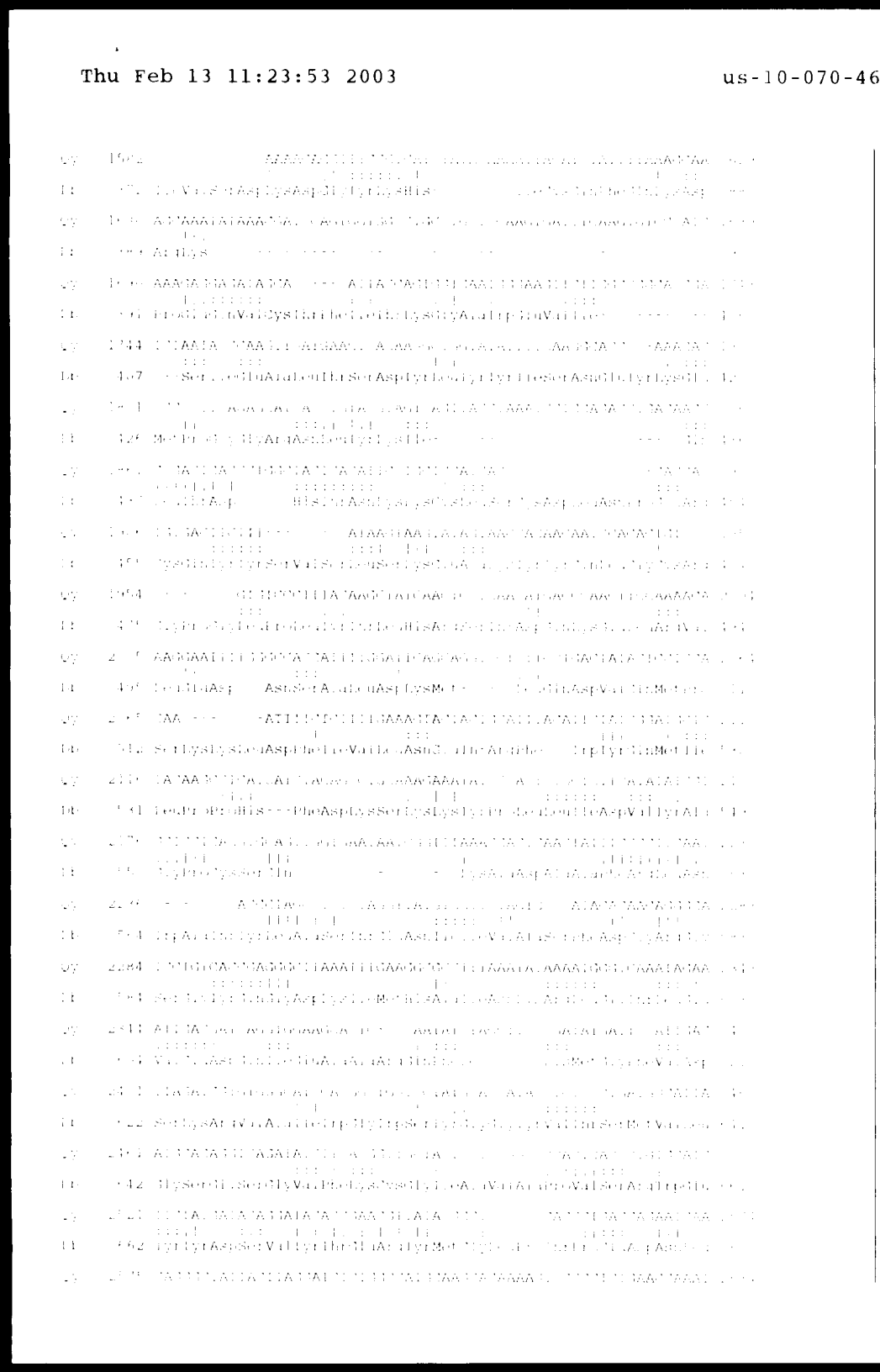


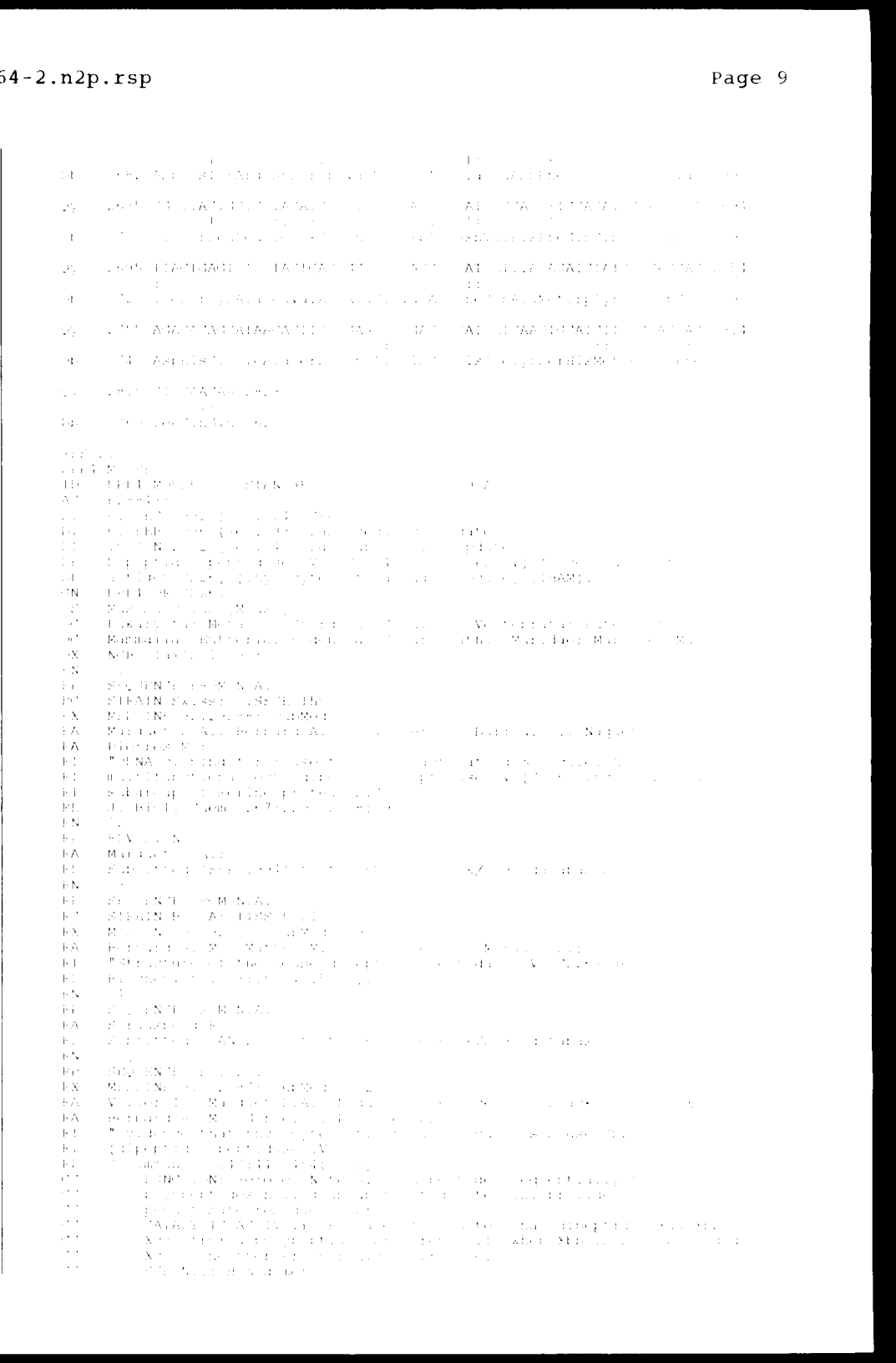


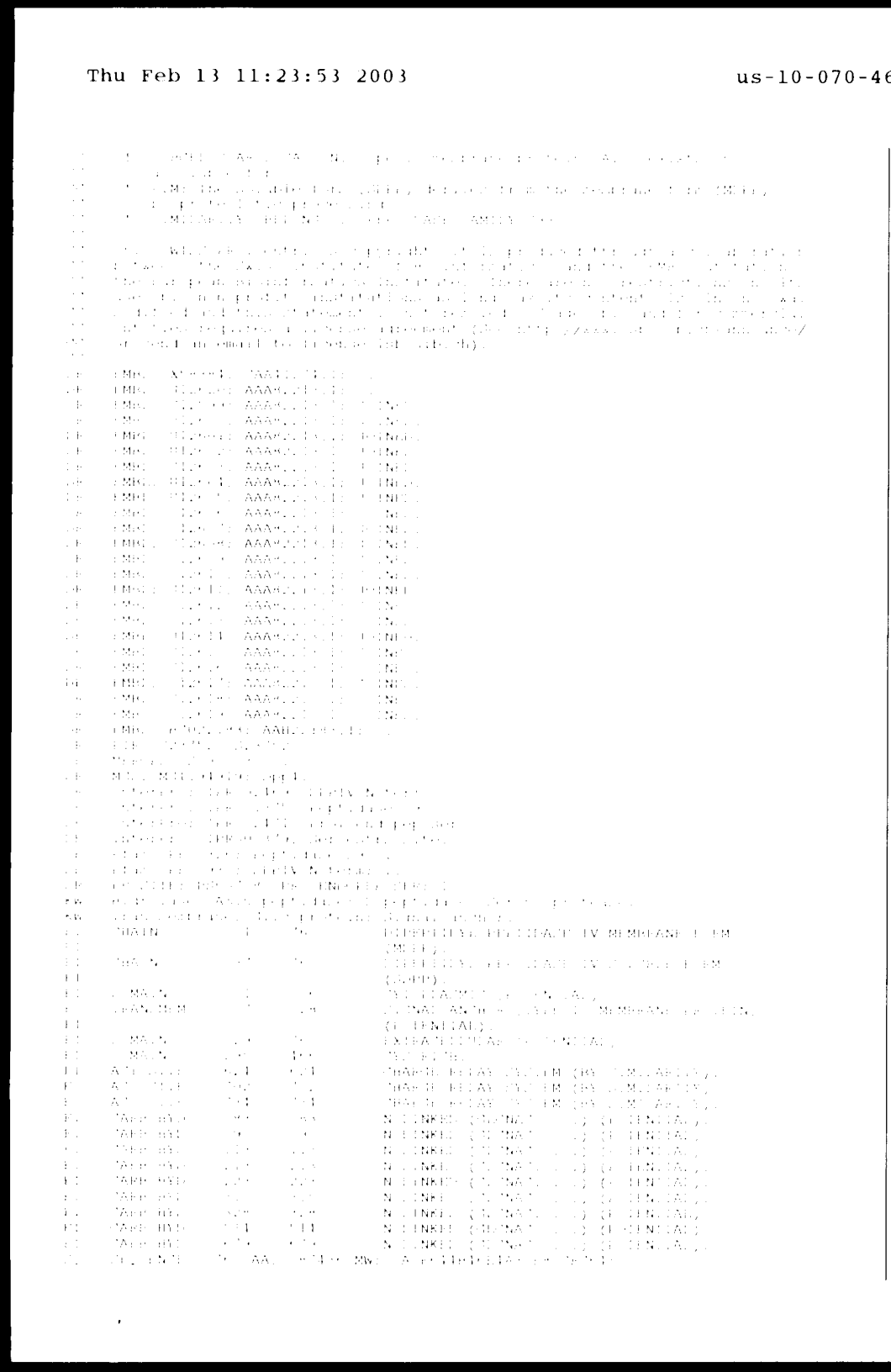


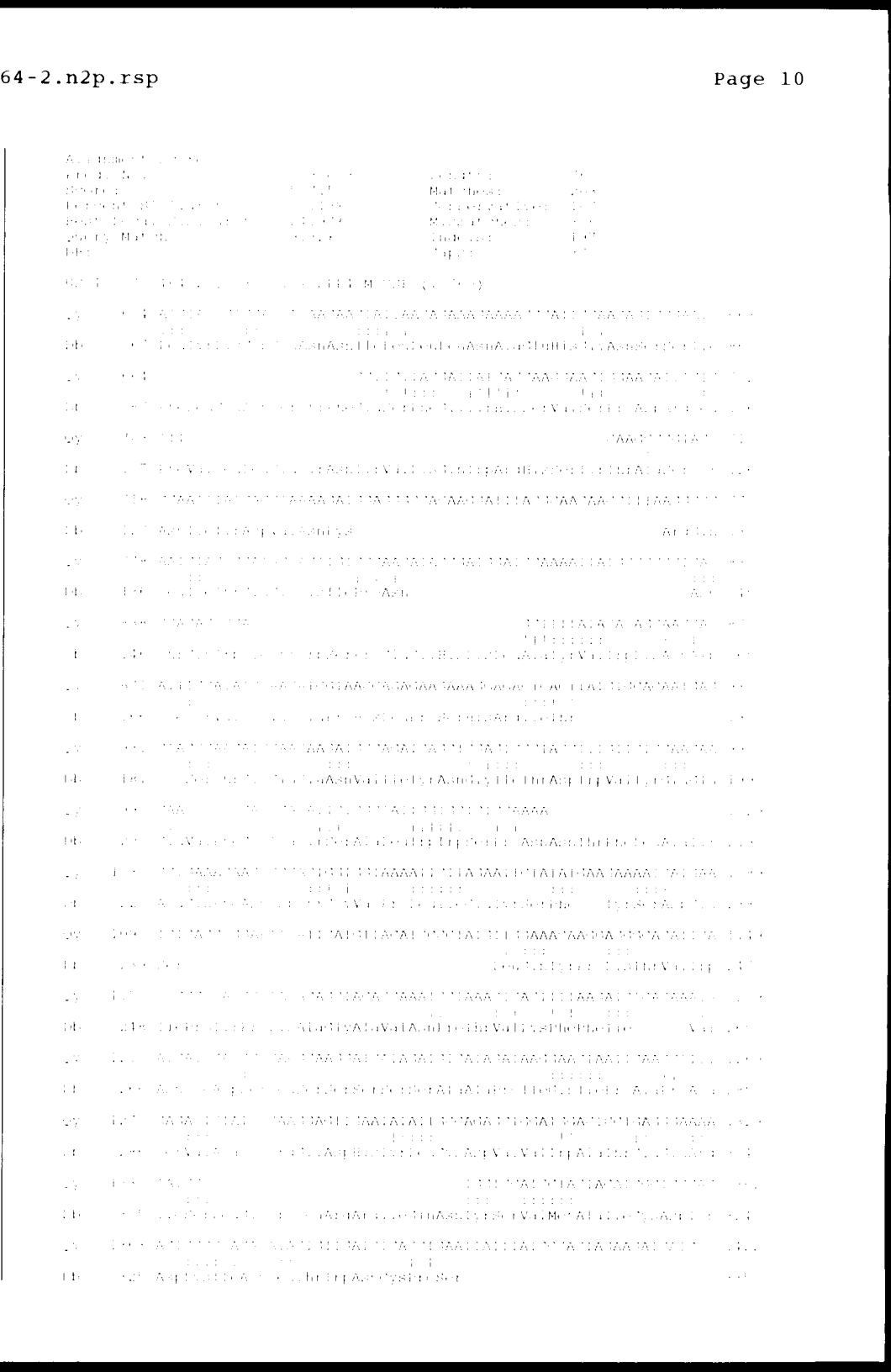


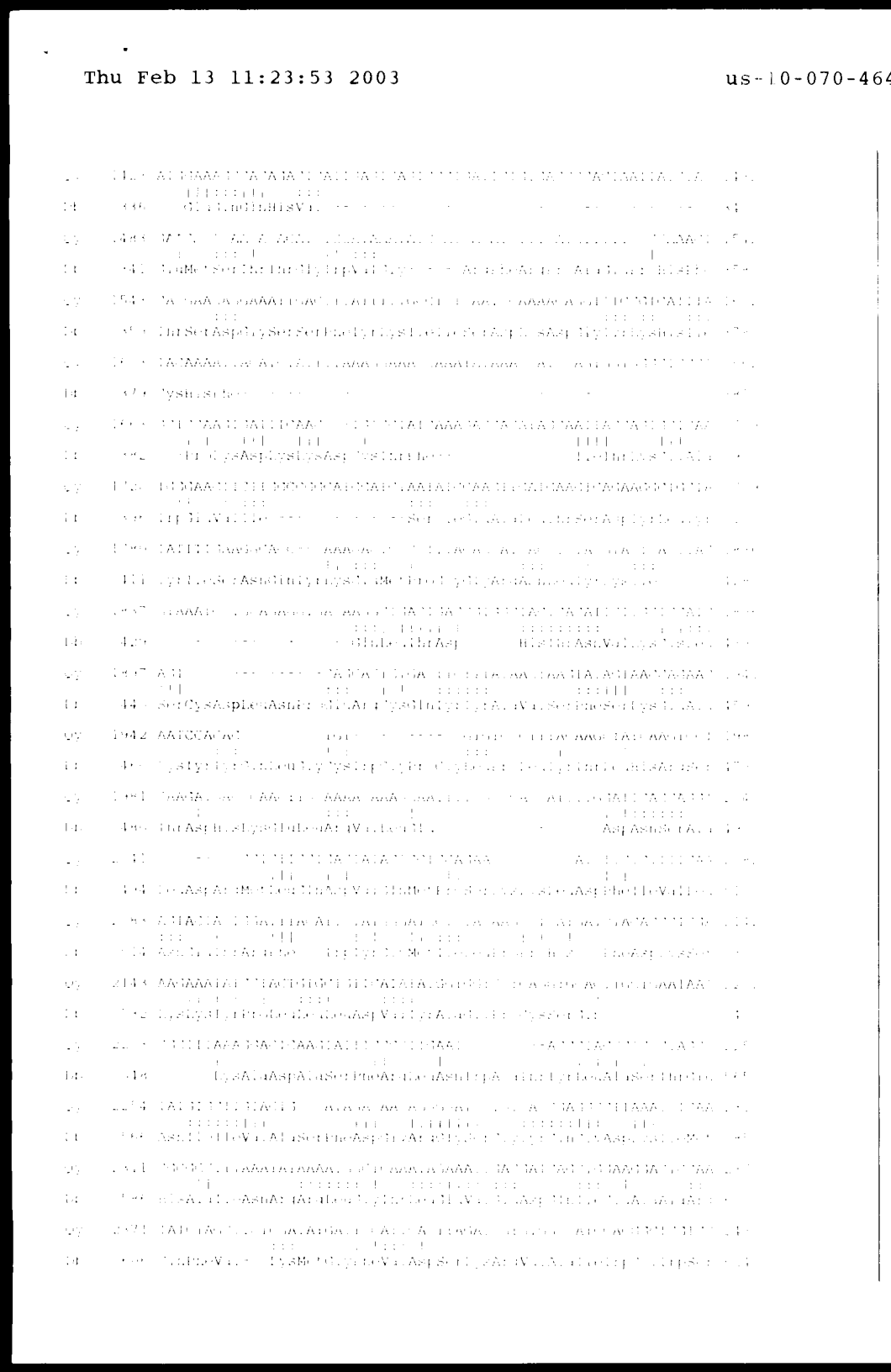


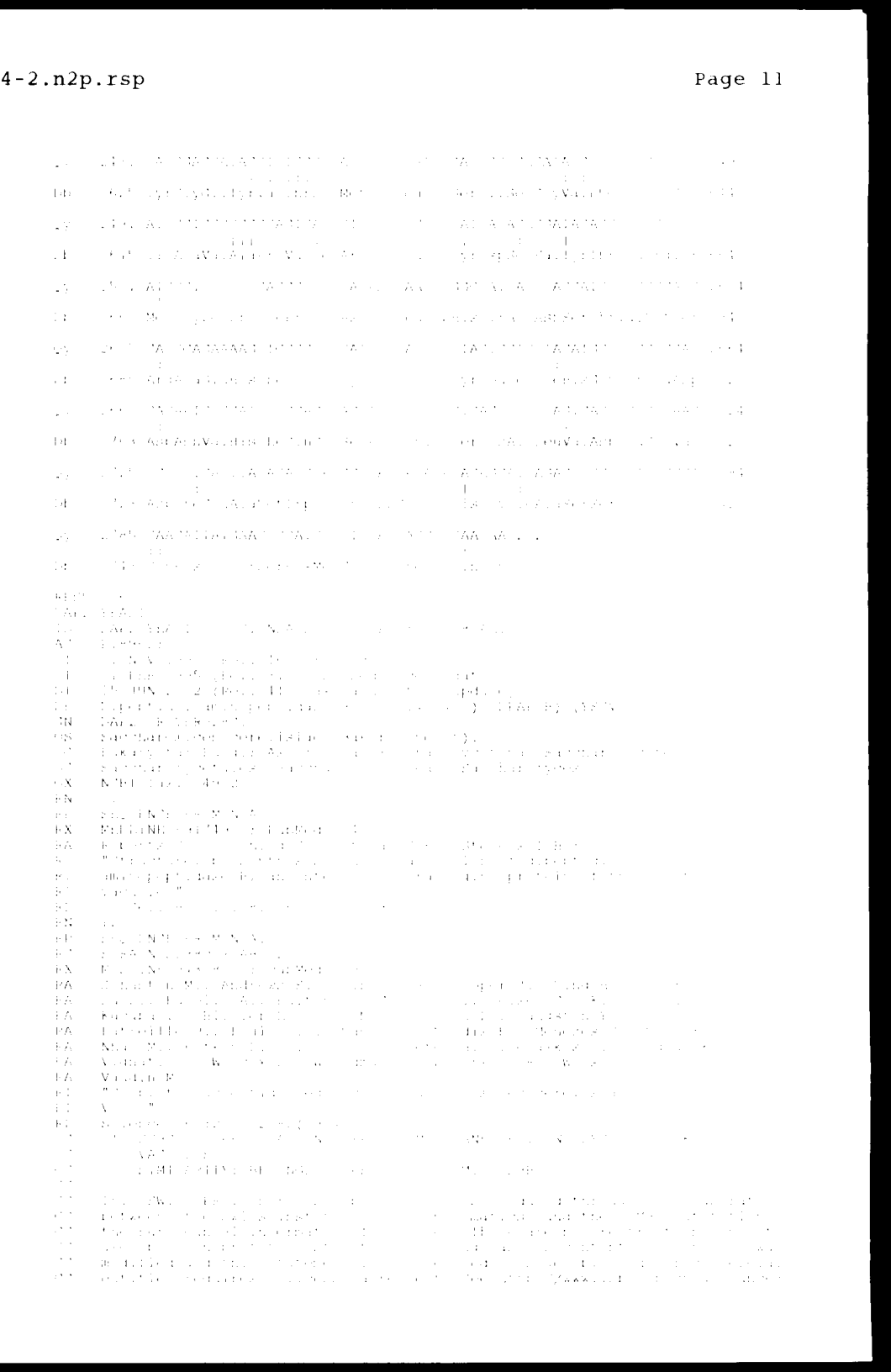


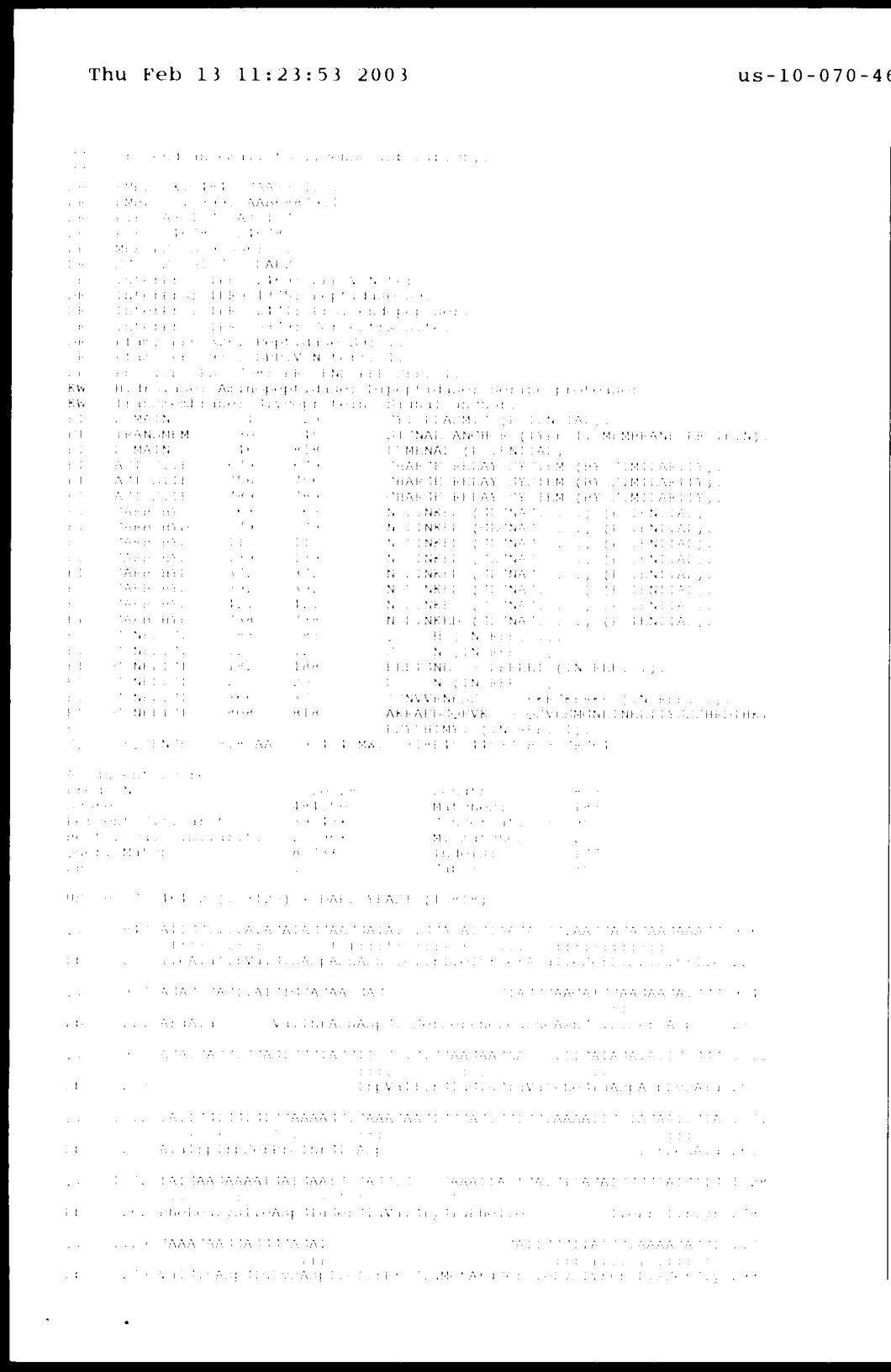


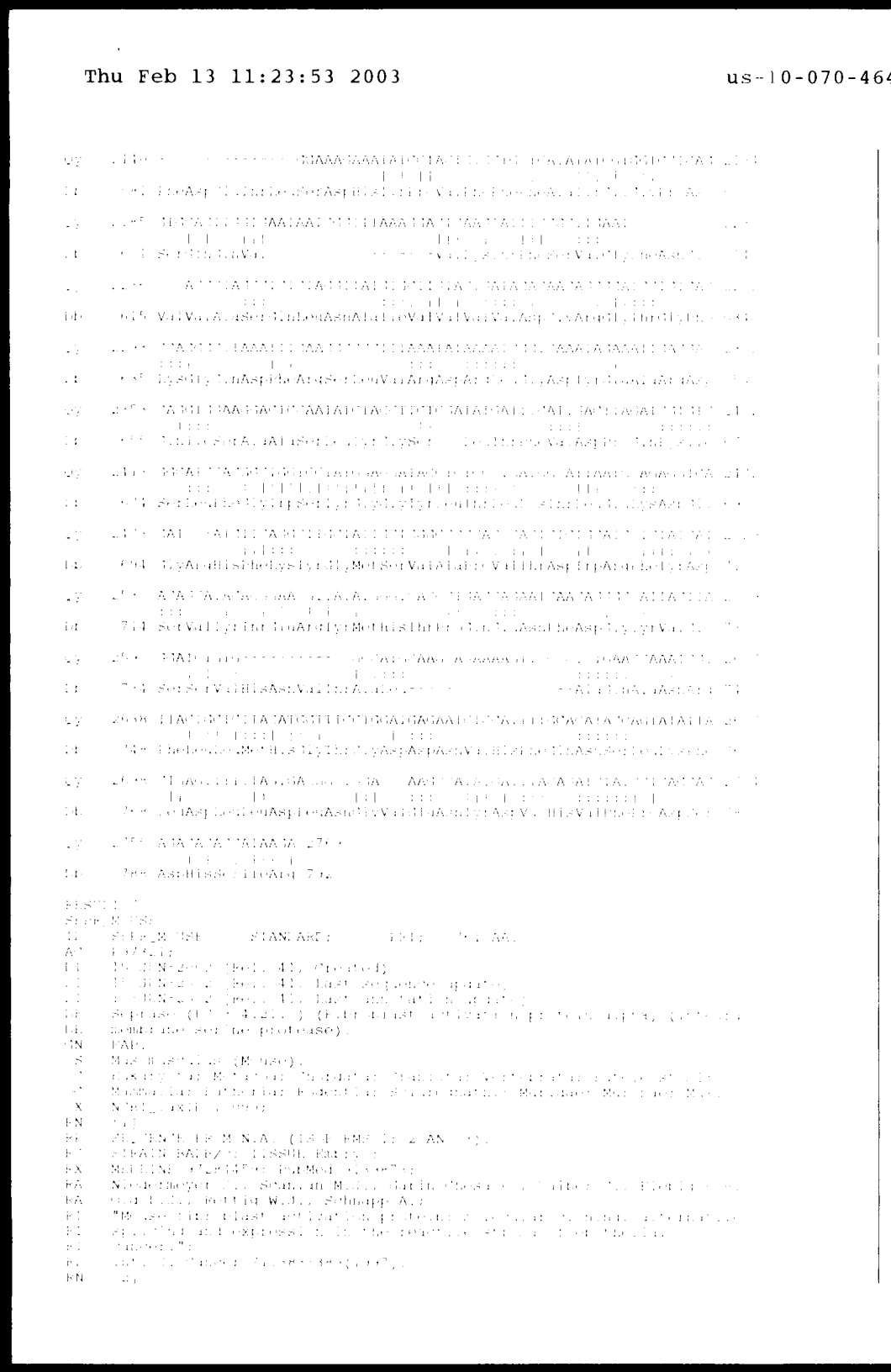


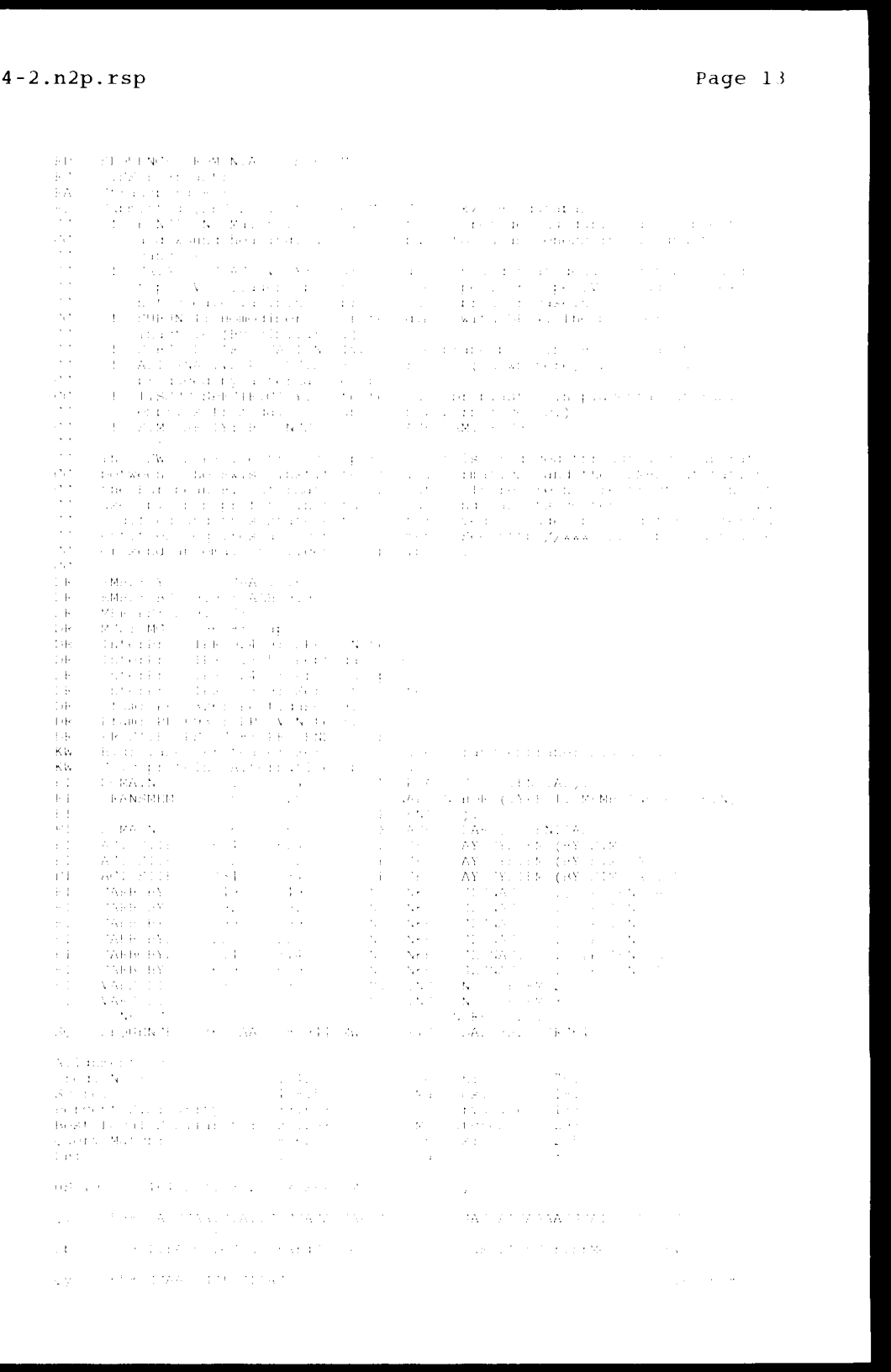


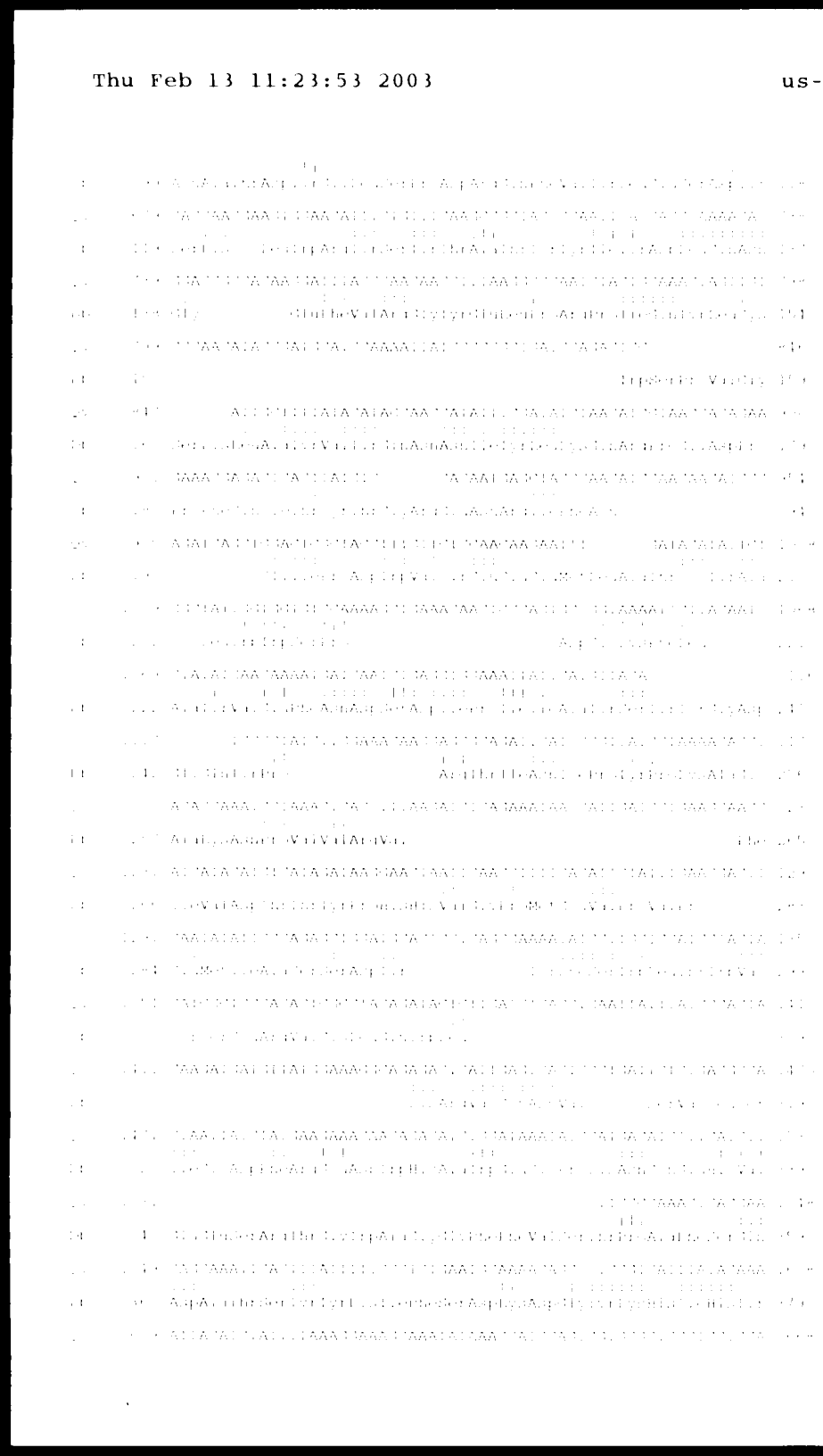


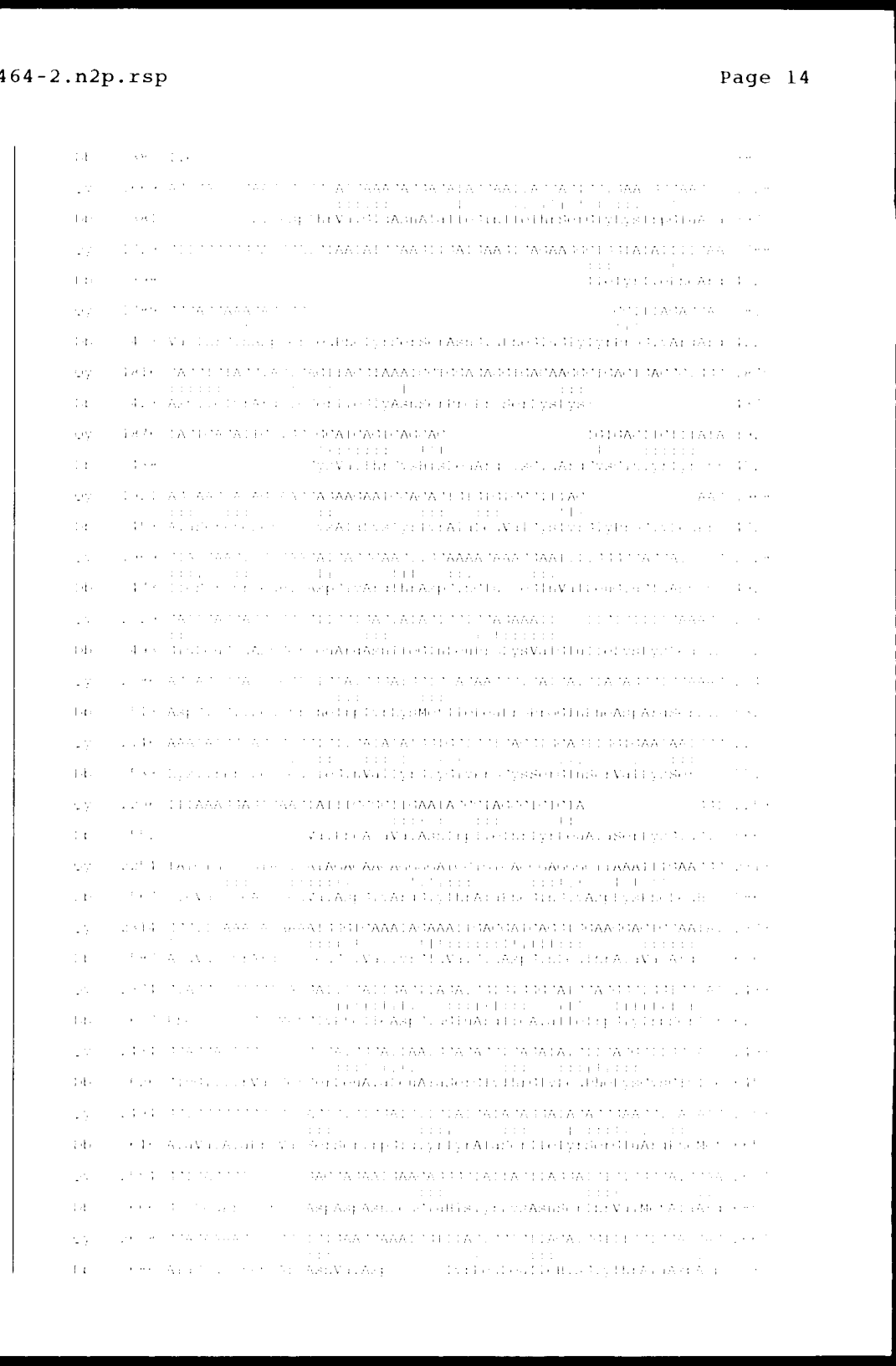


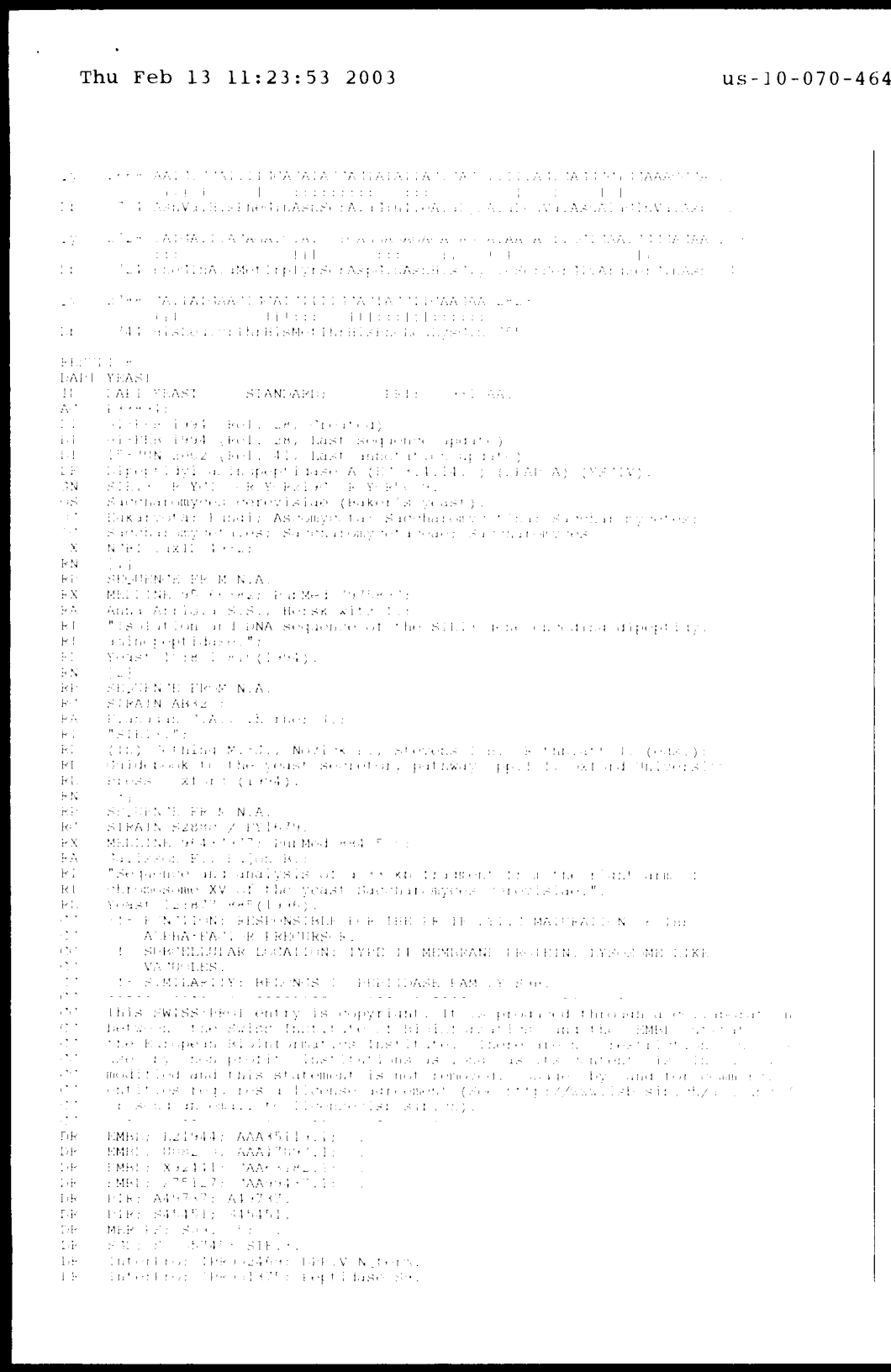


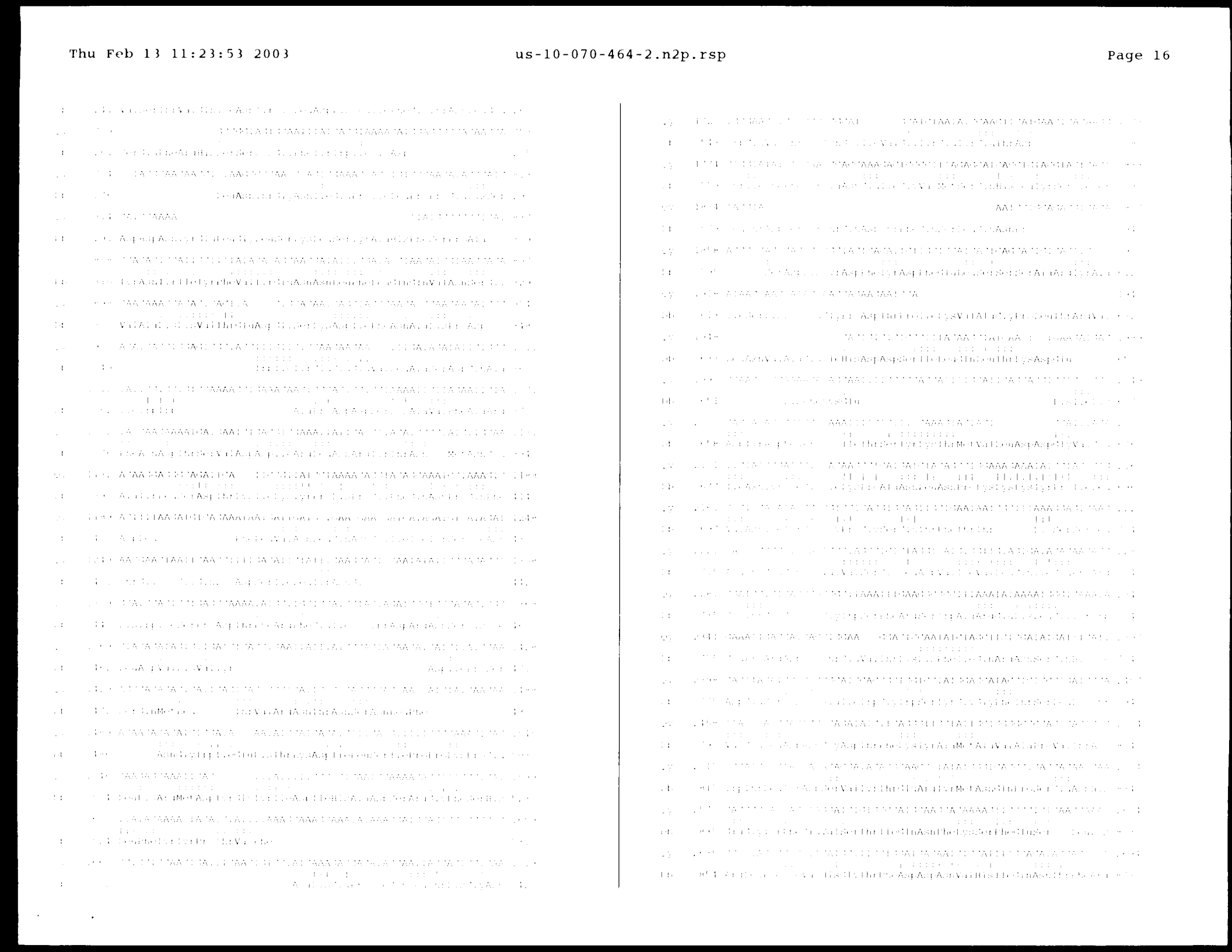


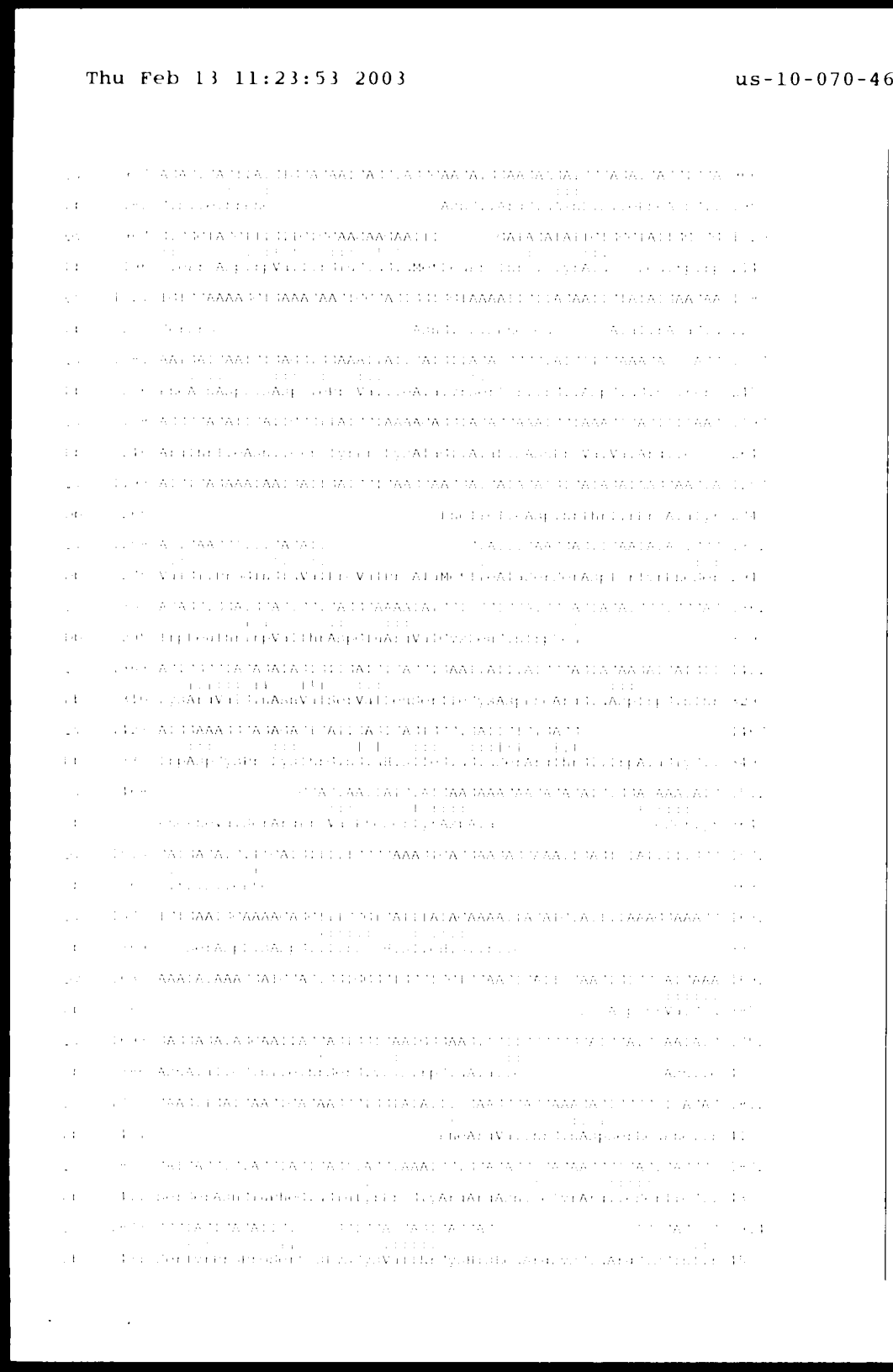


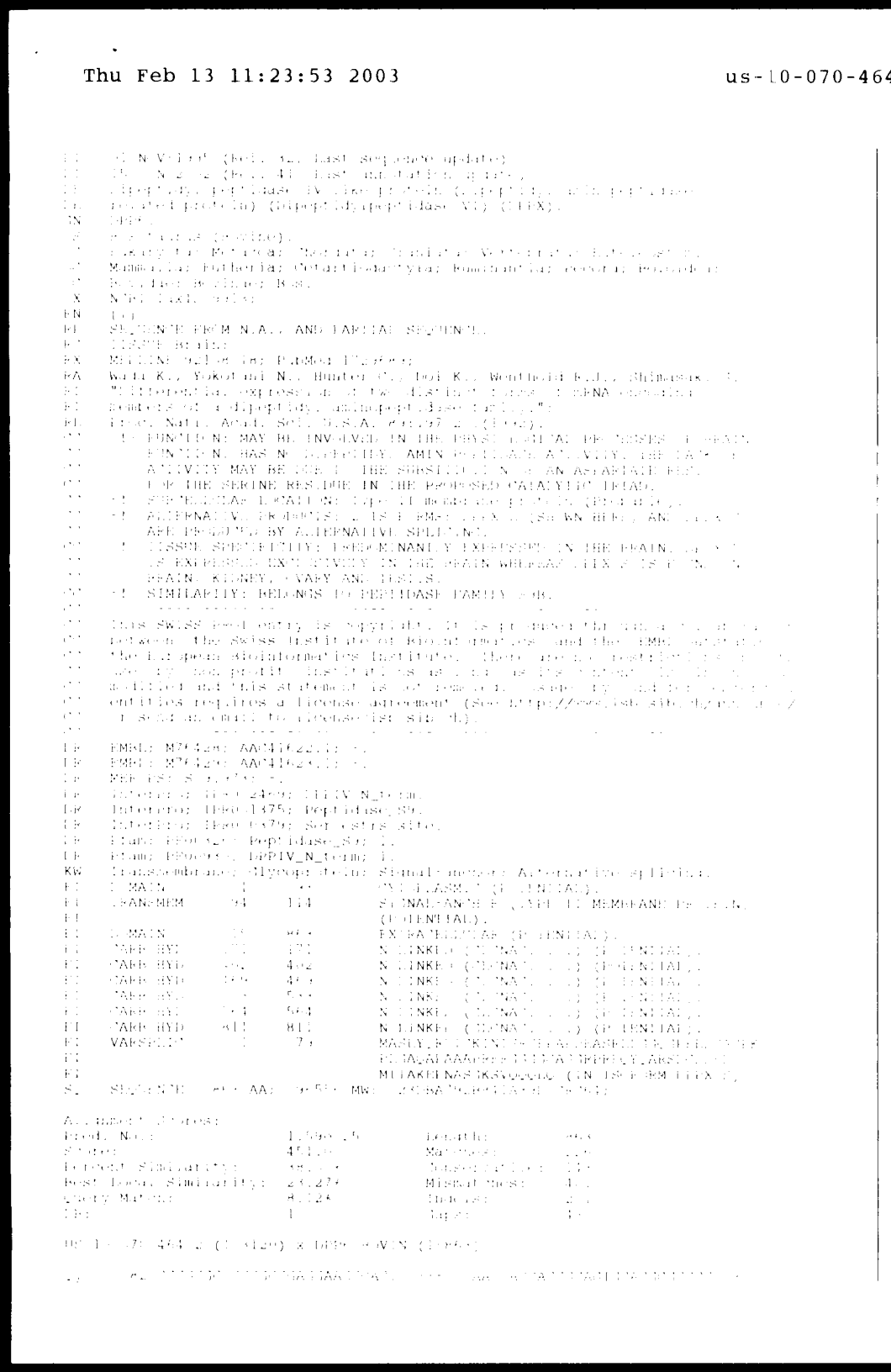


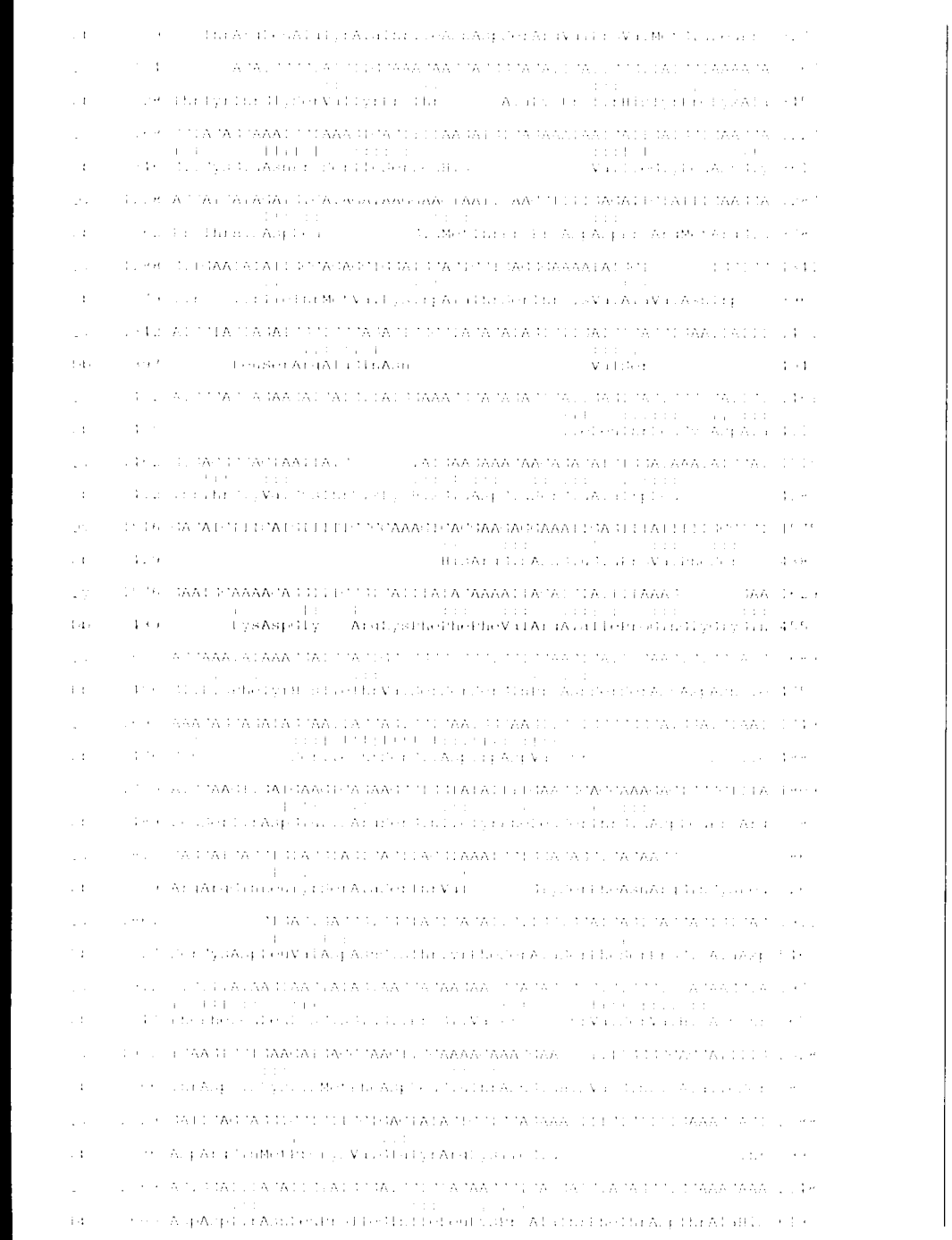


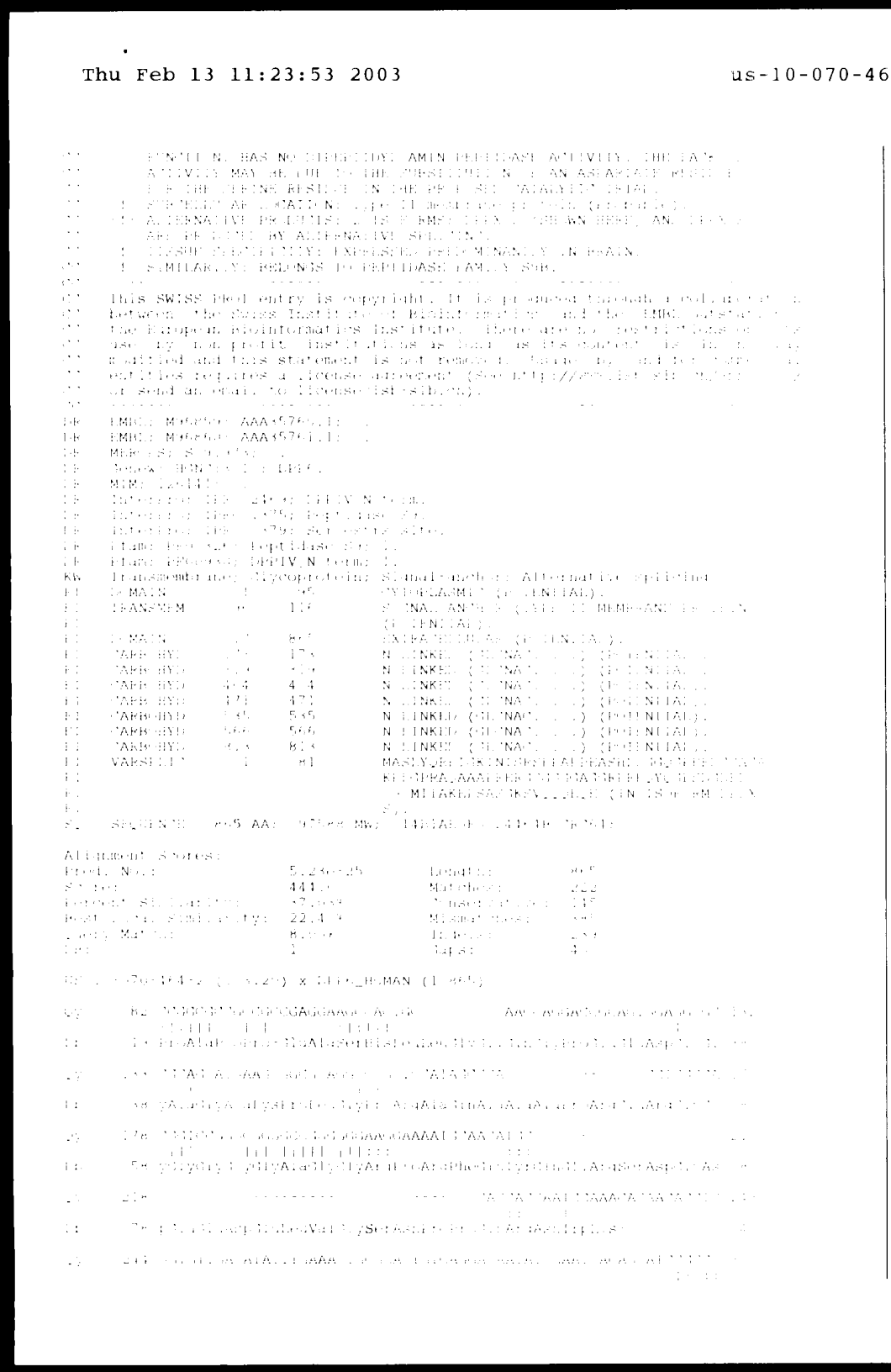


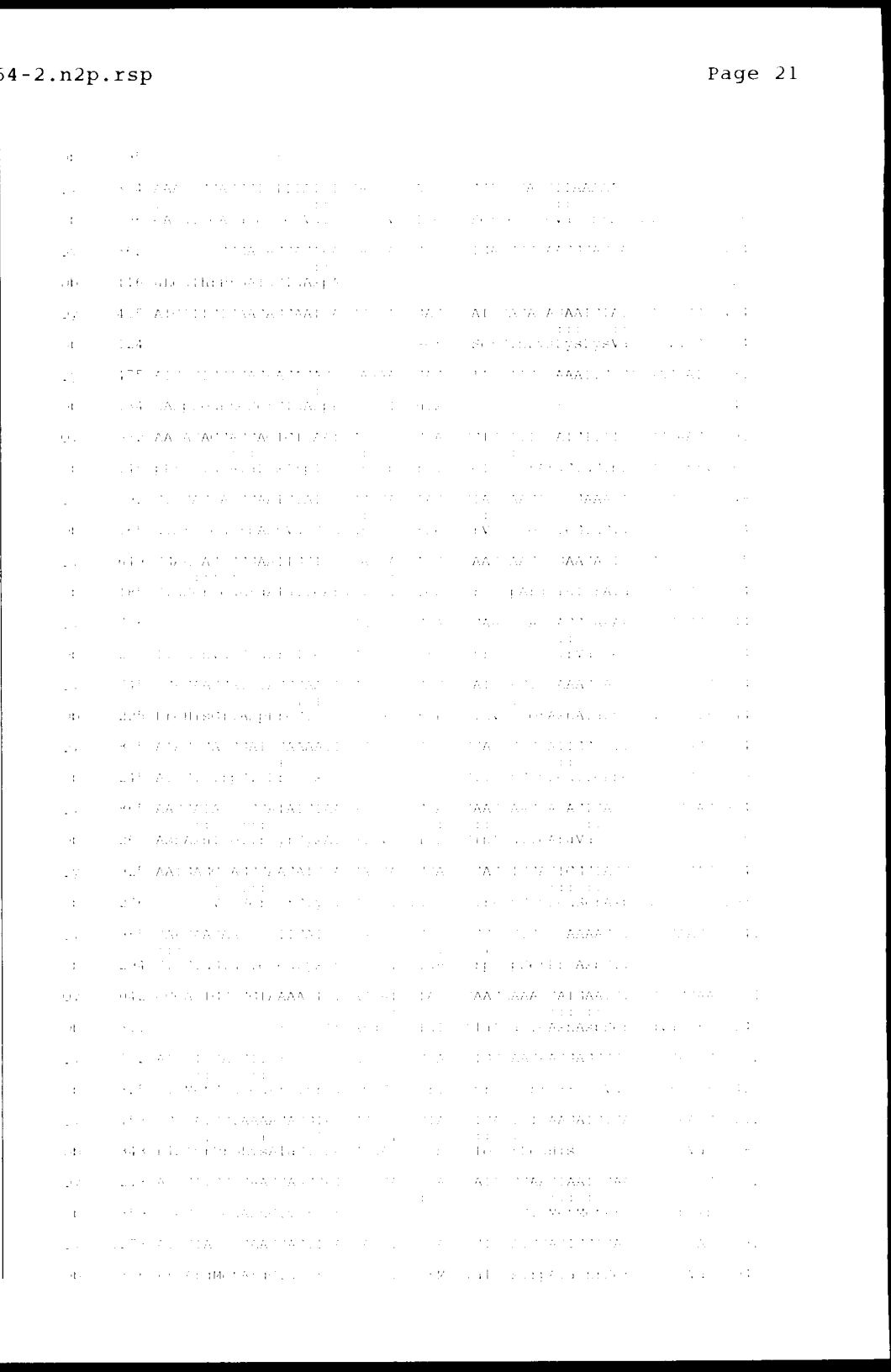


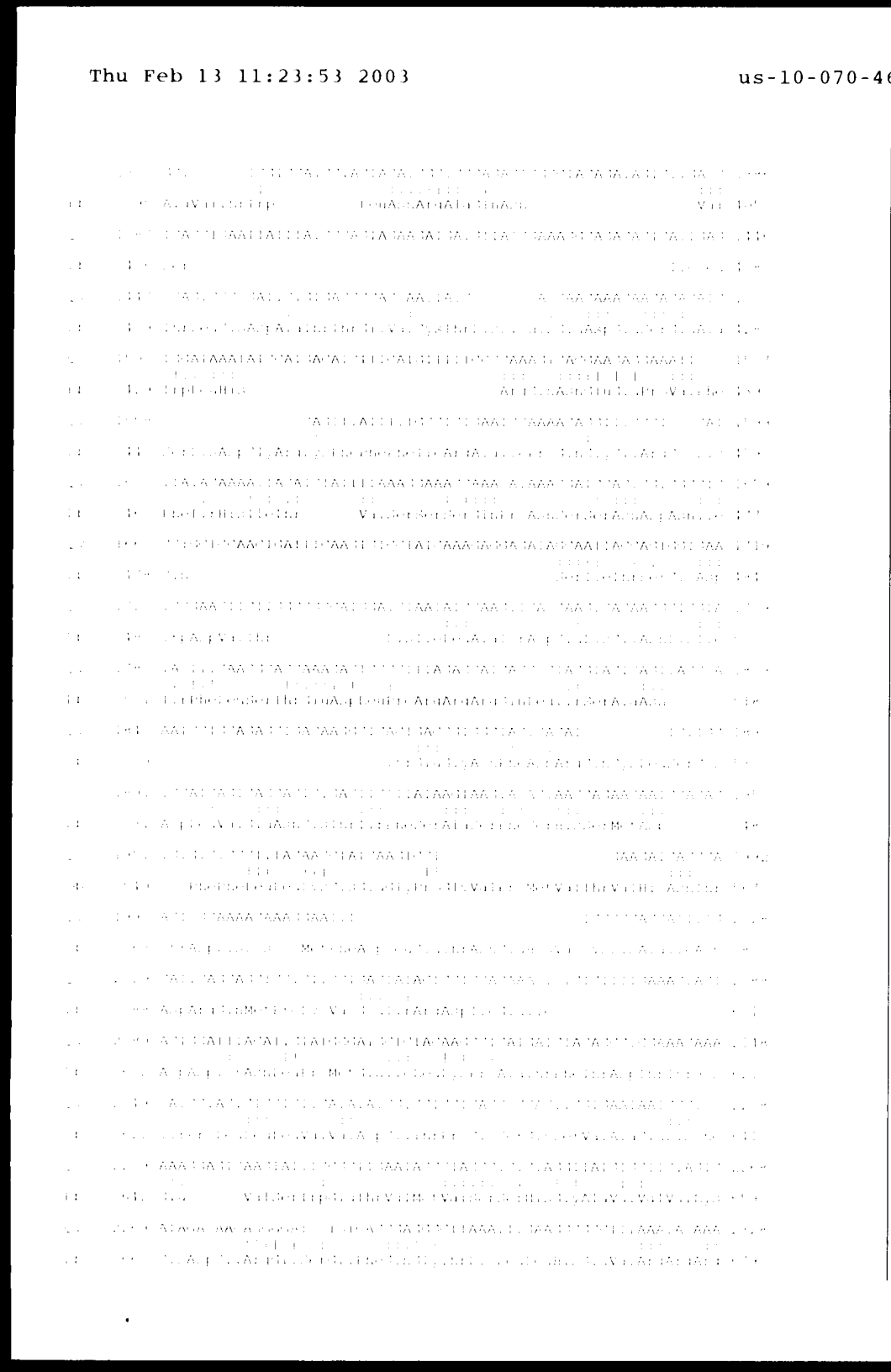


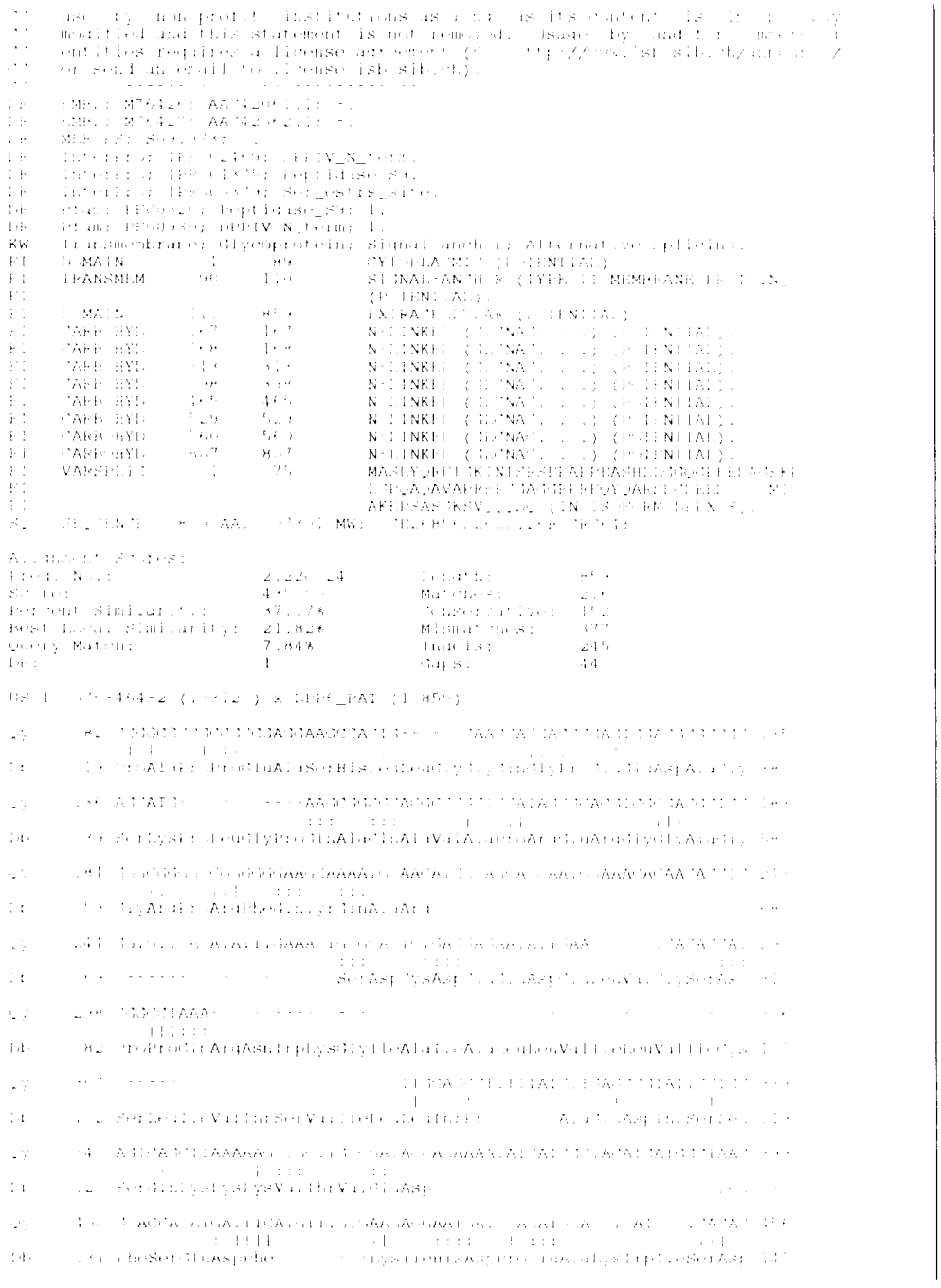


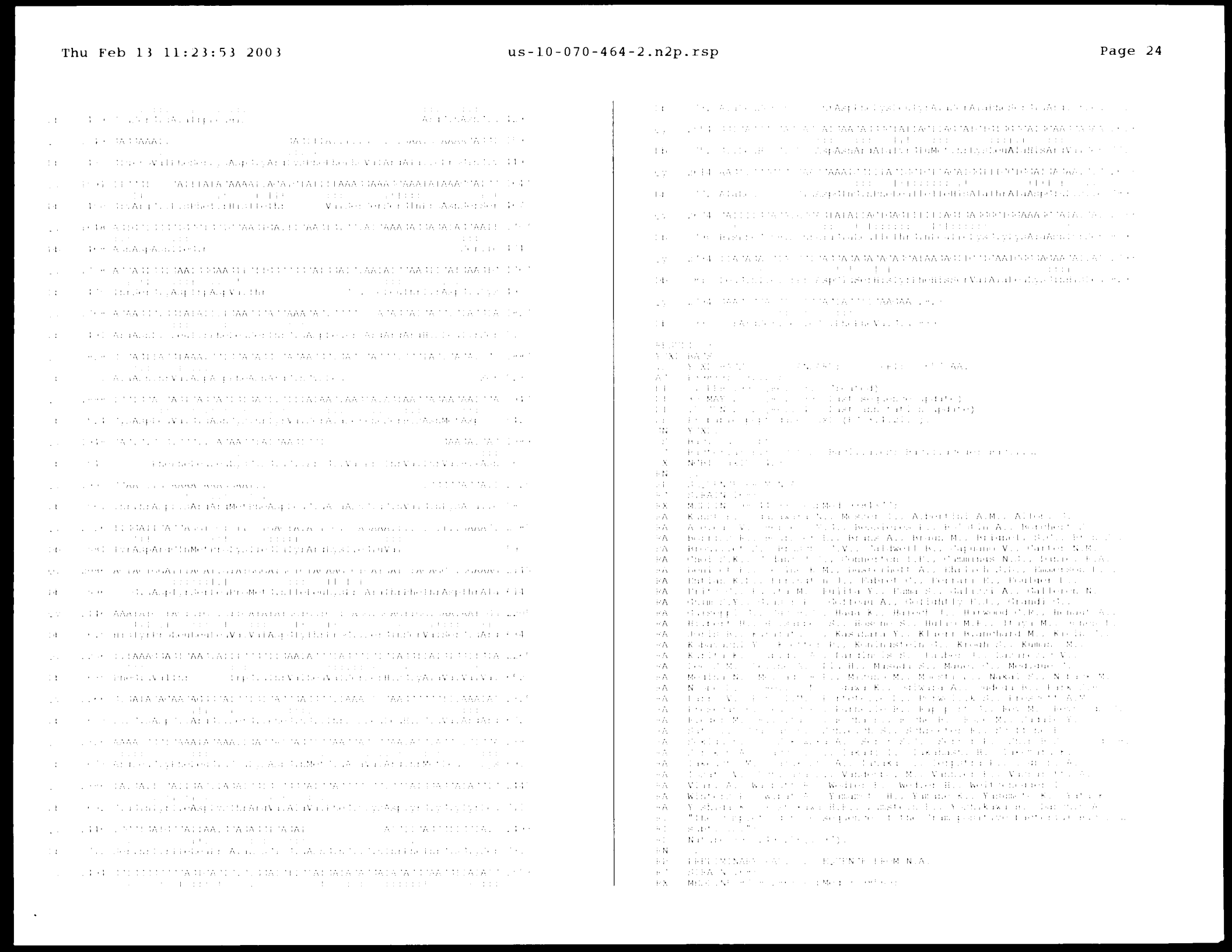


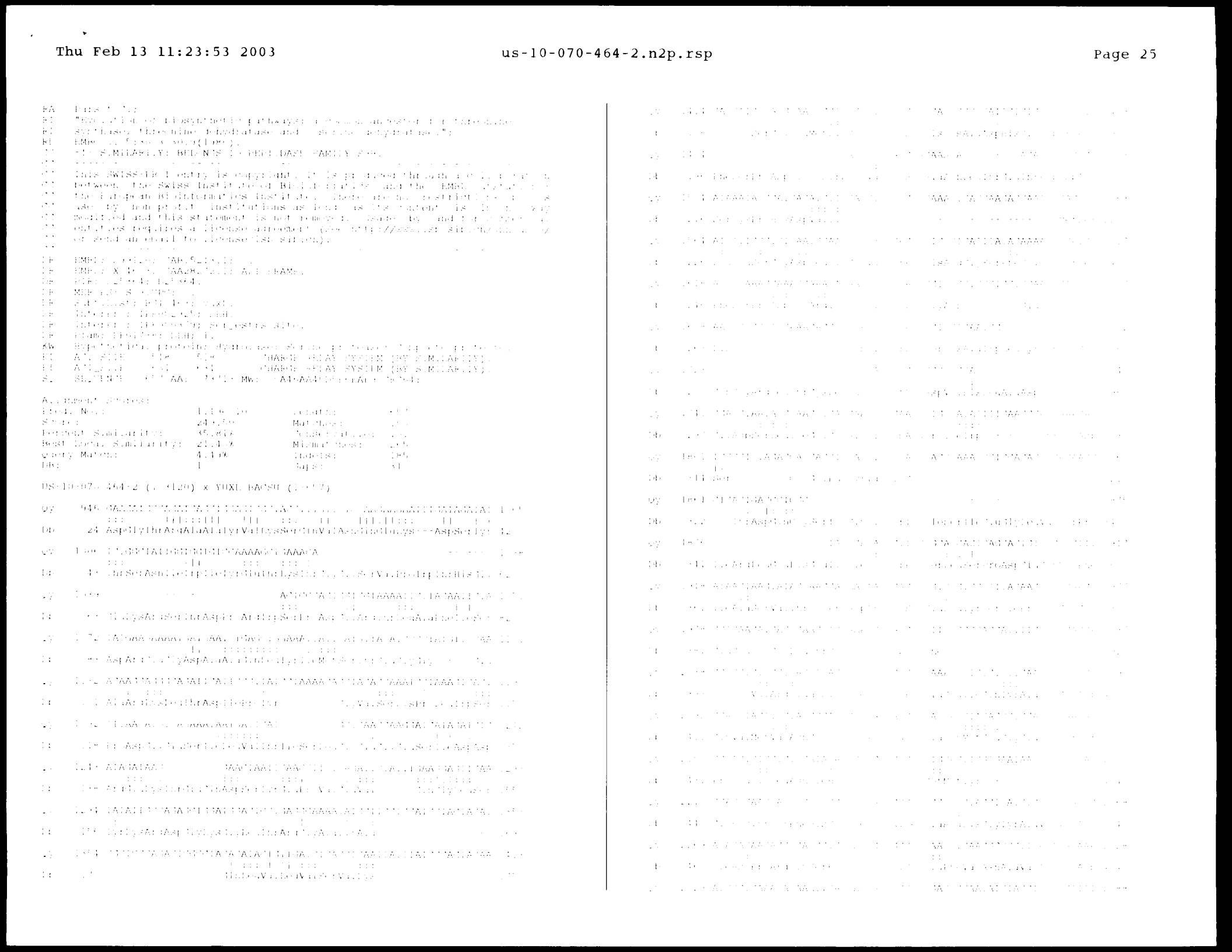


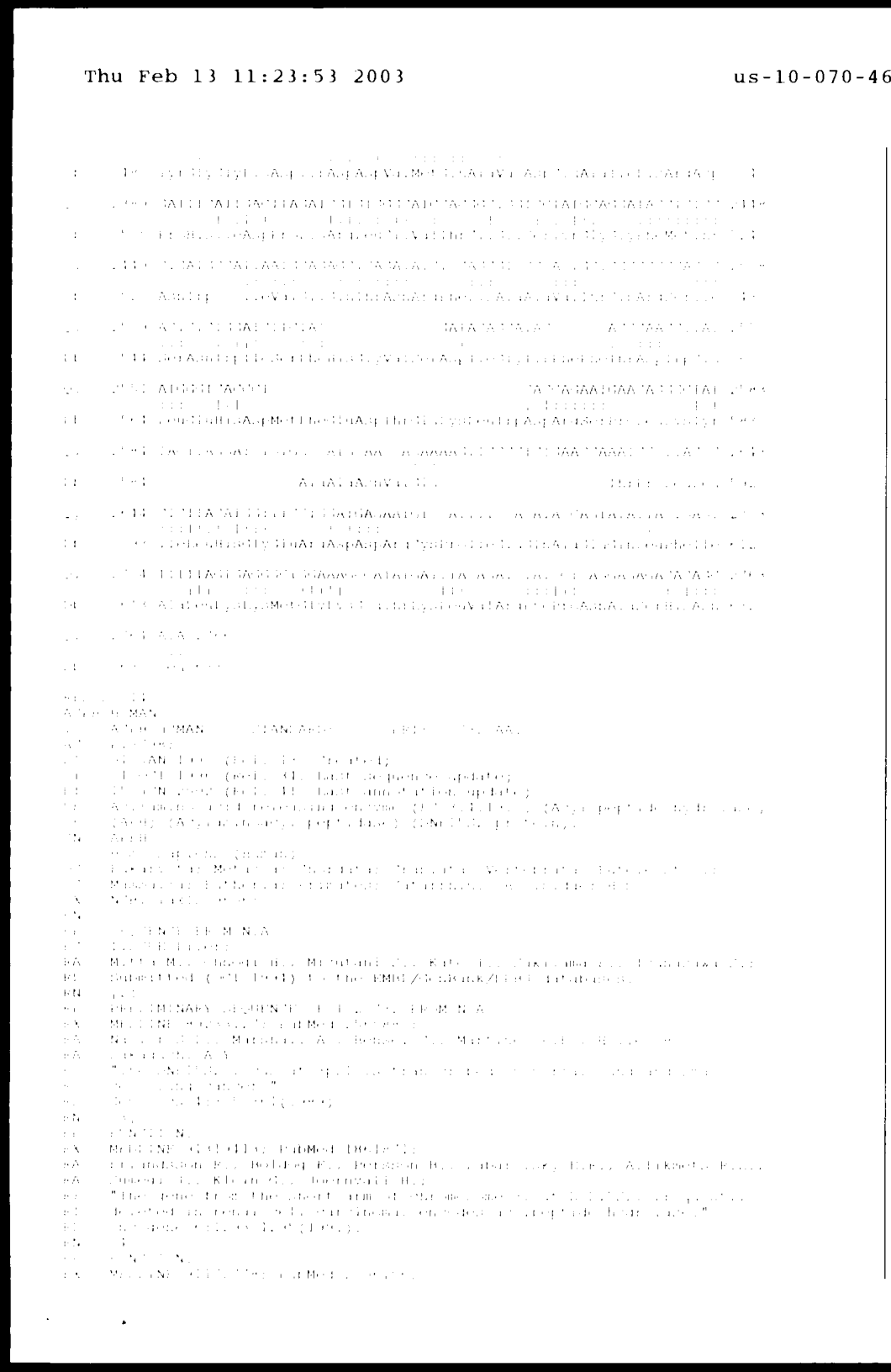


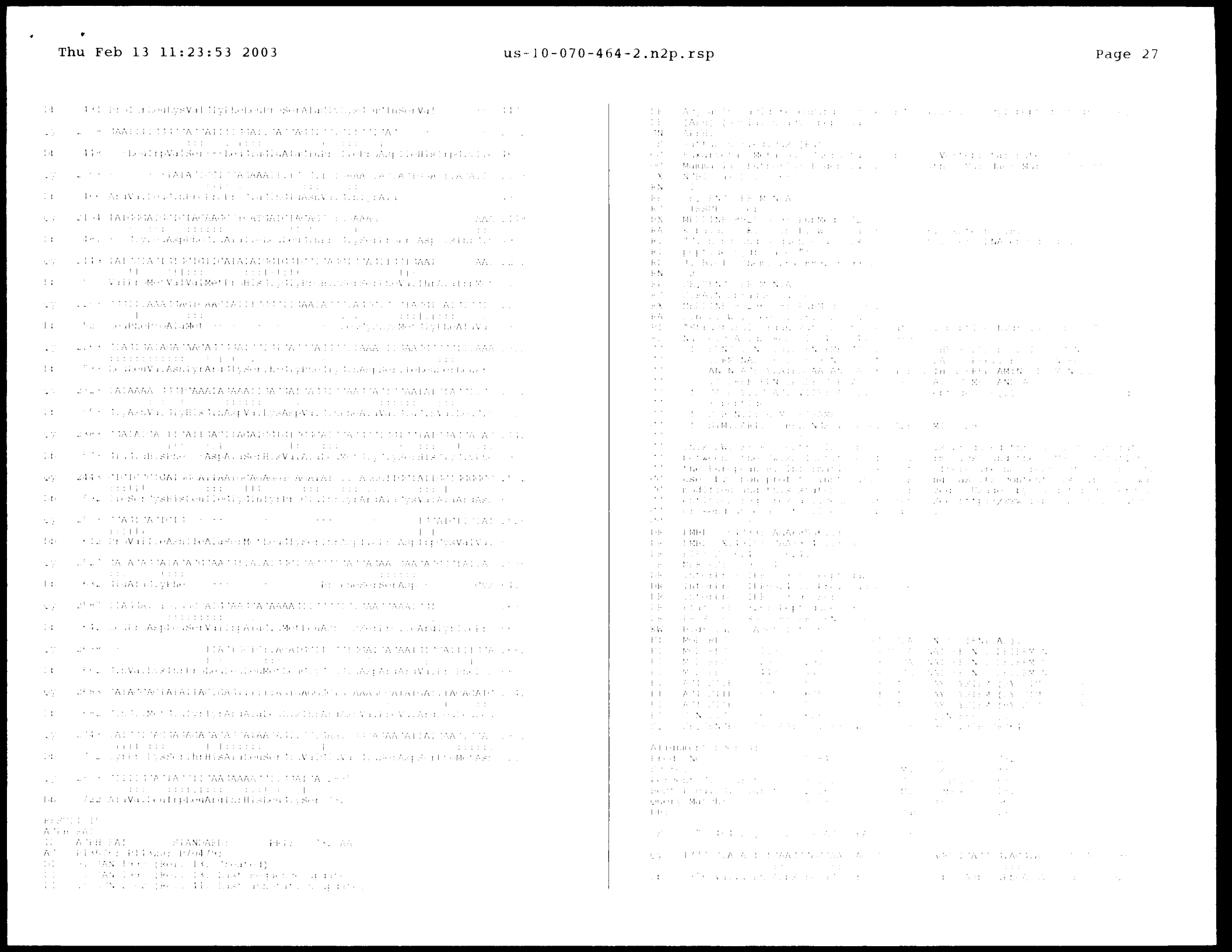


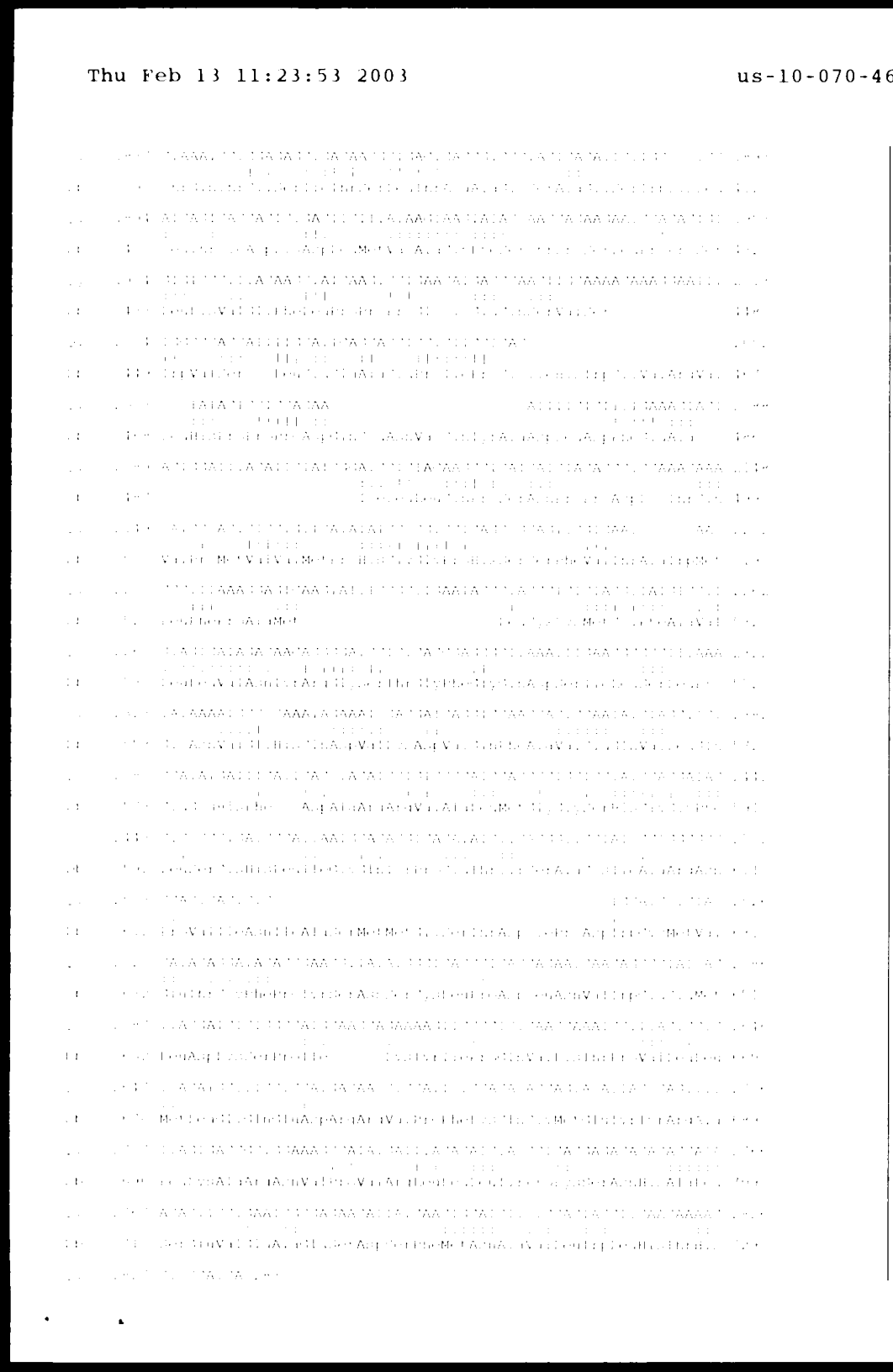


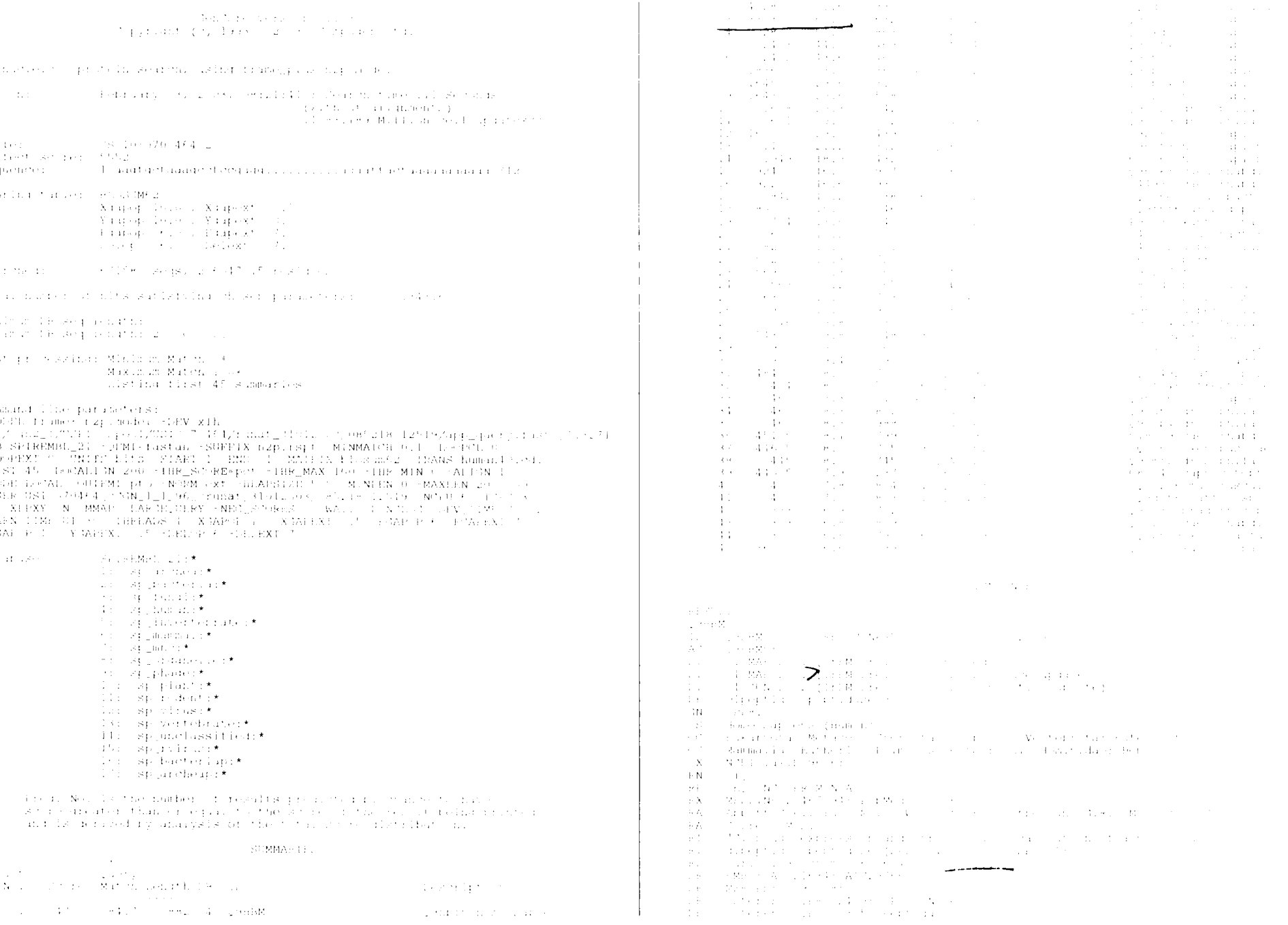


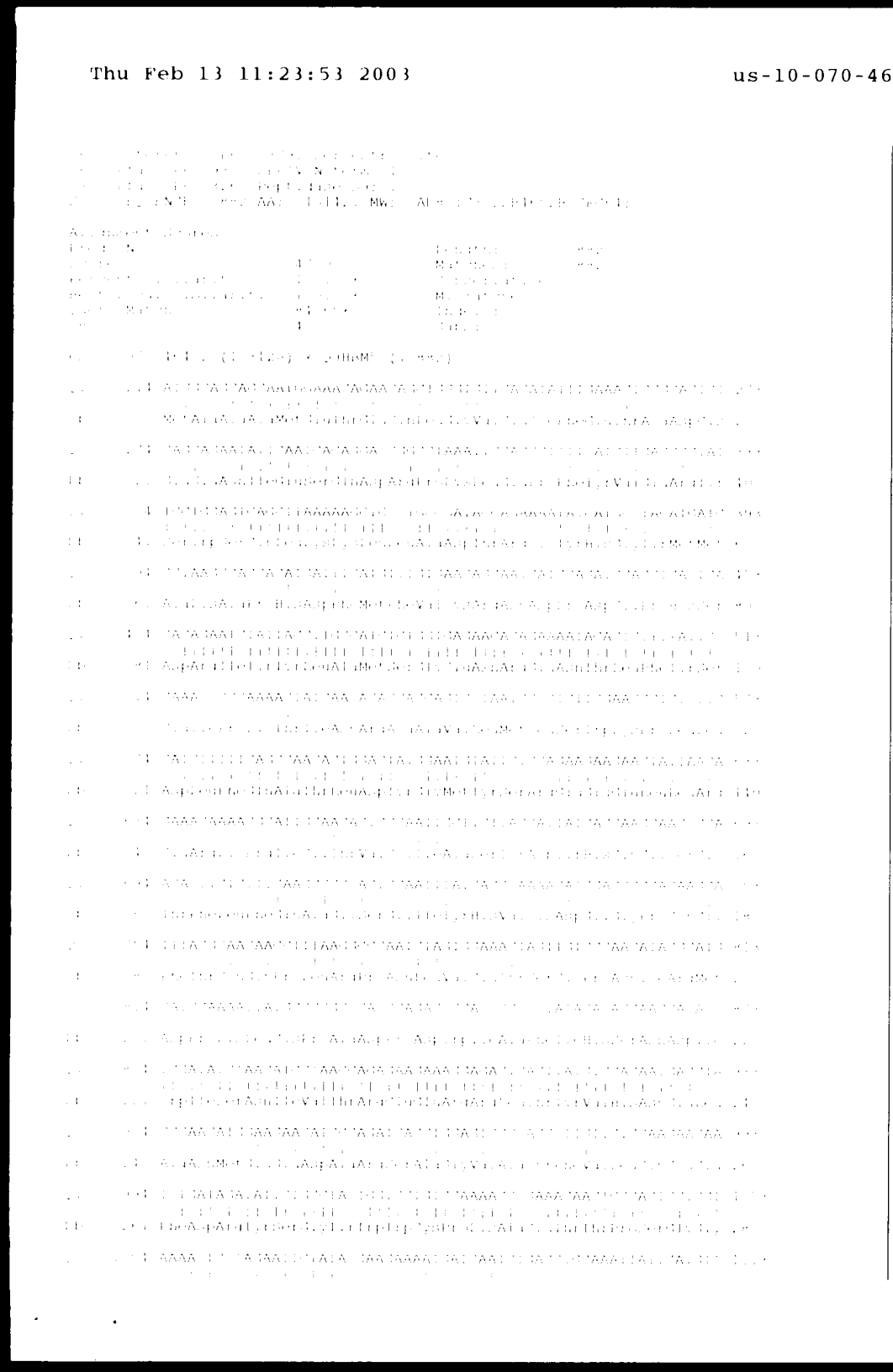


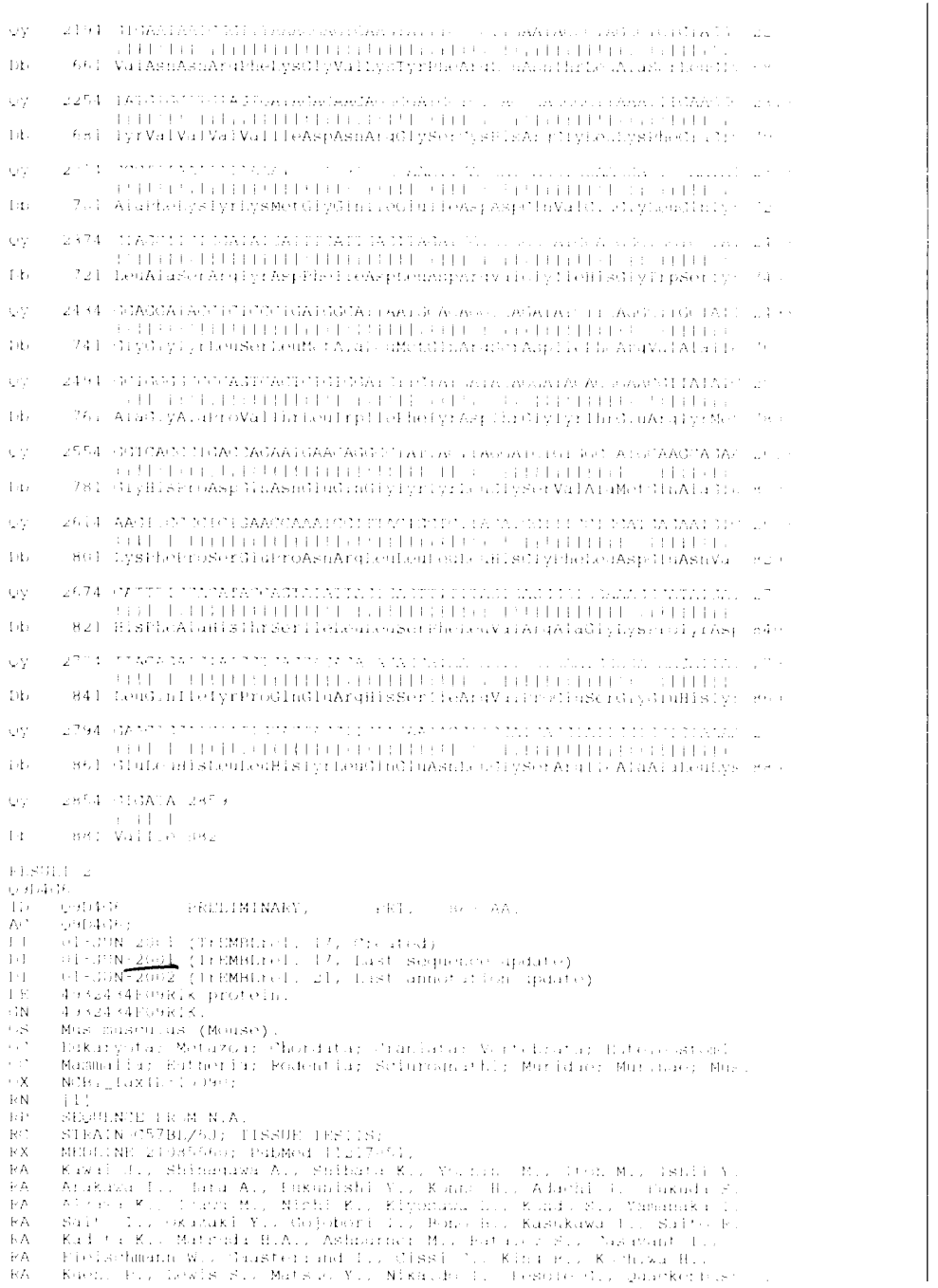


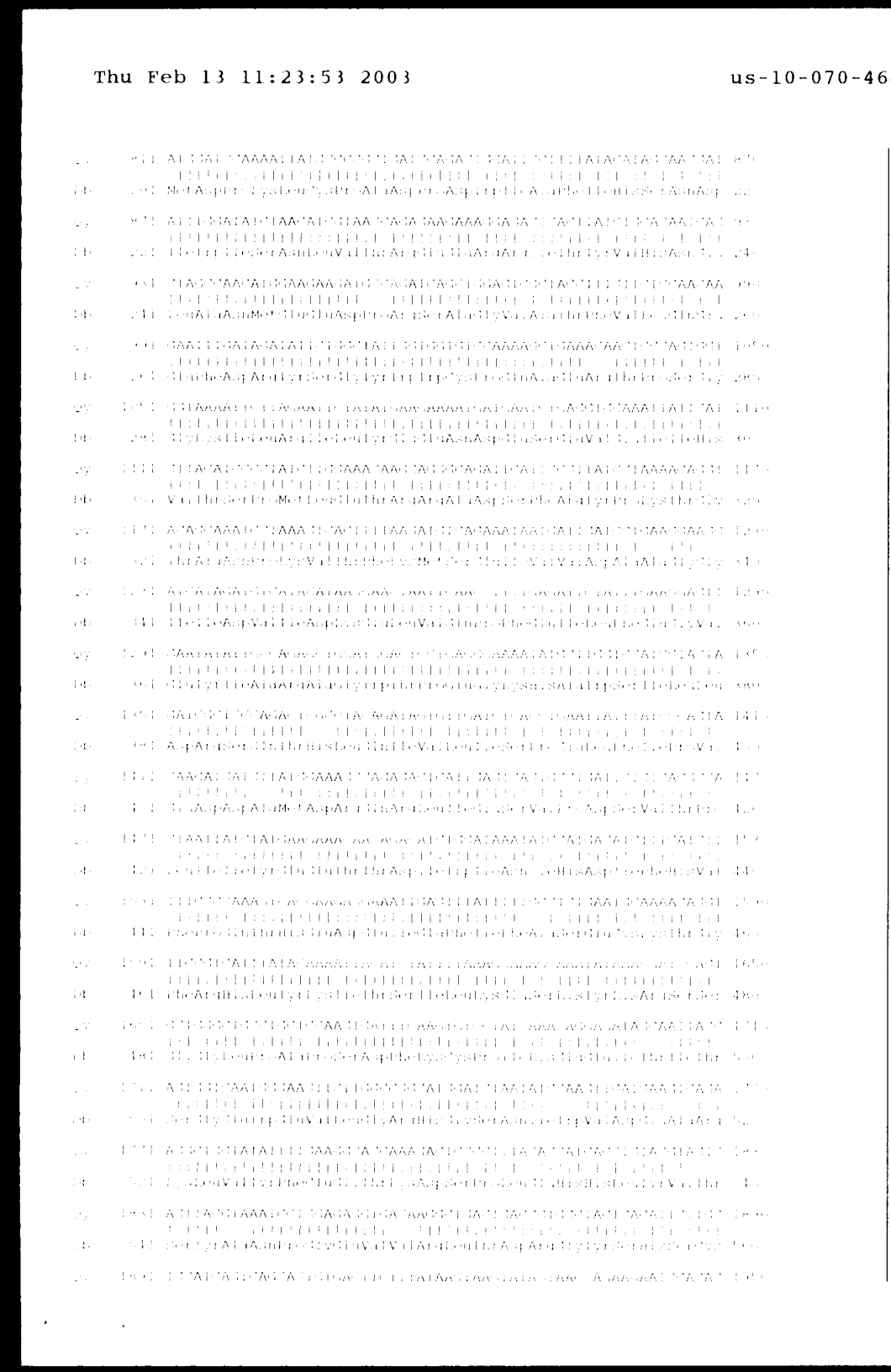




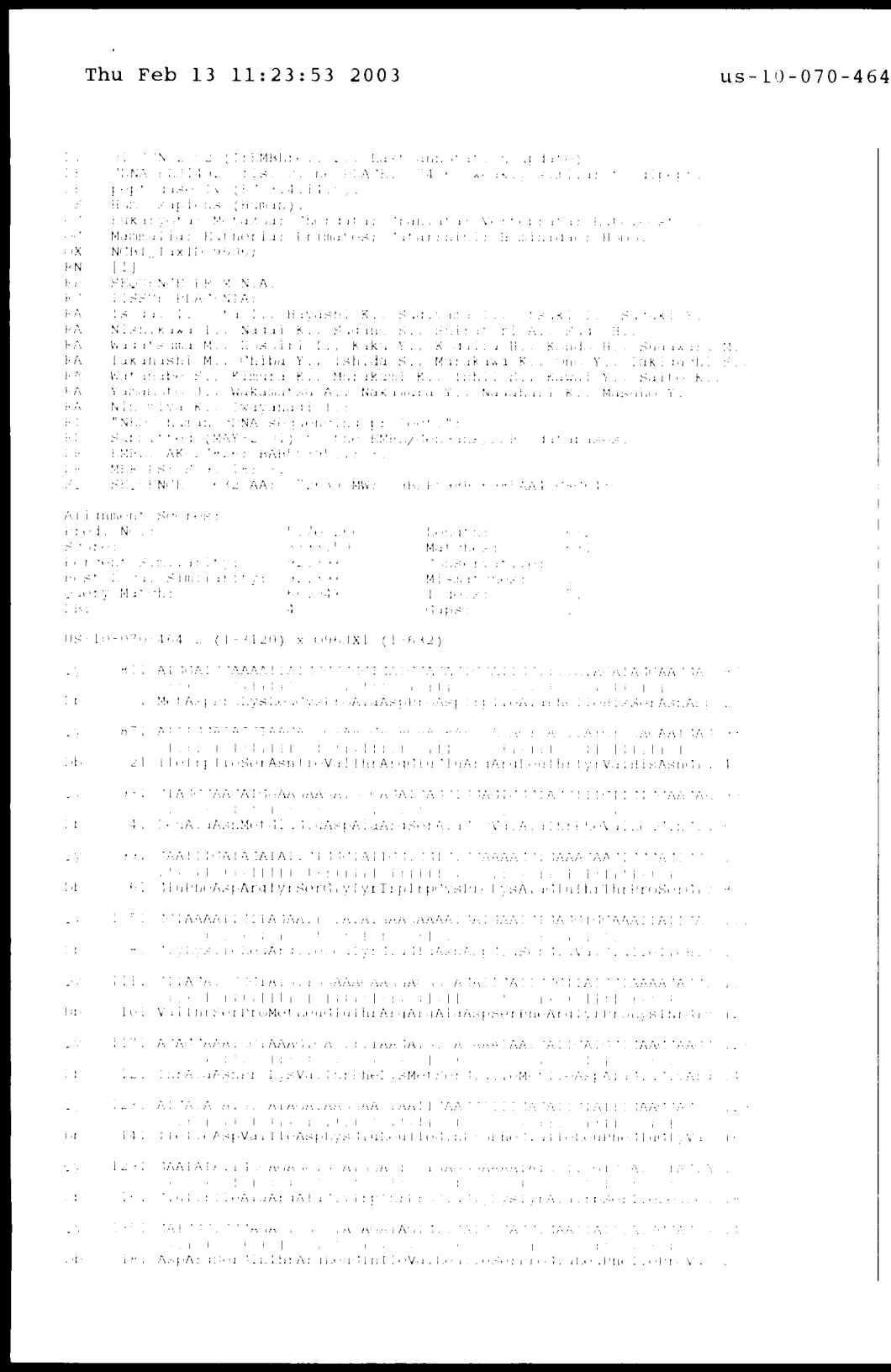


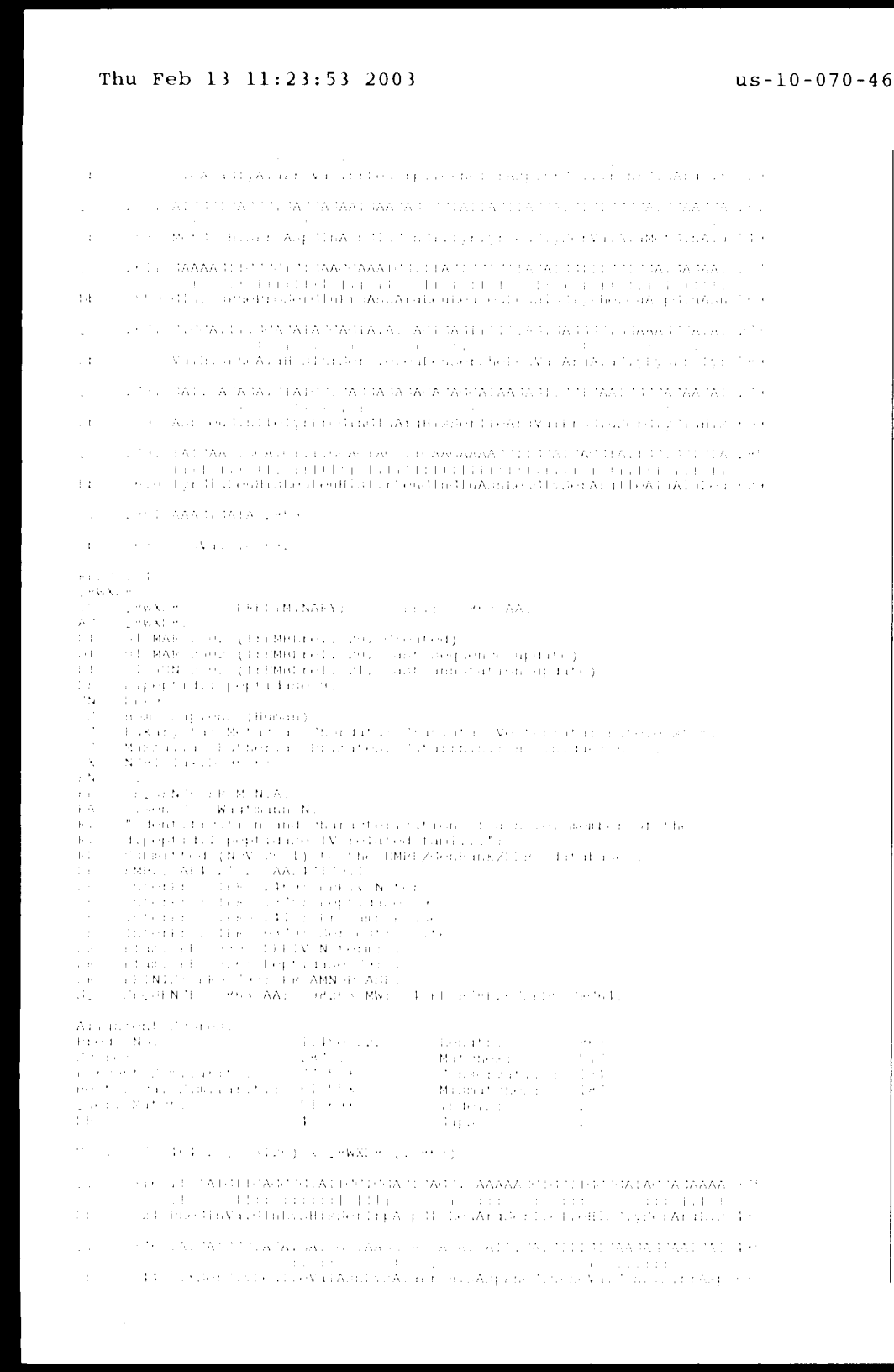


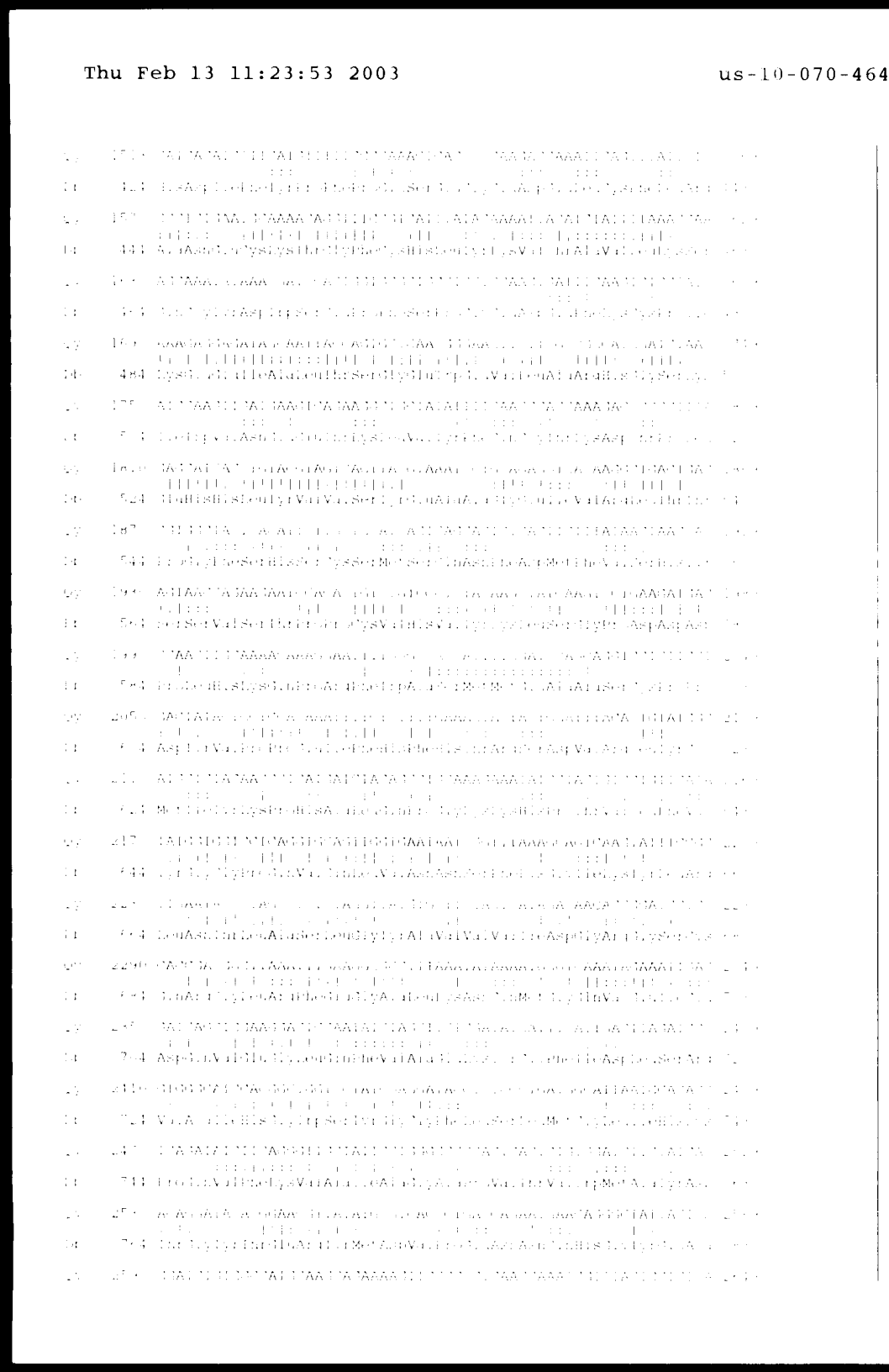


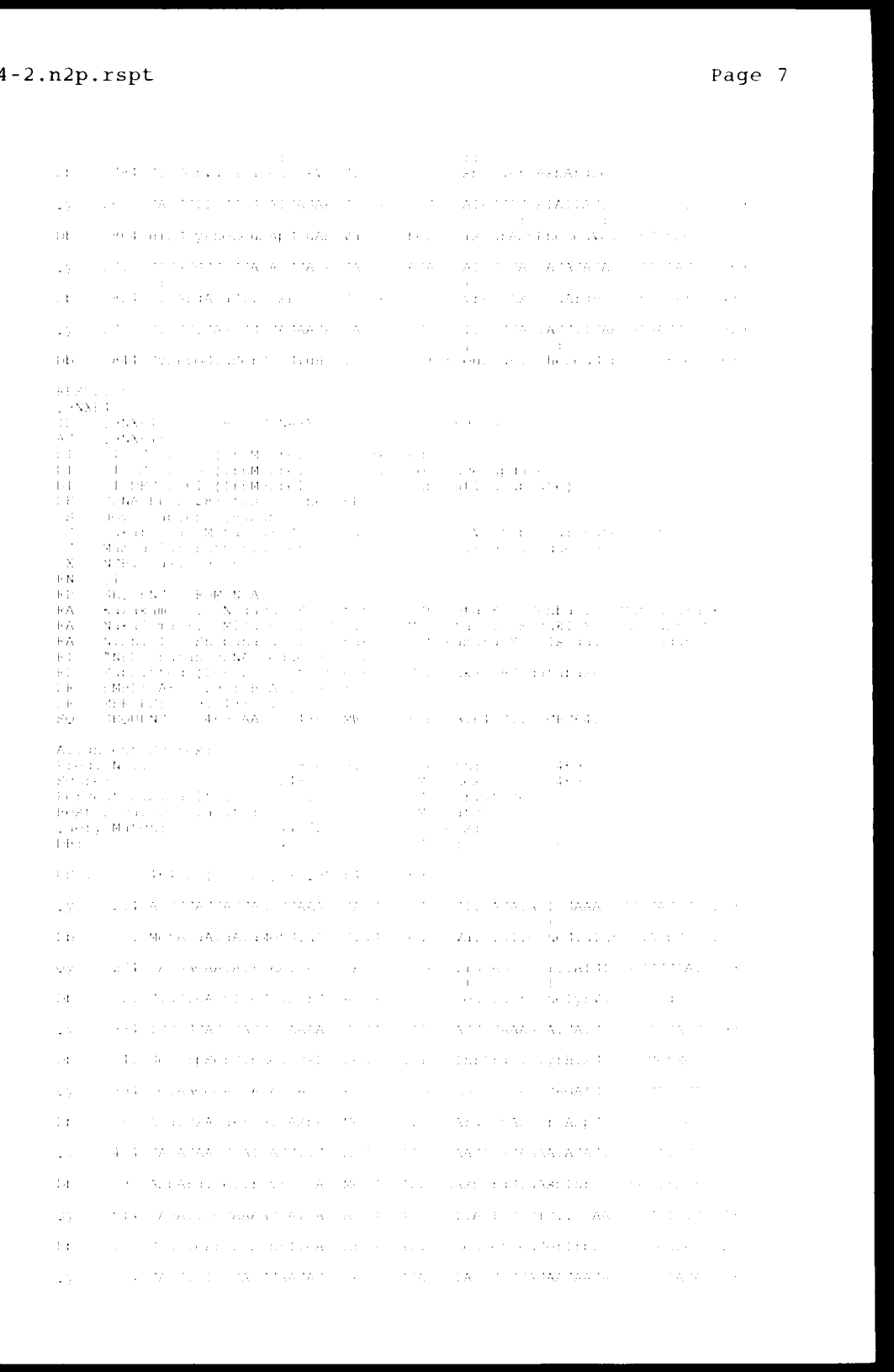


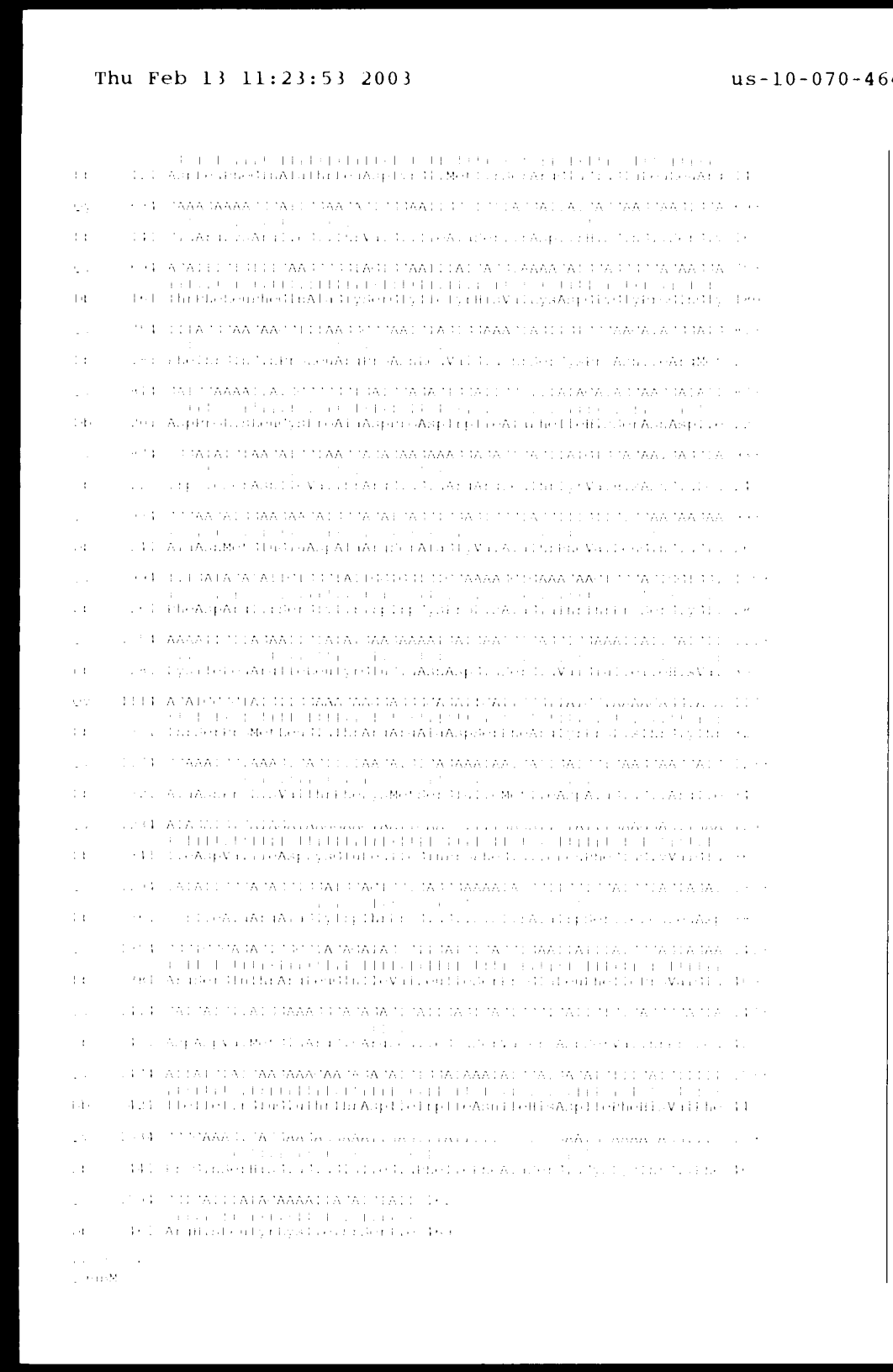
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US-10-070-464-2
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AC US-10-070-464-2
DT 01-DEC-2002 (first entry)
DT 01-DEC-2002 (last sequence update)

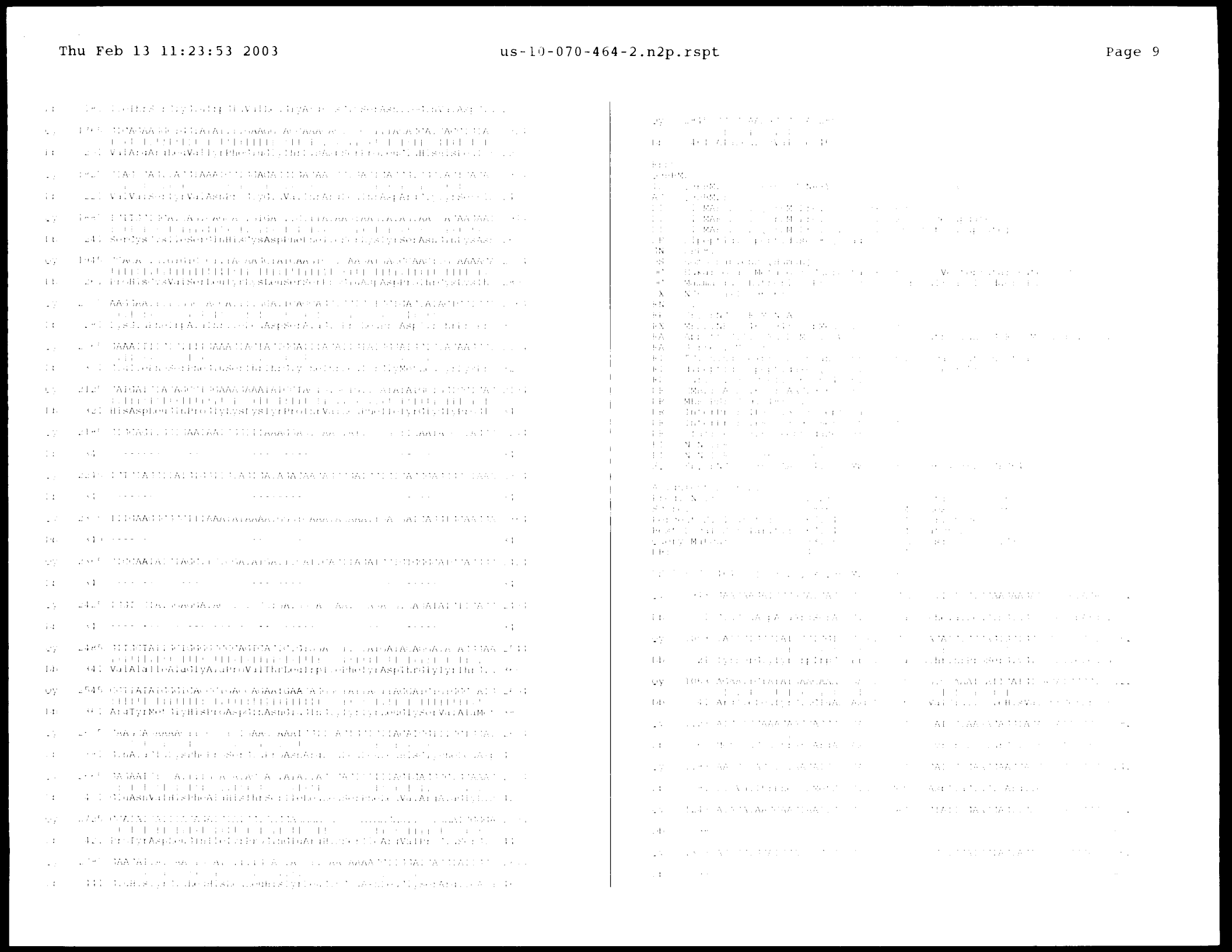


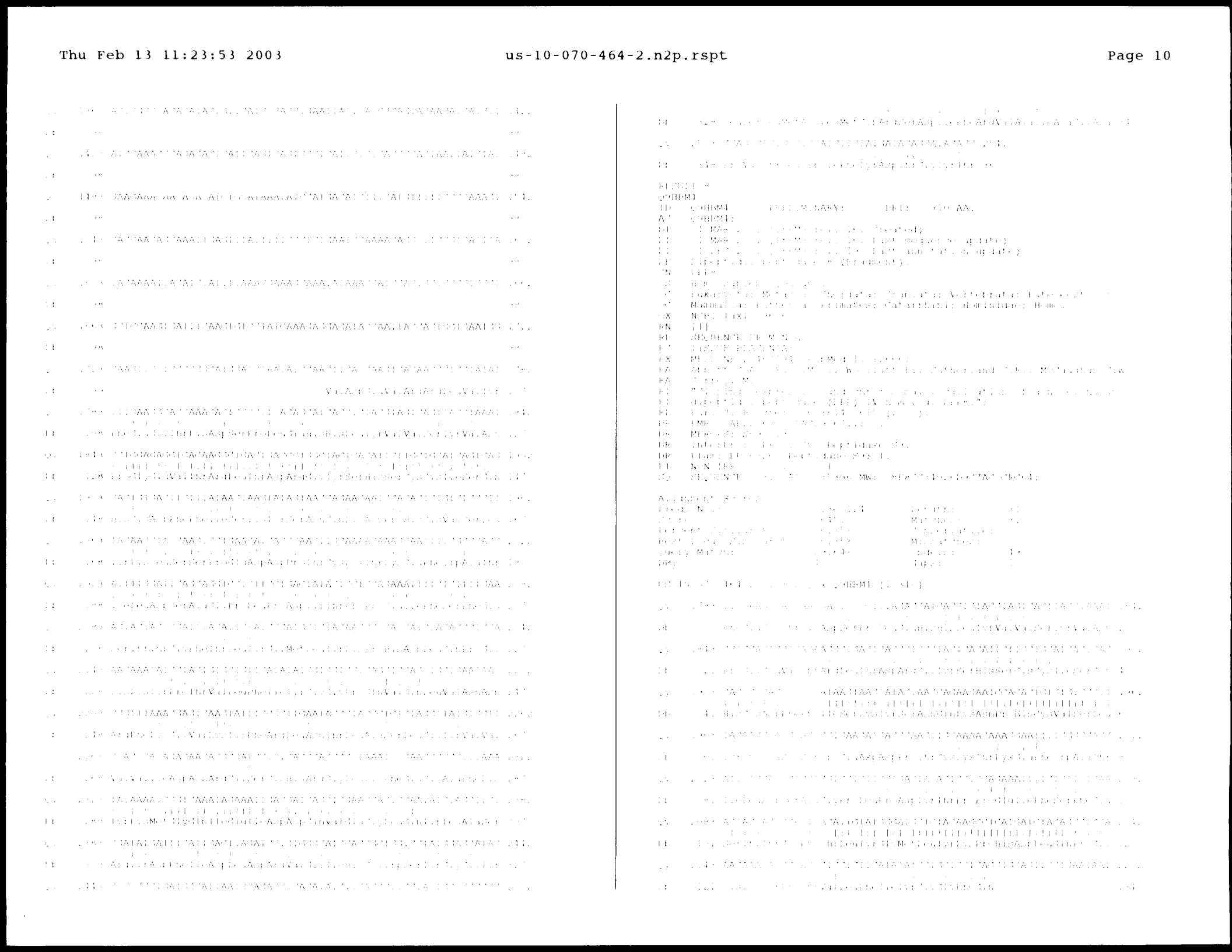


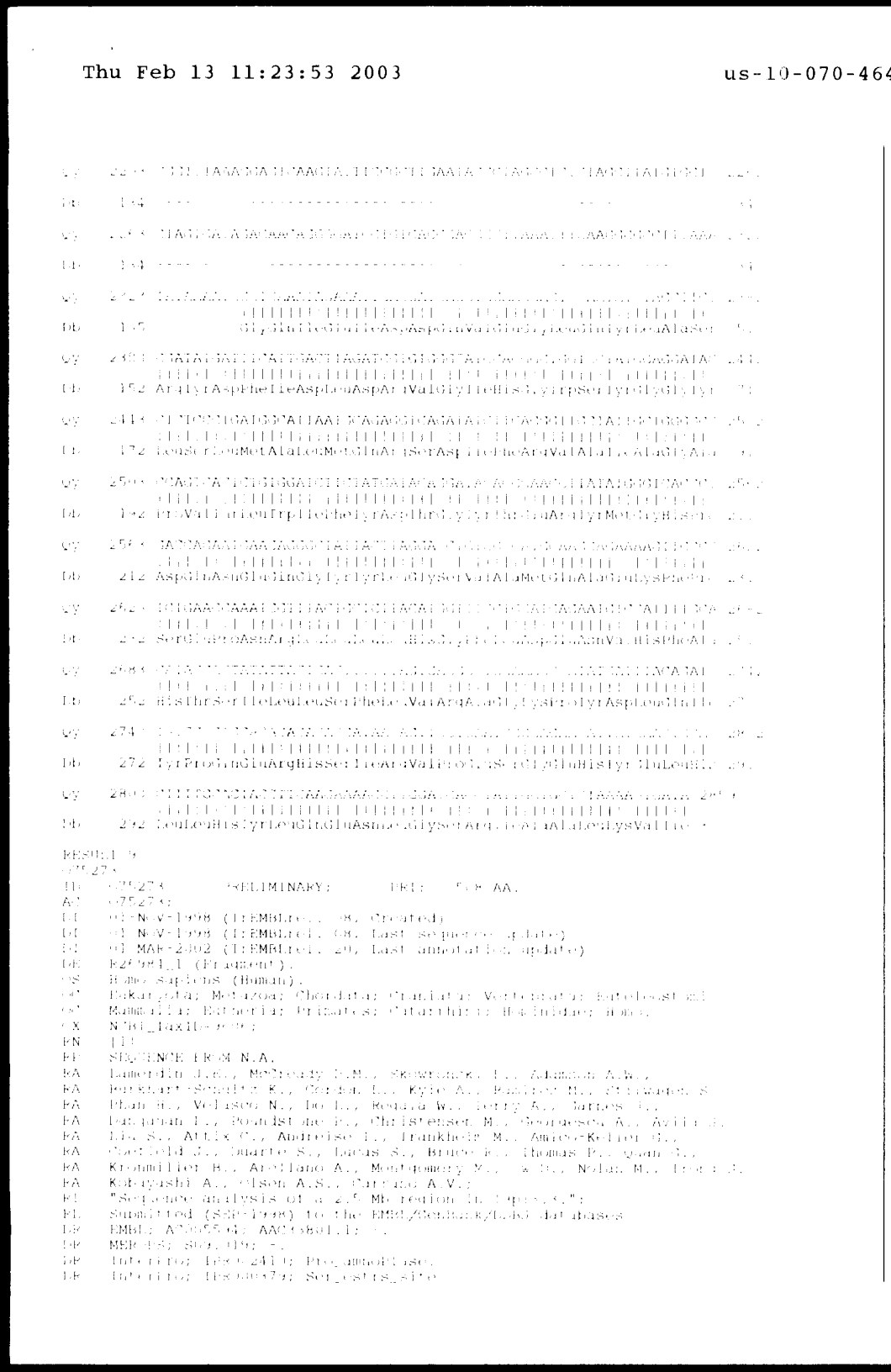


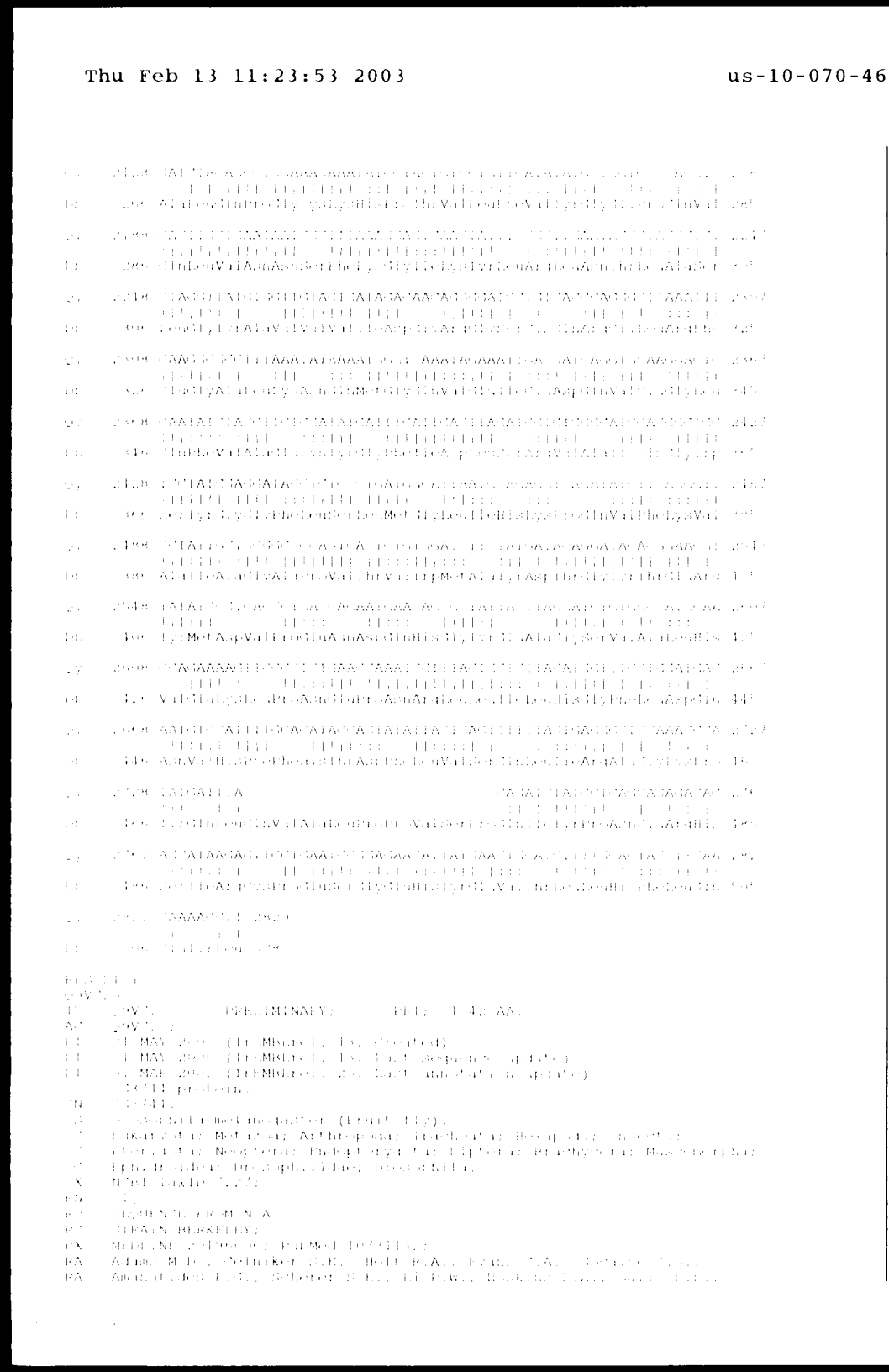


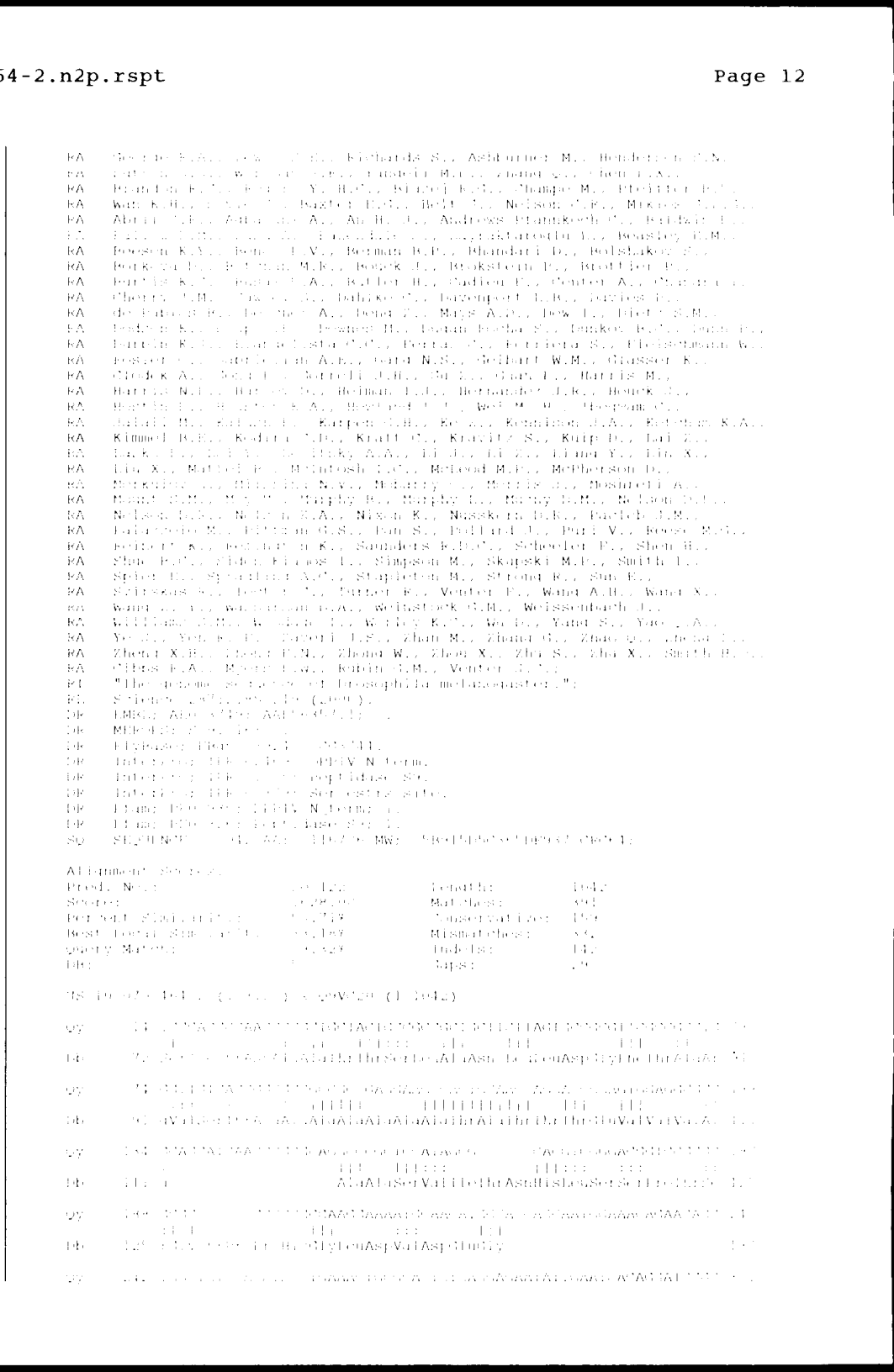


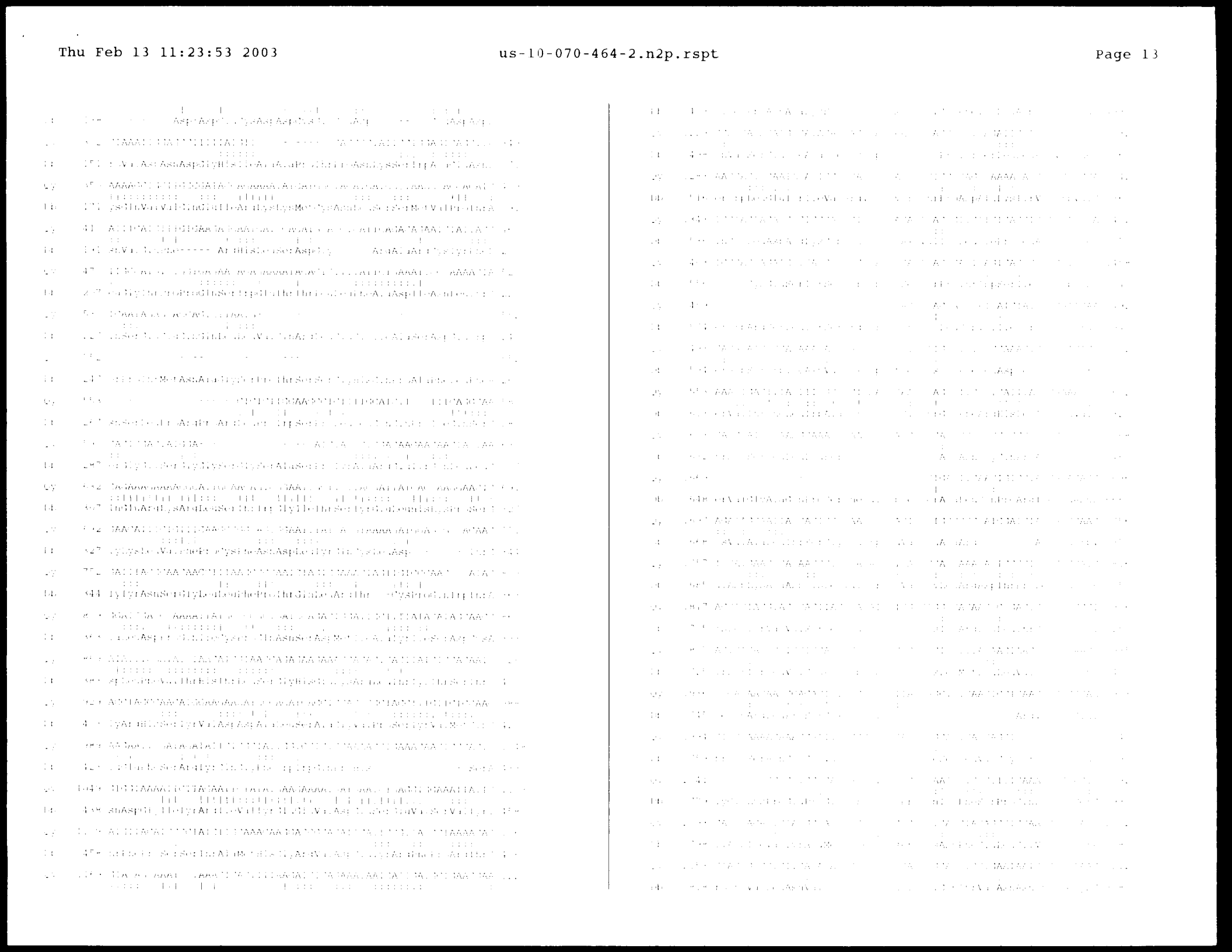


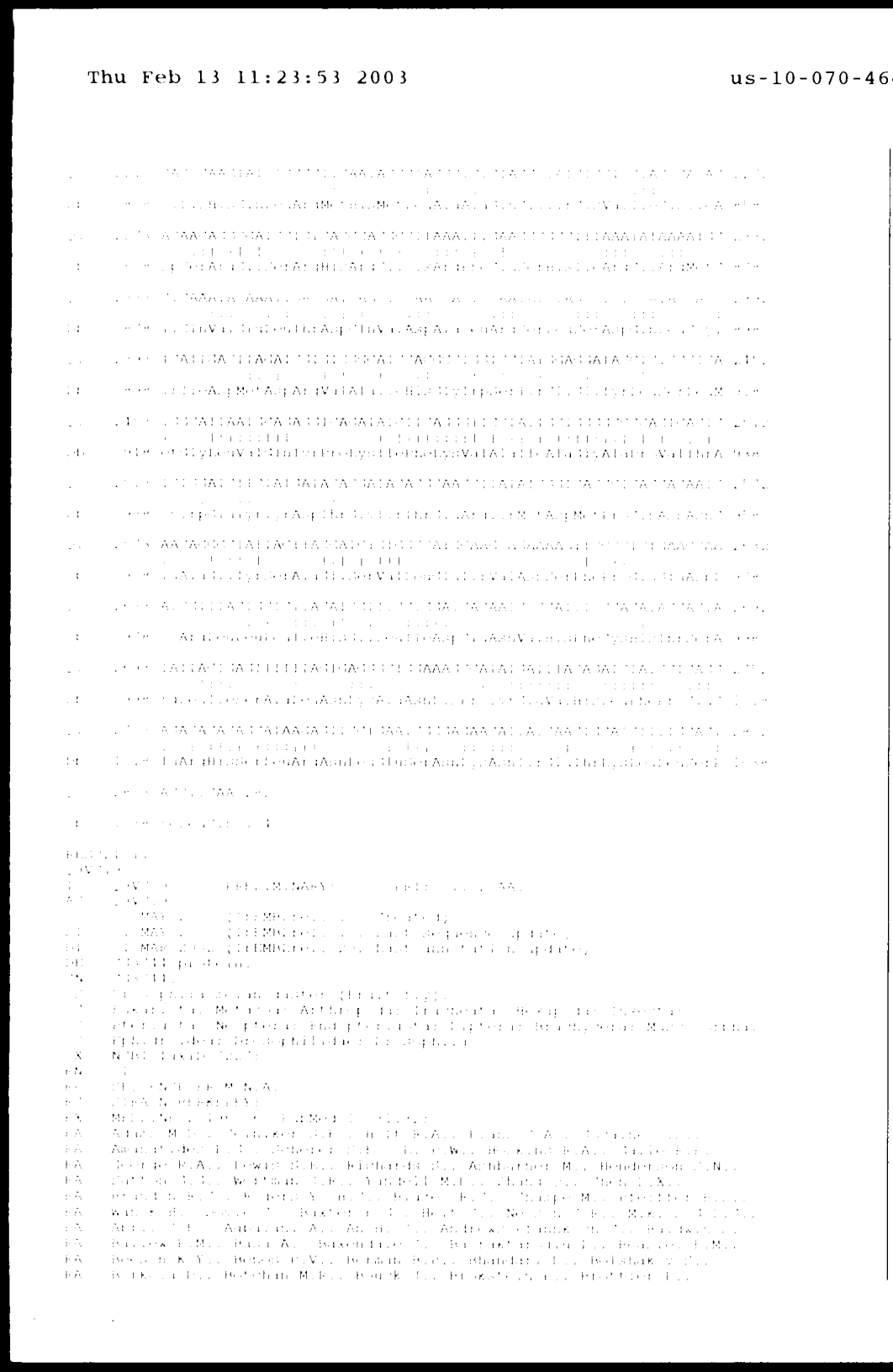


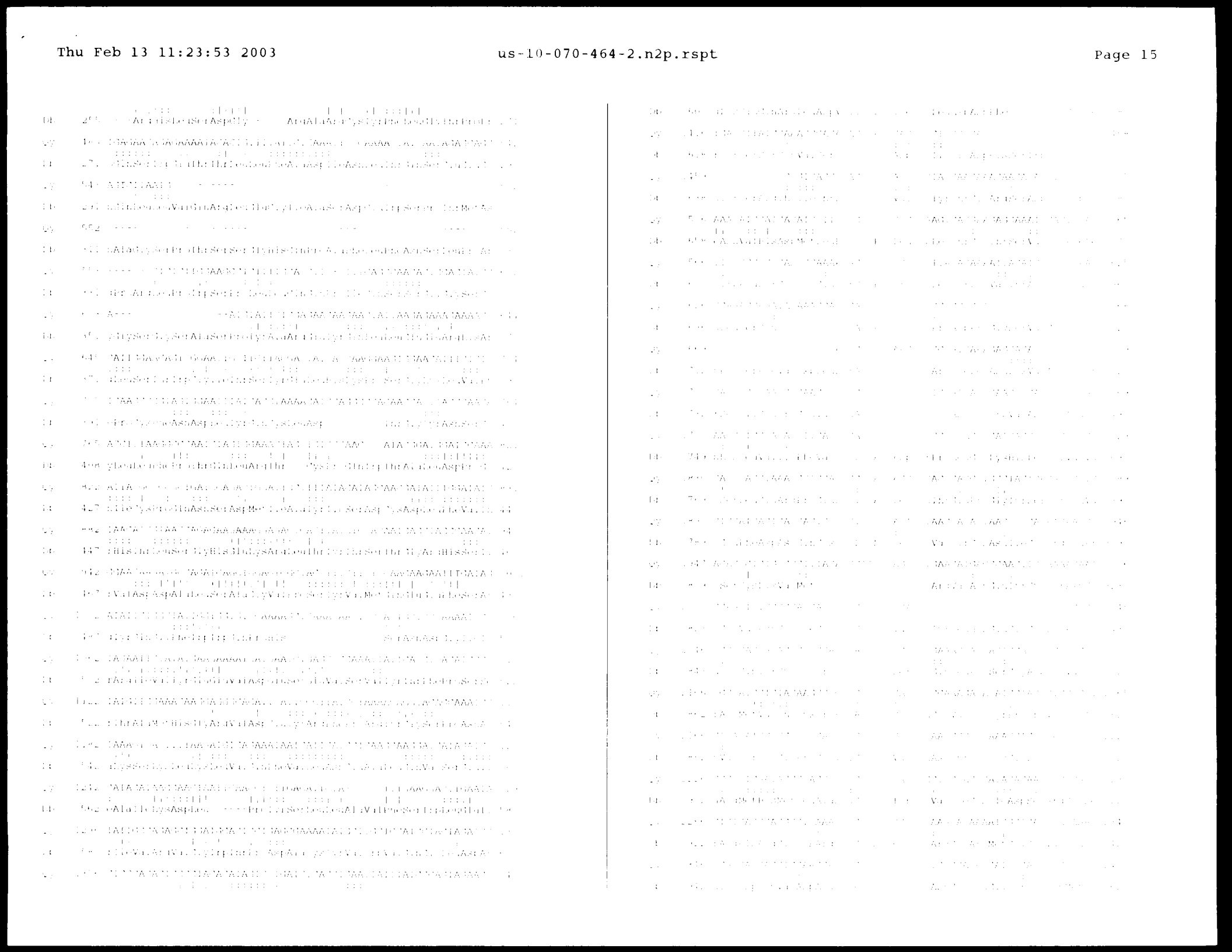


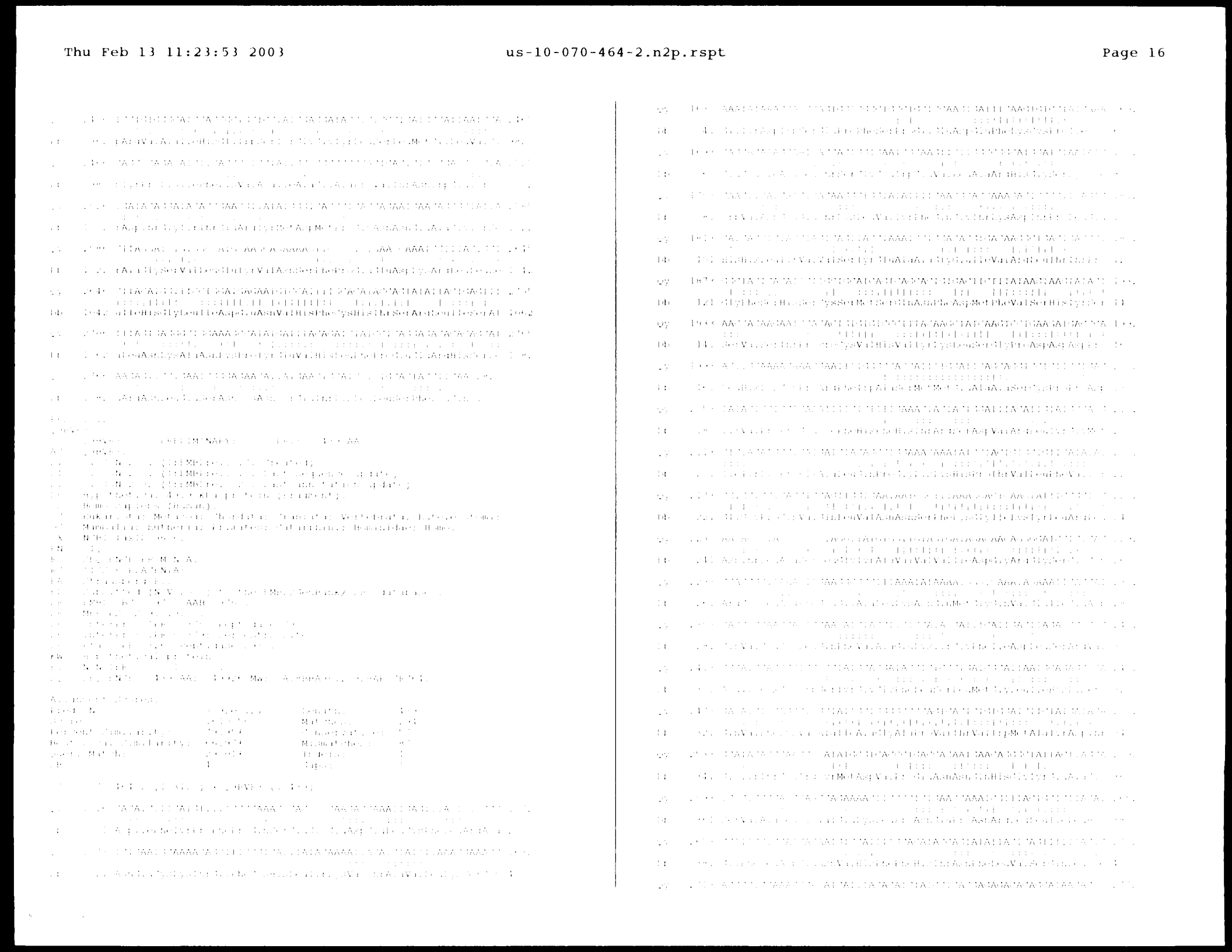


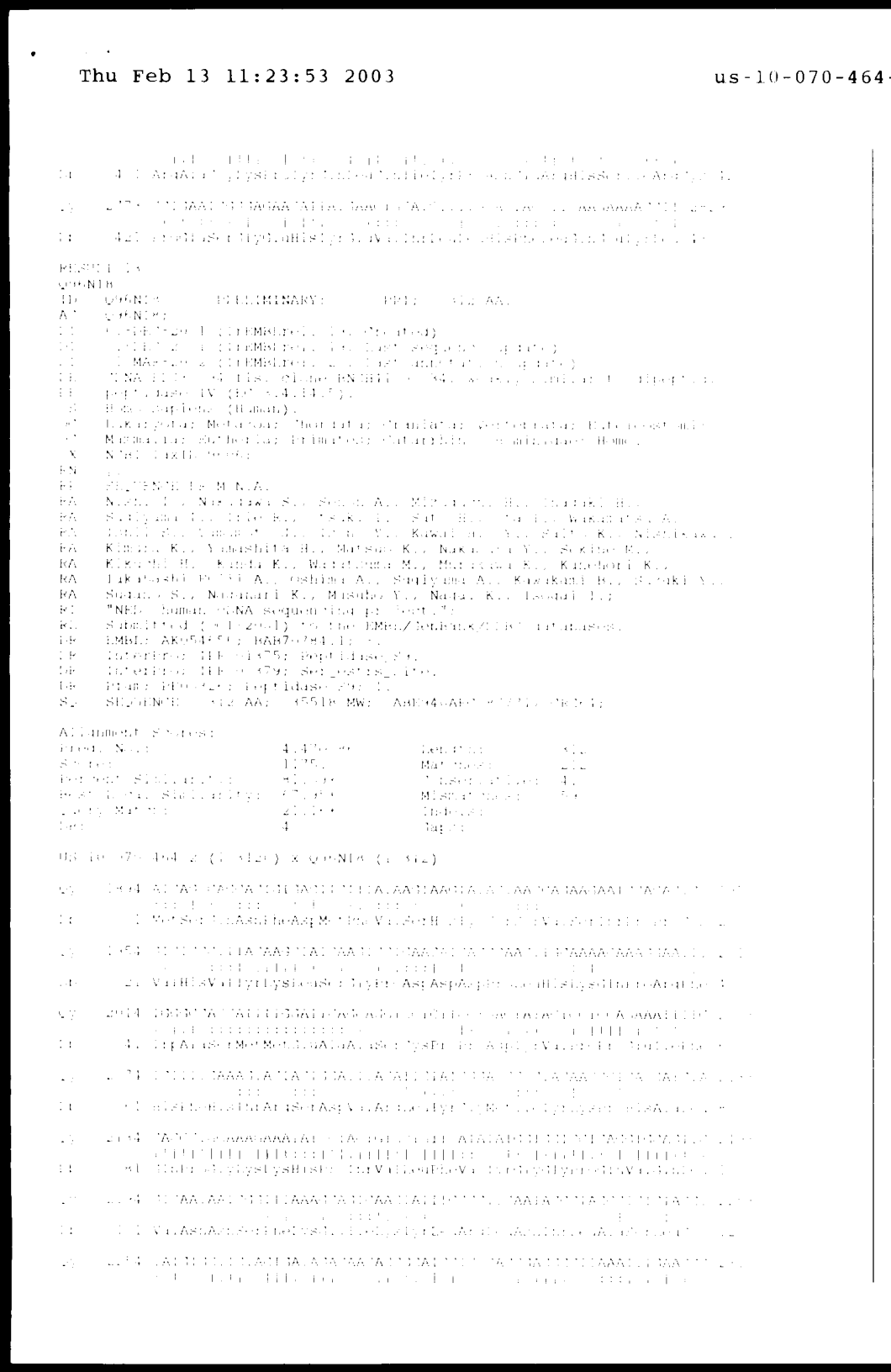


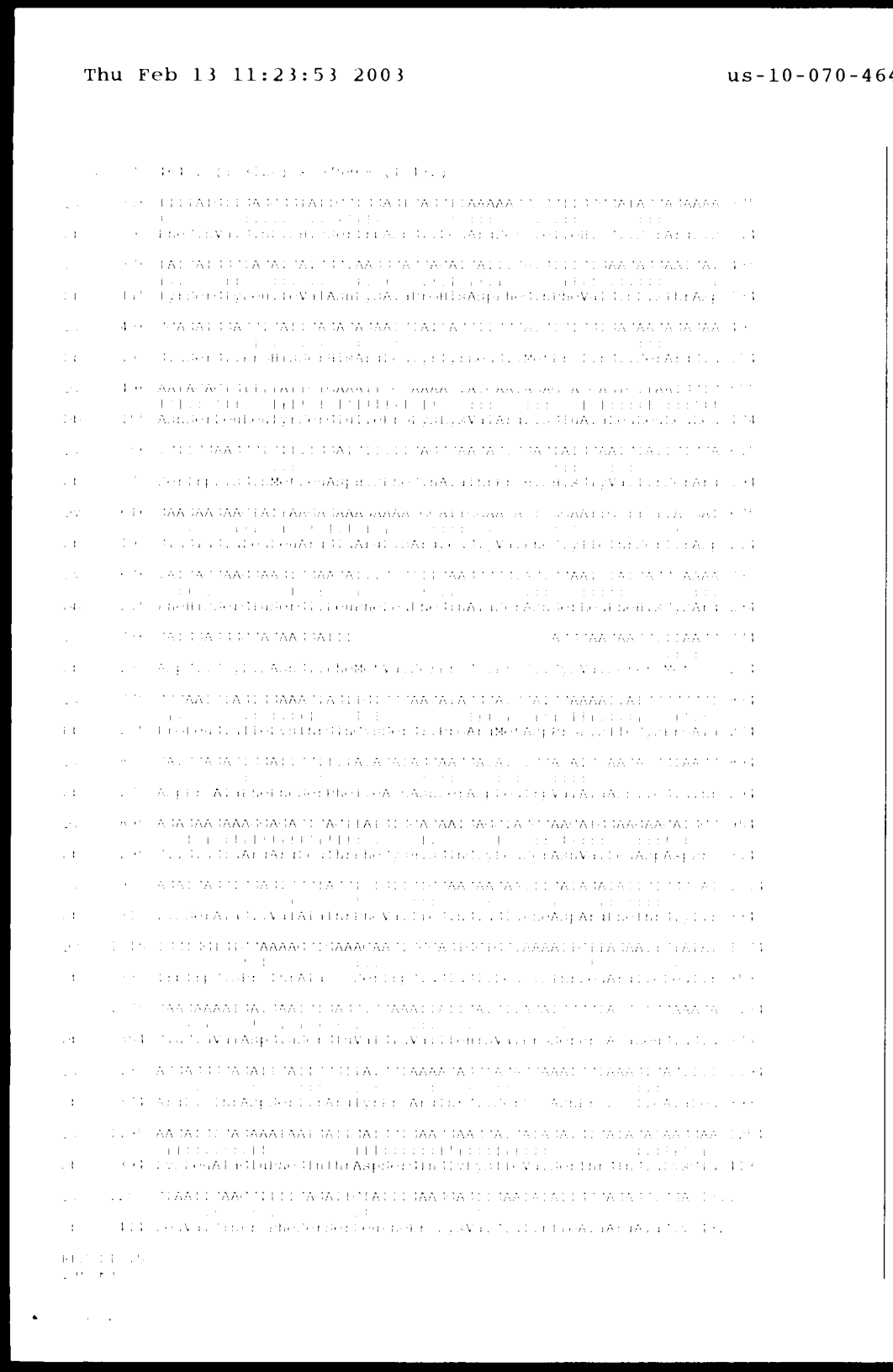


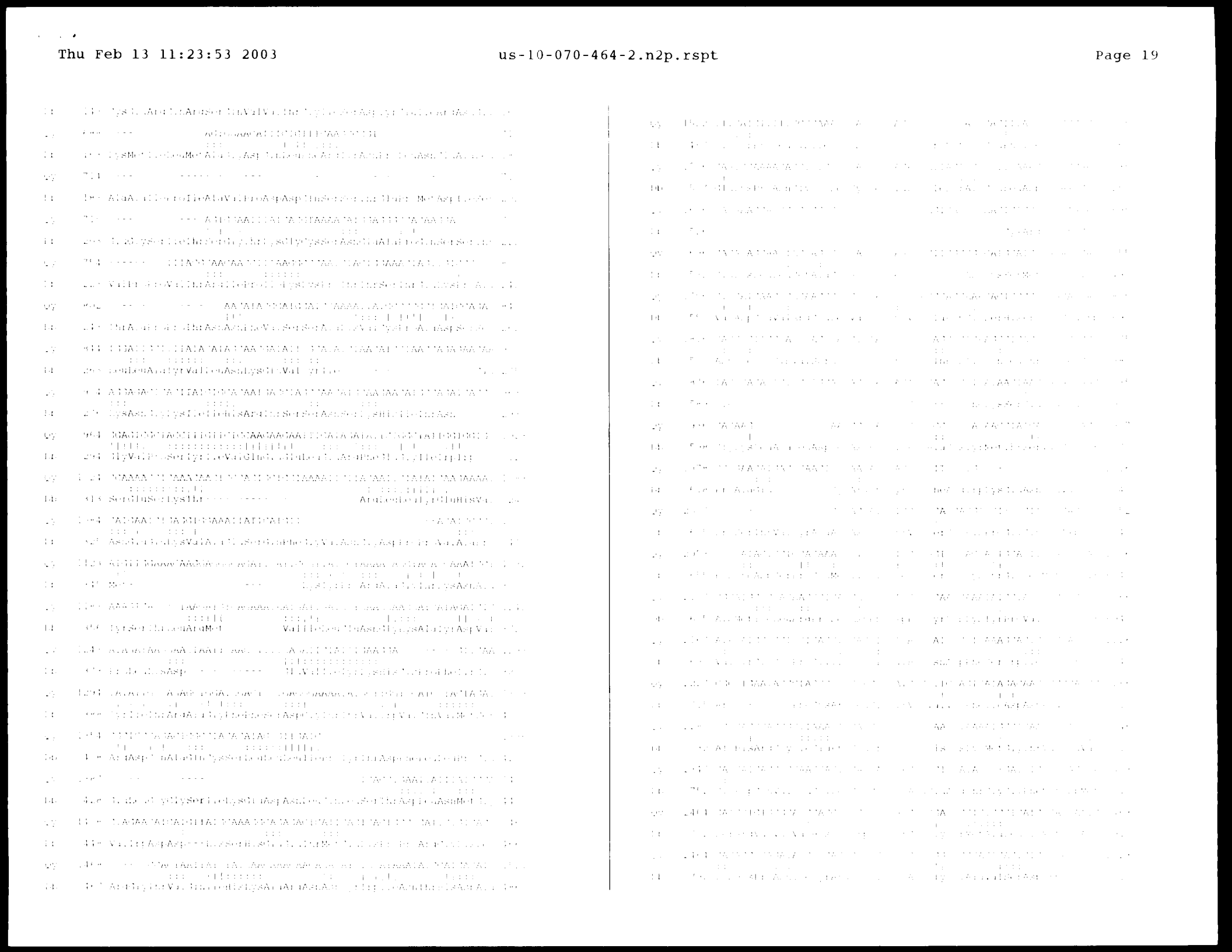


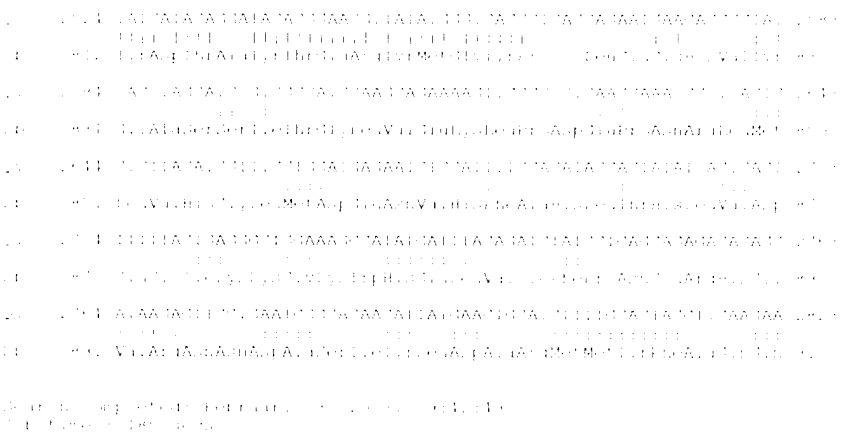












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Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	982.5	19.0	221	4	US-09-472-284-2	Sequence 2, Appl
3	529	9.5	755	5	PCT-US99-07942-2	Sequence 2, Appl
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5	526	9.5	766	1	US-08-220-443A-5	Sequence 5, Appl
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7	526	9.5	766	2	US-08-941-[illegible]	Sequence 5, Appl
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13	279.5	5.1	647	4	US-09-[illegible]	Sequence 3, Appl
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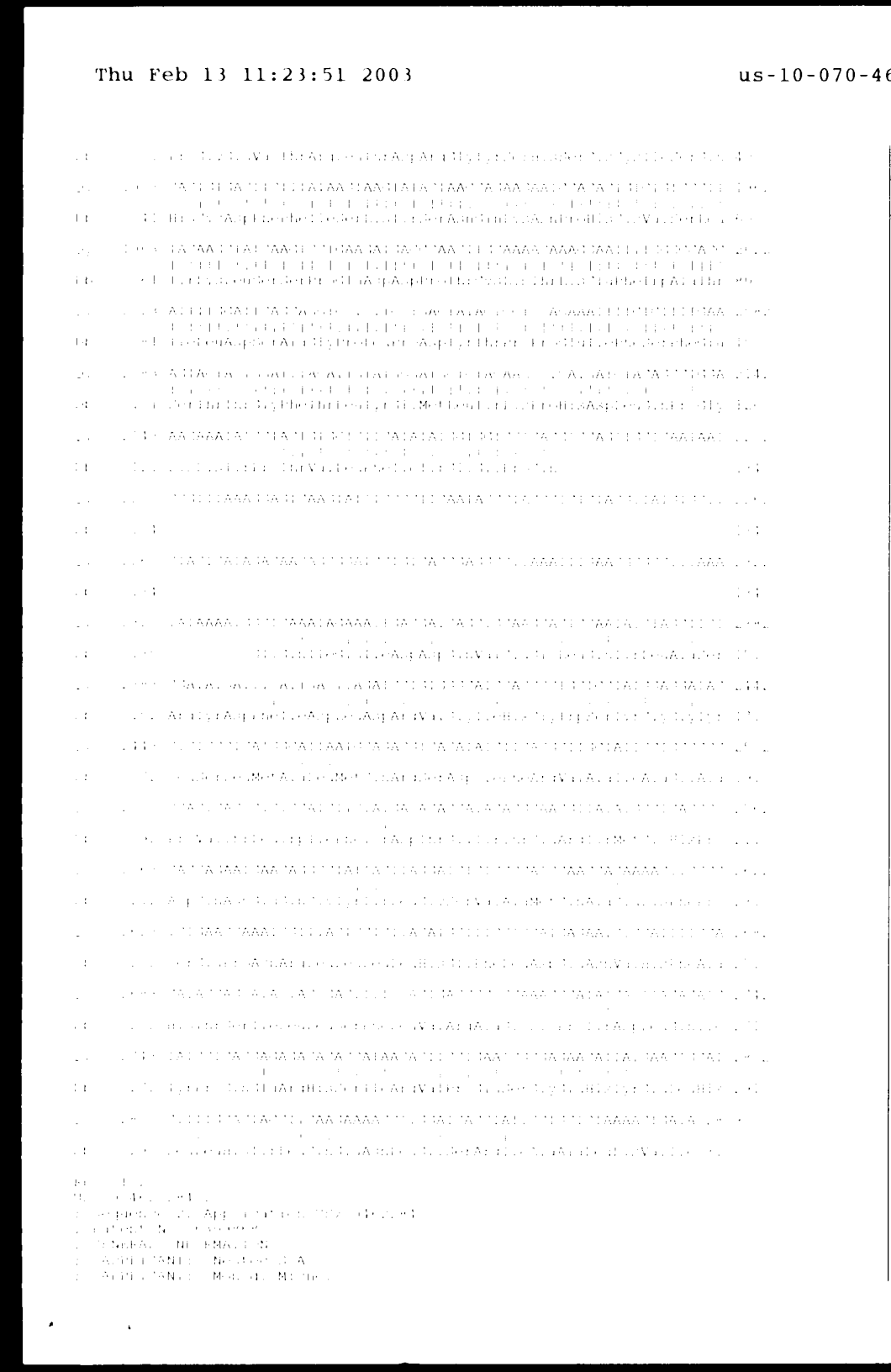
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; APPLICANT: Yeo, Gene, et al
; APPLICANT: Burge, Christopher, B.
; APPLICANT: Modular Genetics
; TITLE OF INVENTION: Methods and Compositions for the Discovery of Alternative Splicing Events
; FILE REFERENCE: 4150.1.1.1/GEN
; CURRENT APPLICATION NUMBER: US/09/794,230
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 35
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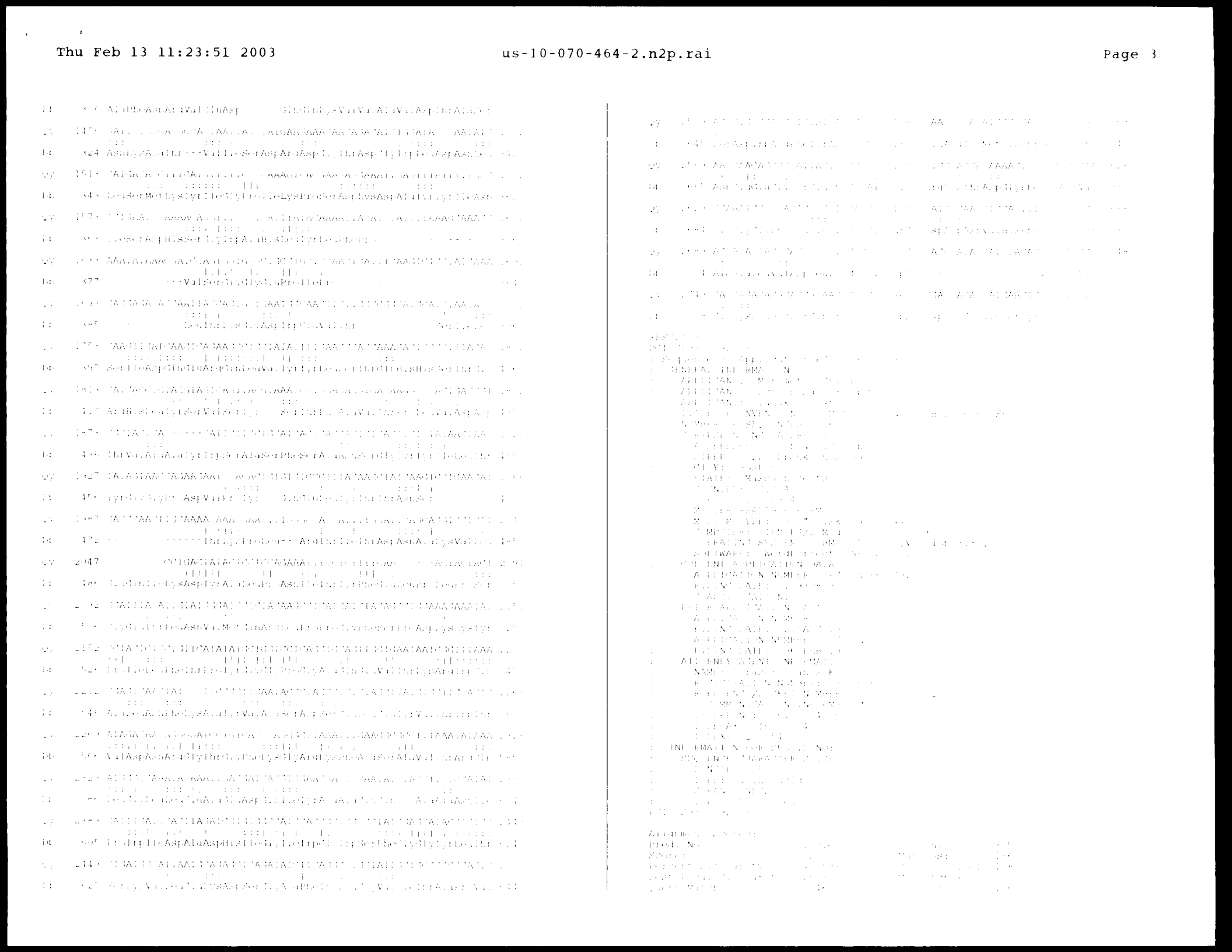
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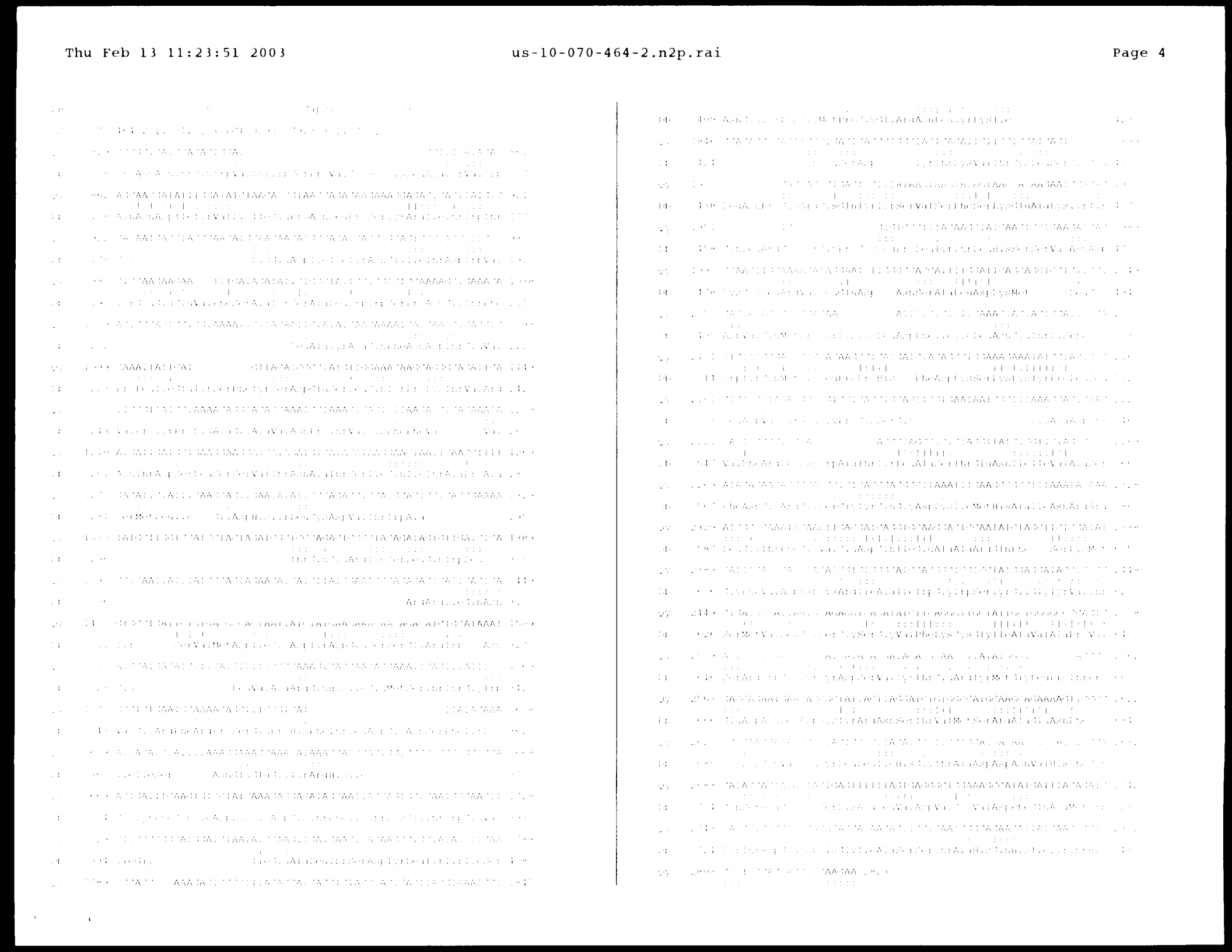
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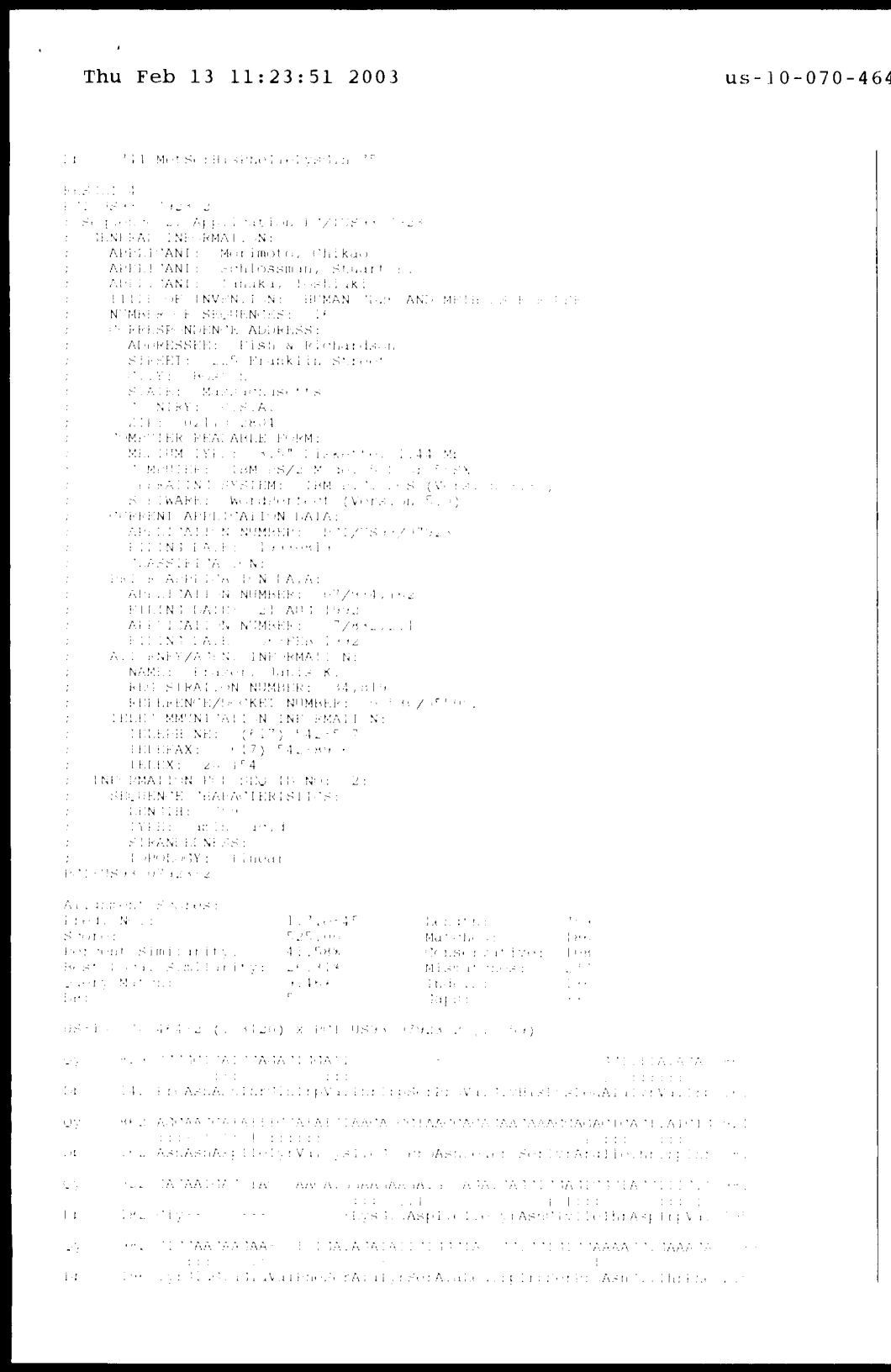
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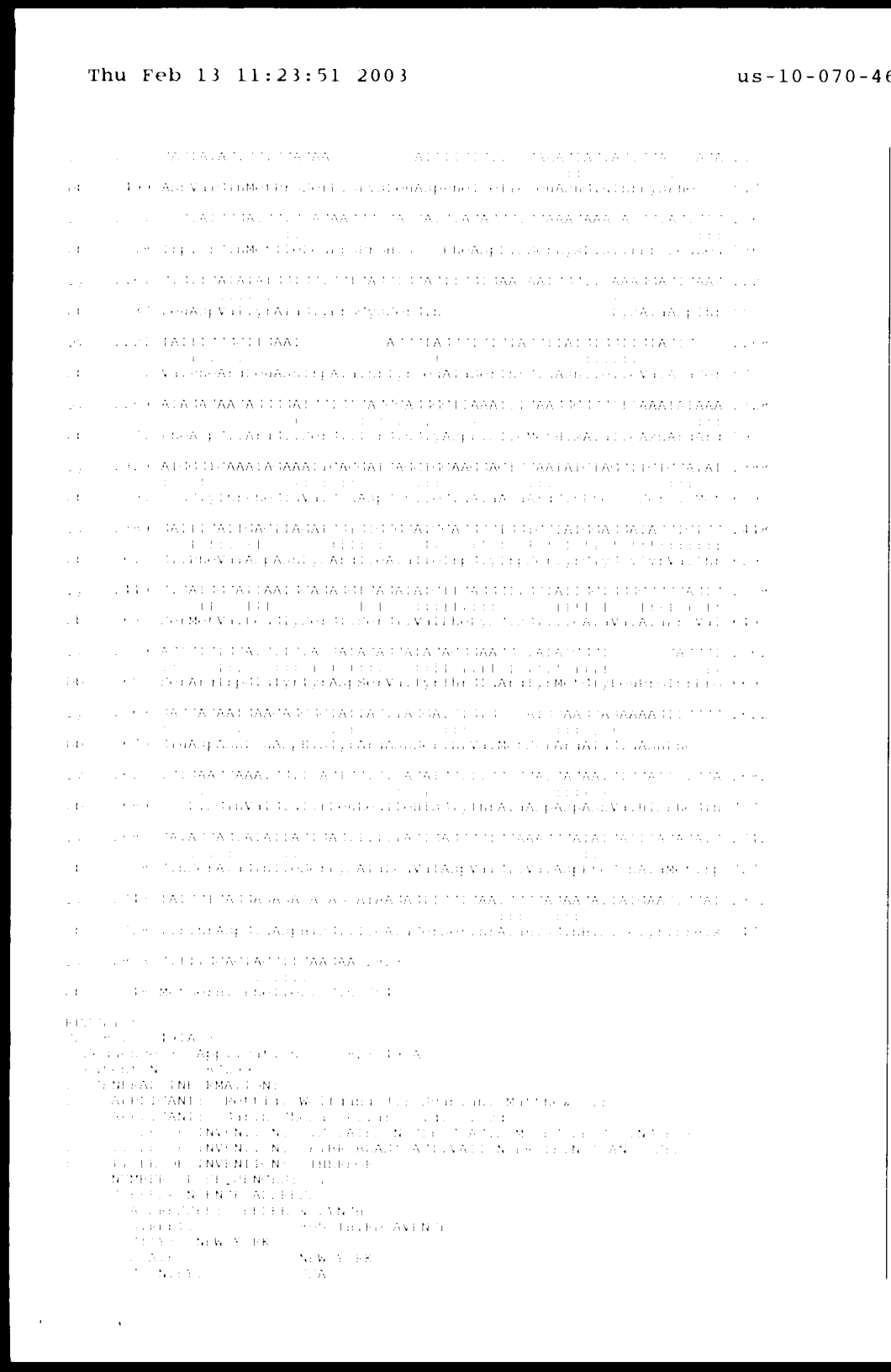
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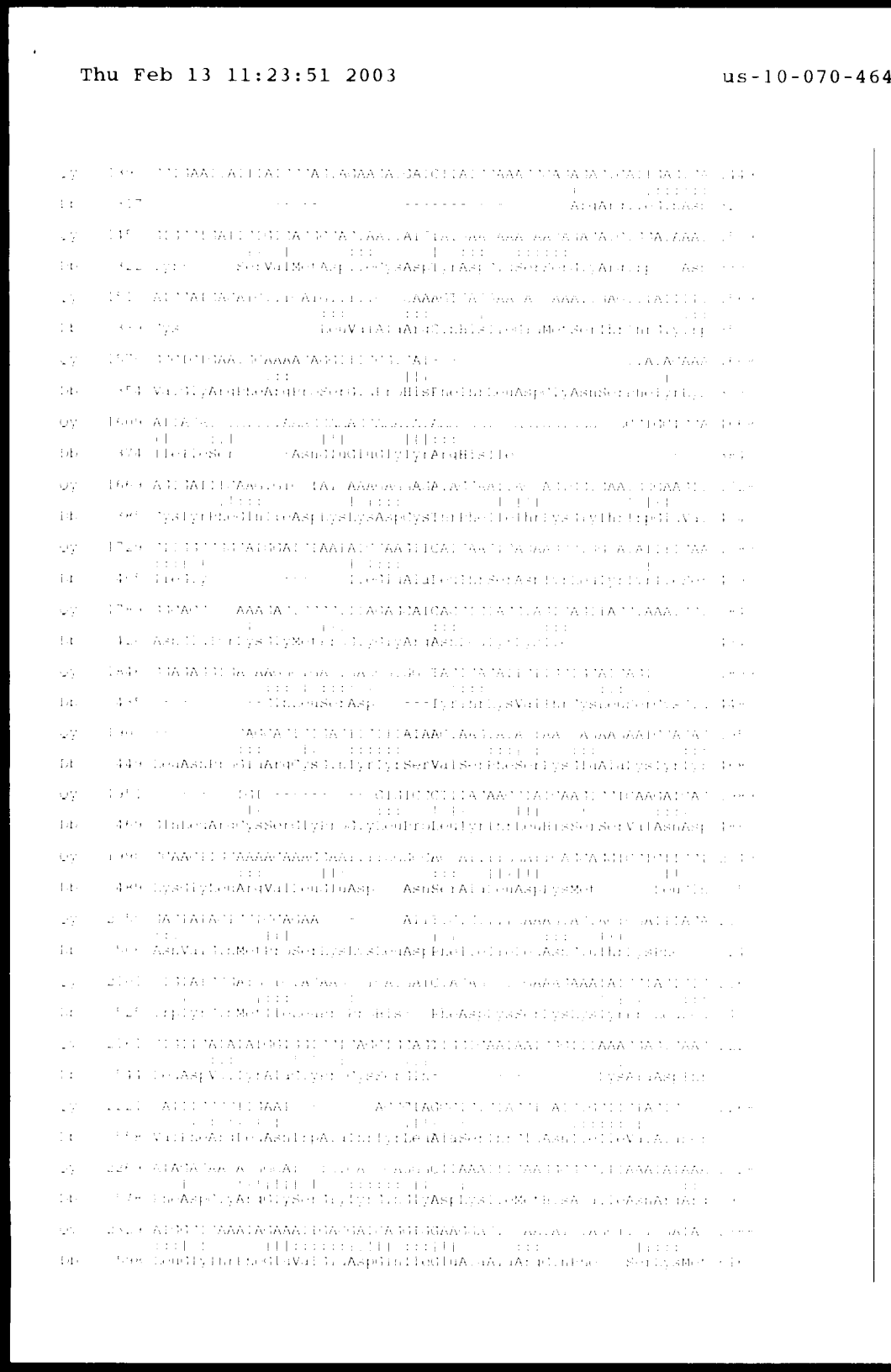


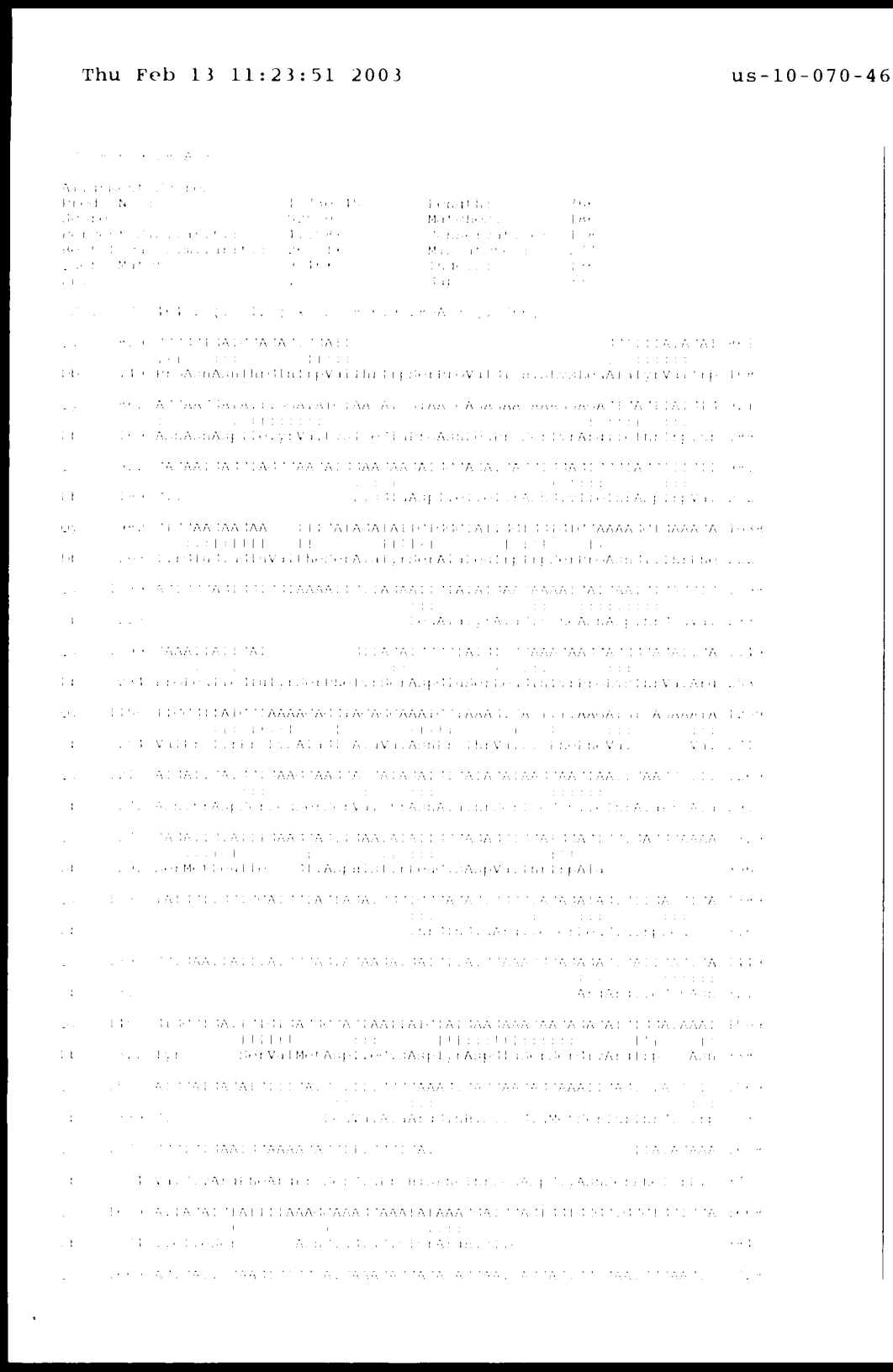


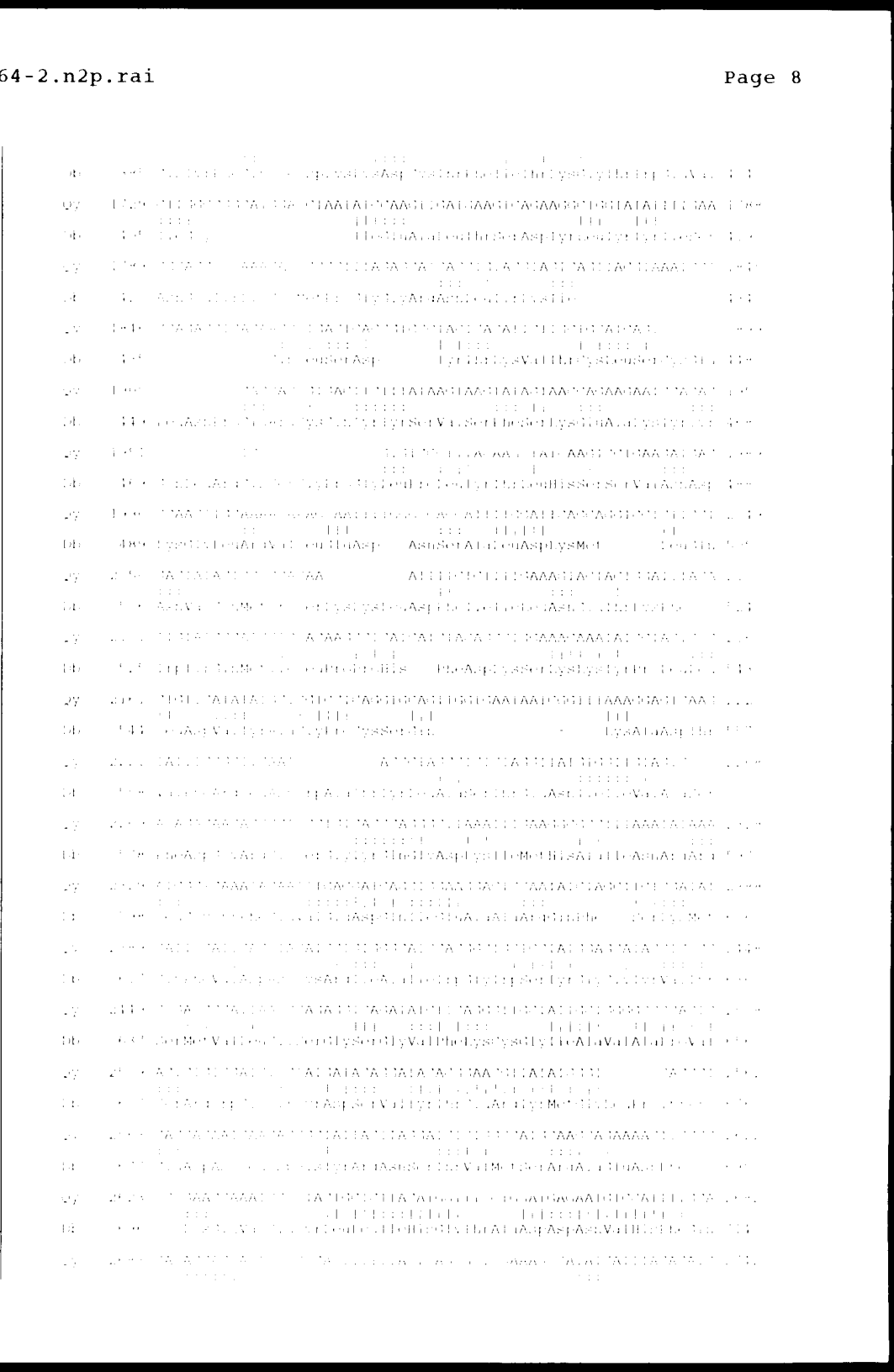


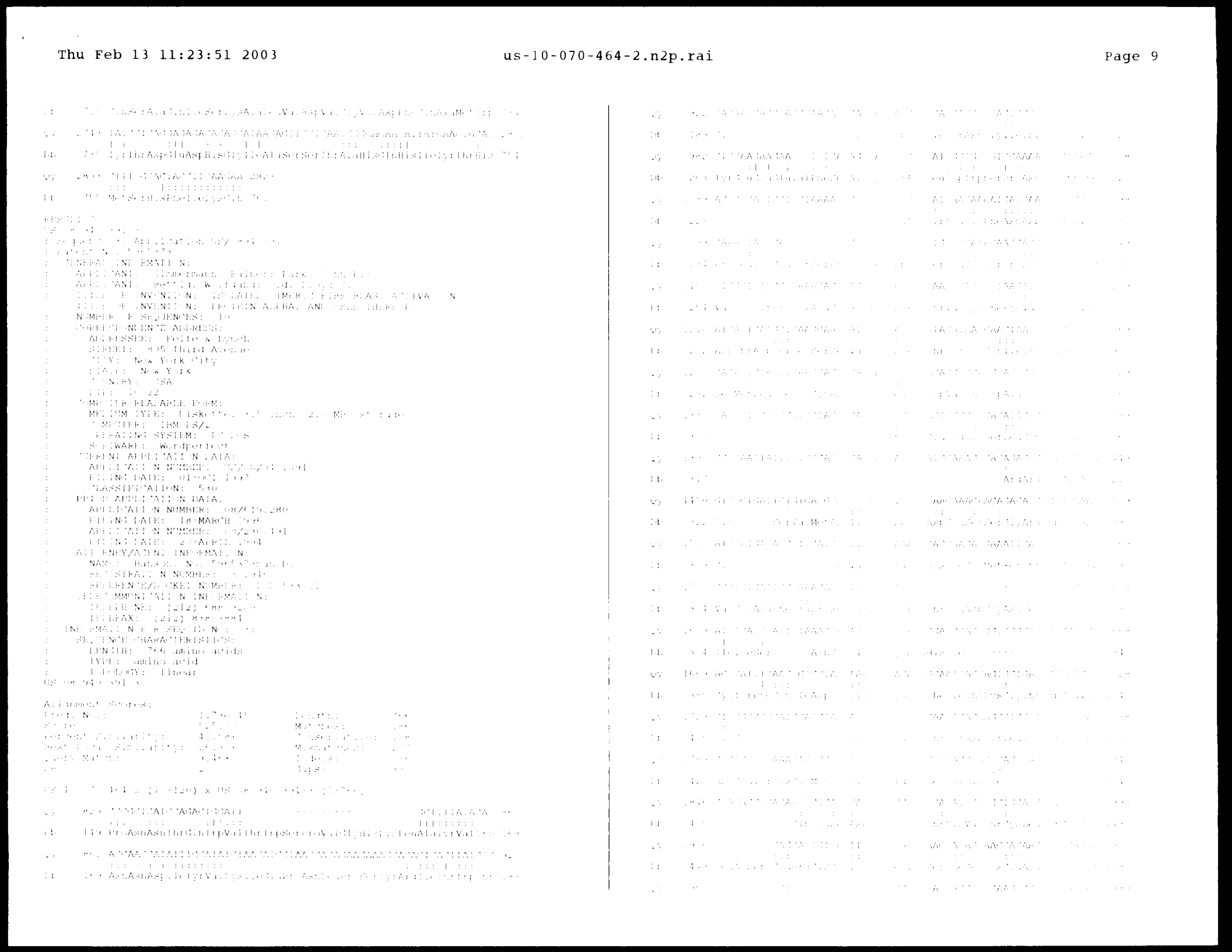


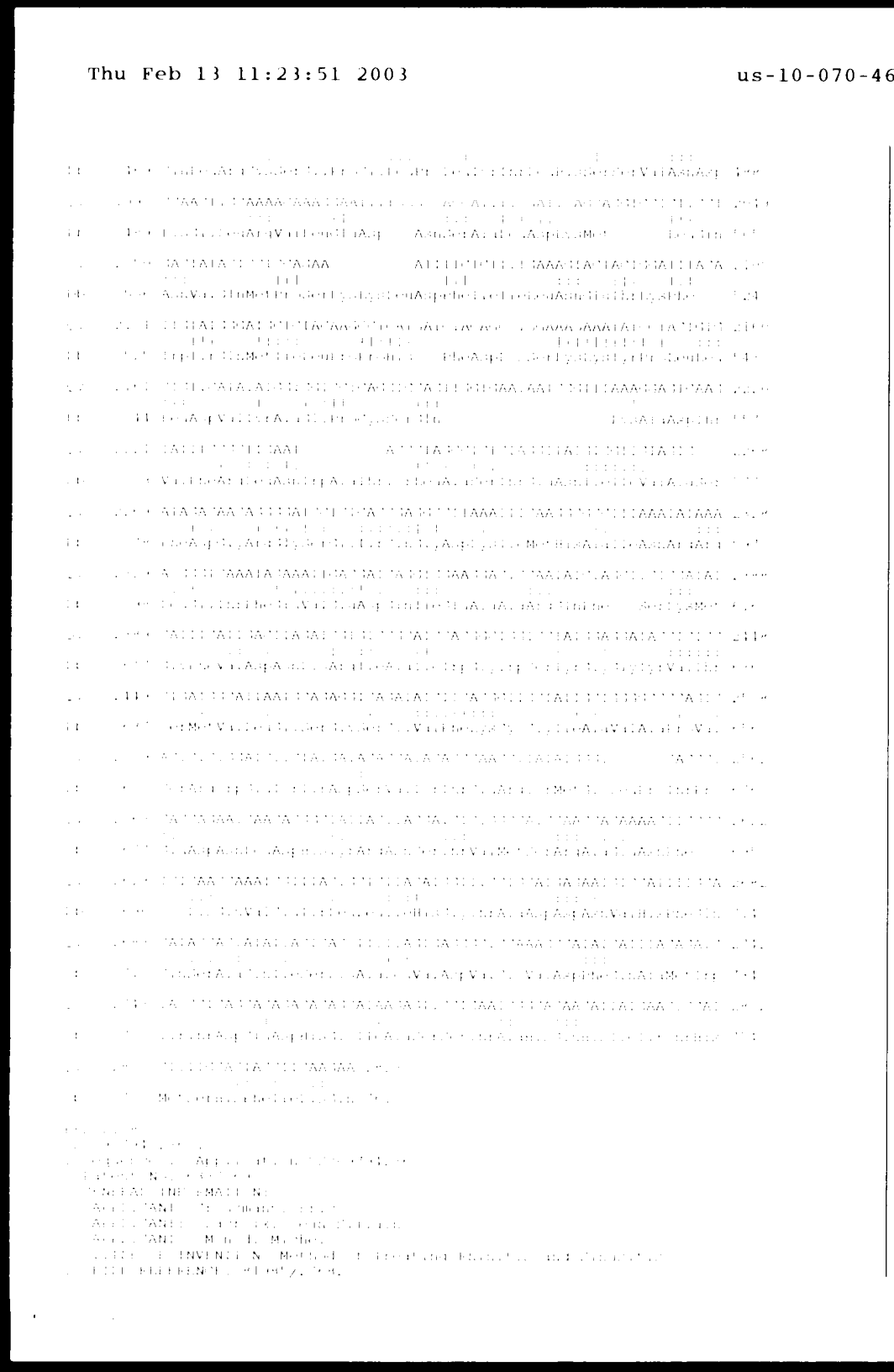


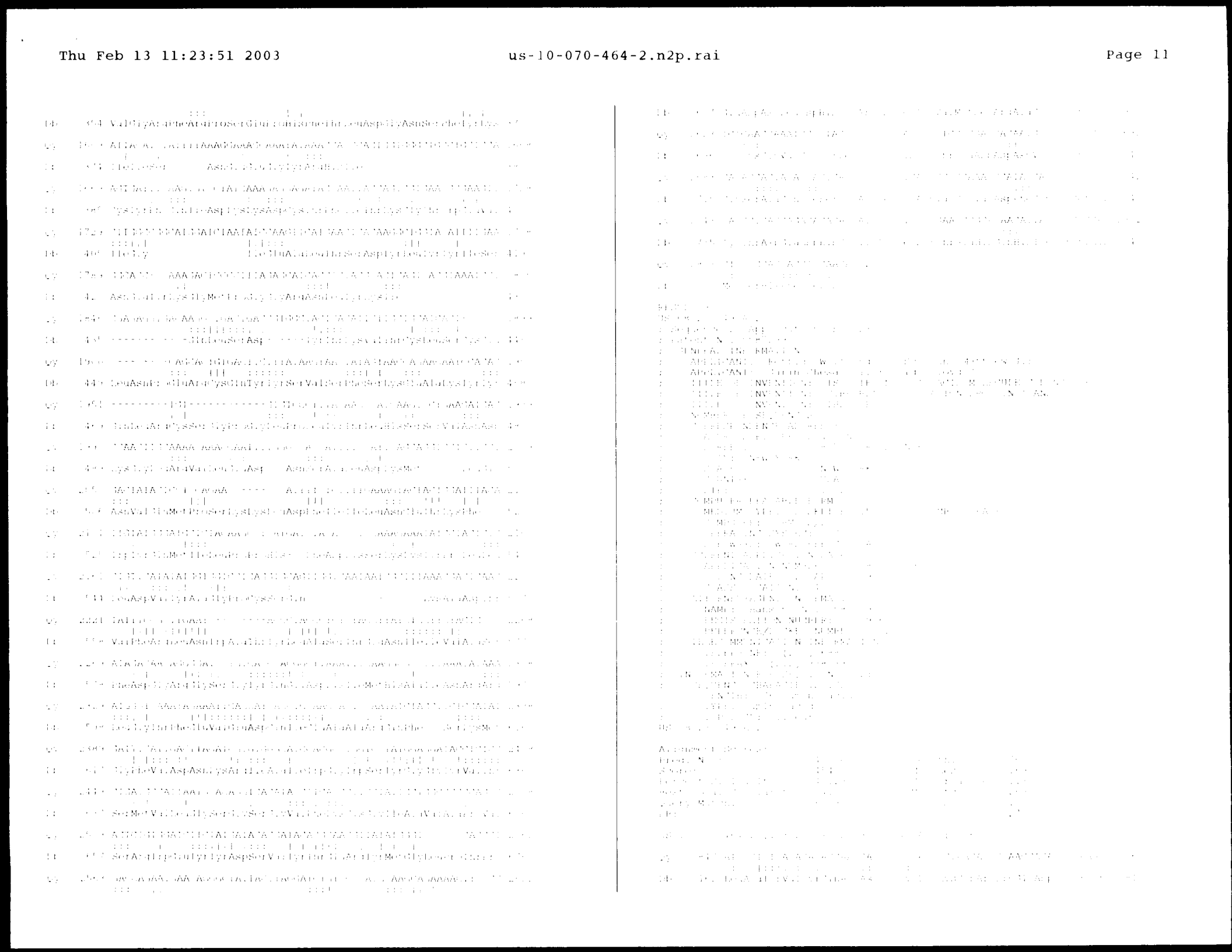


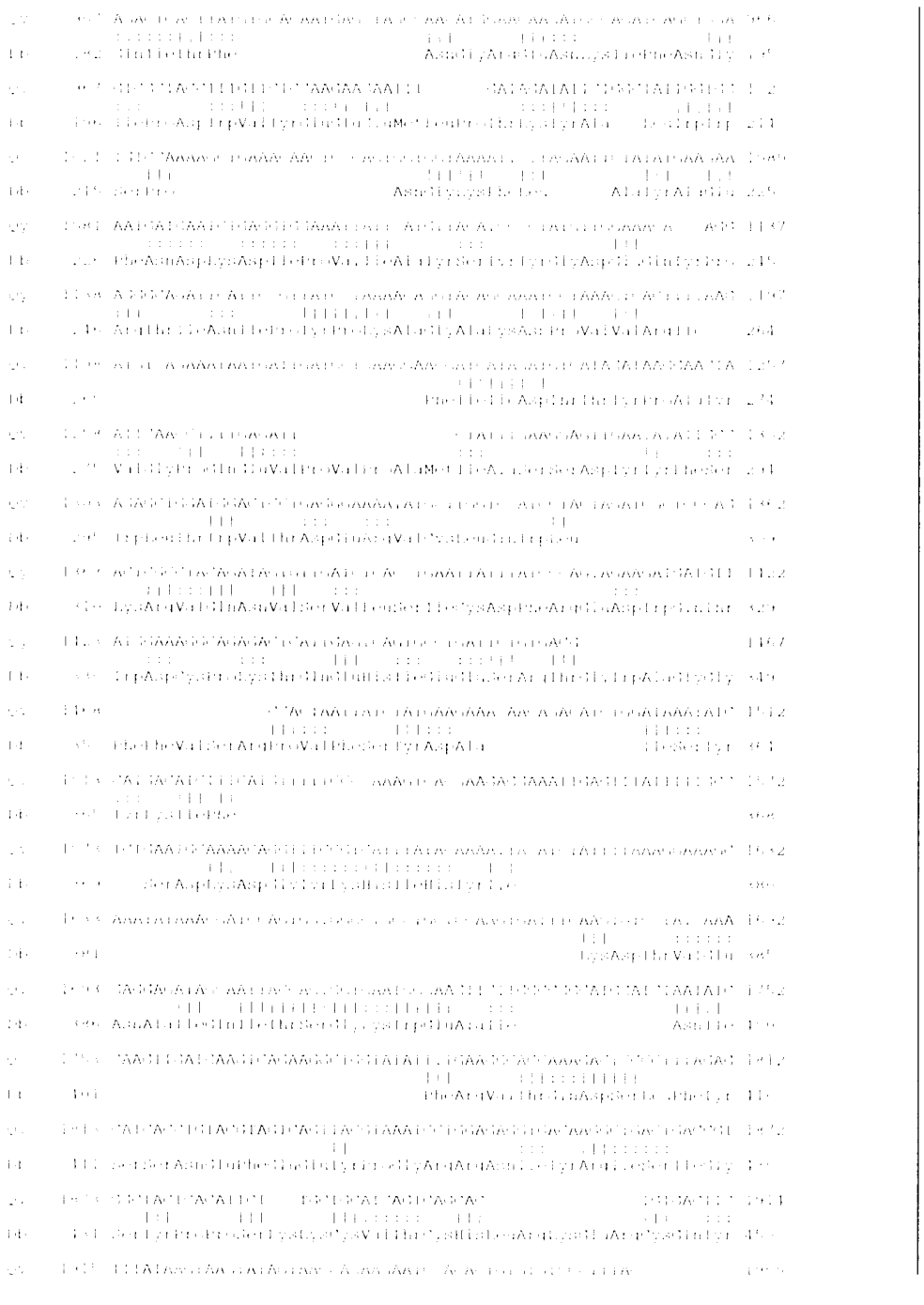


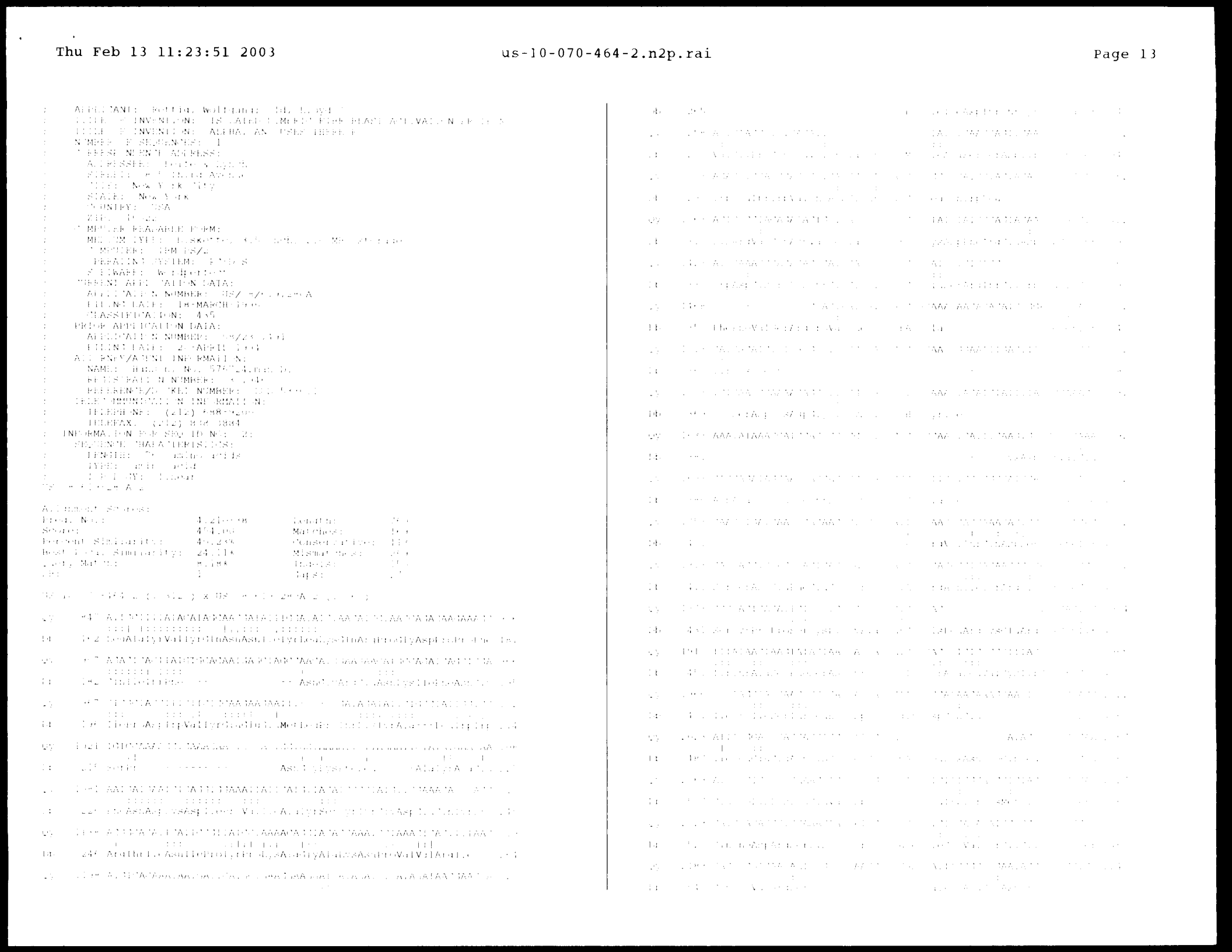


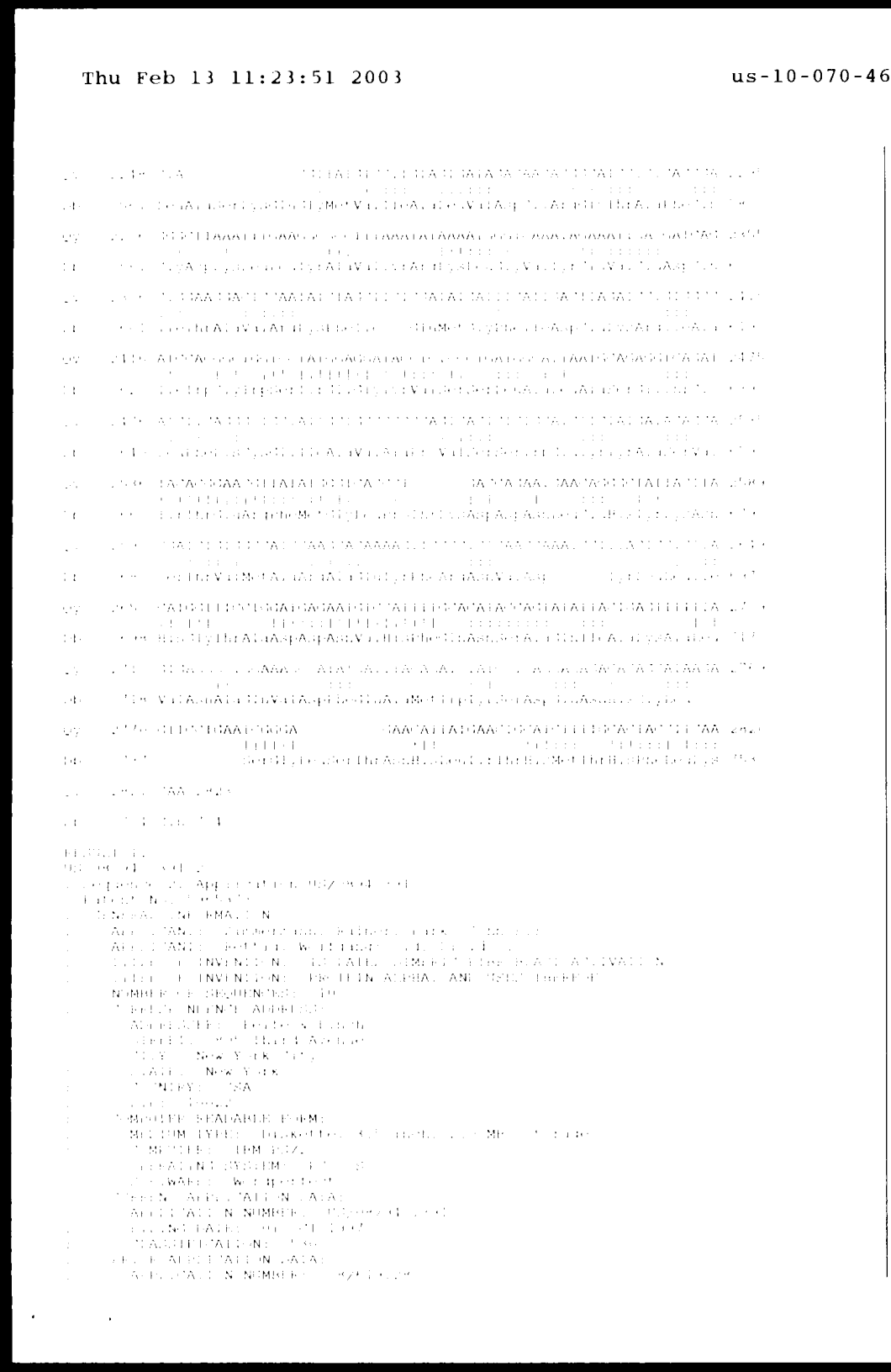


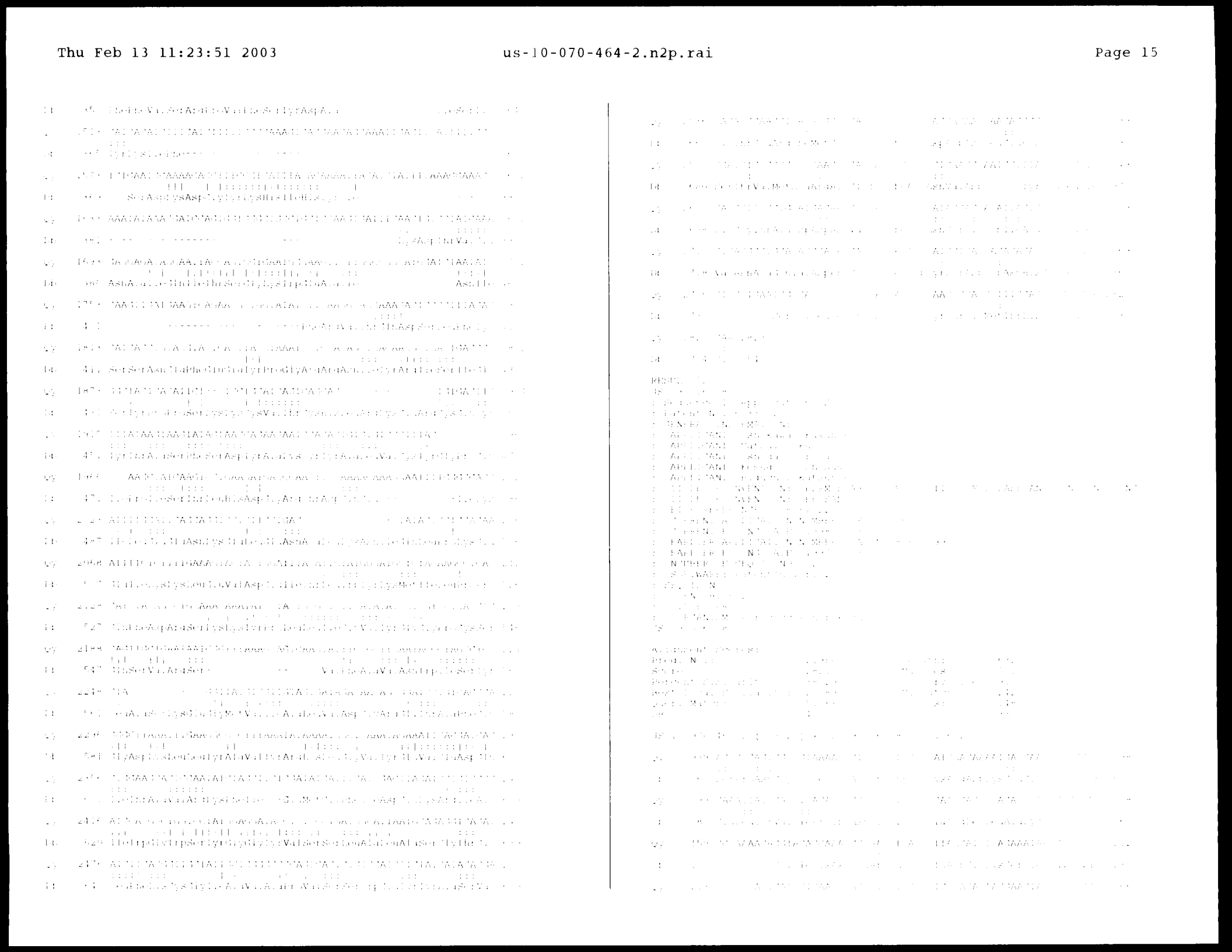


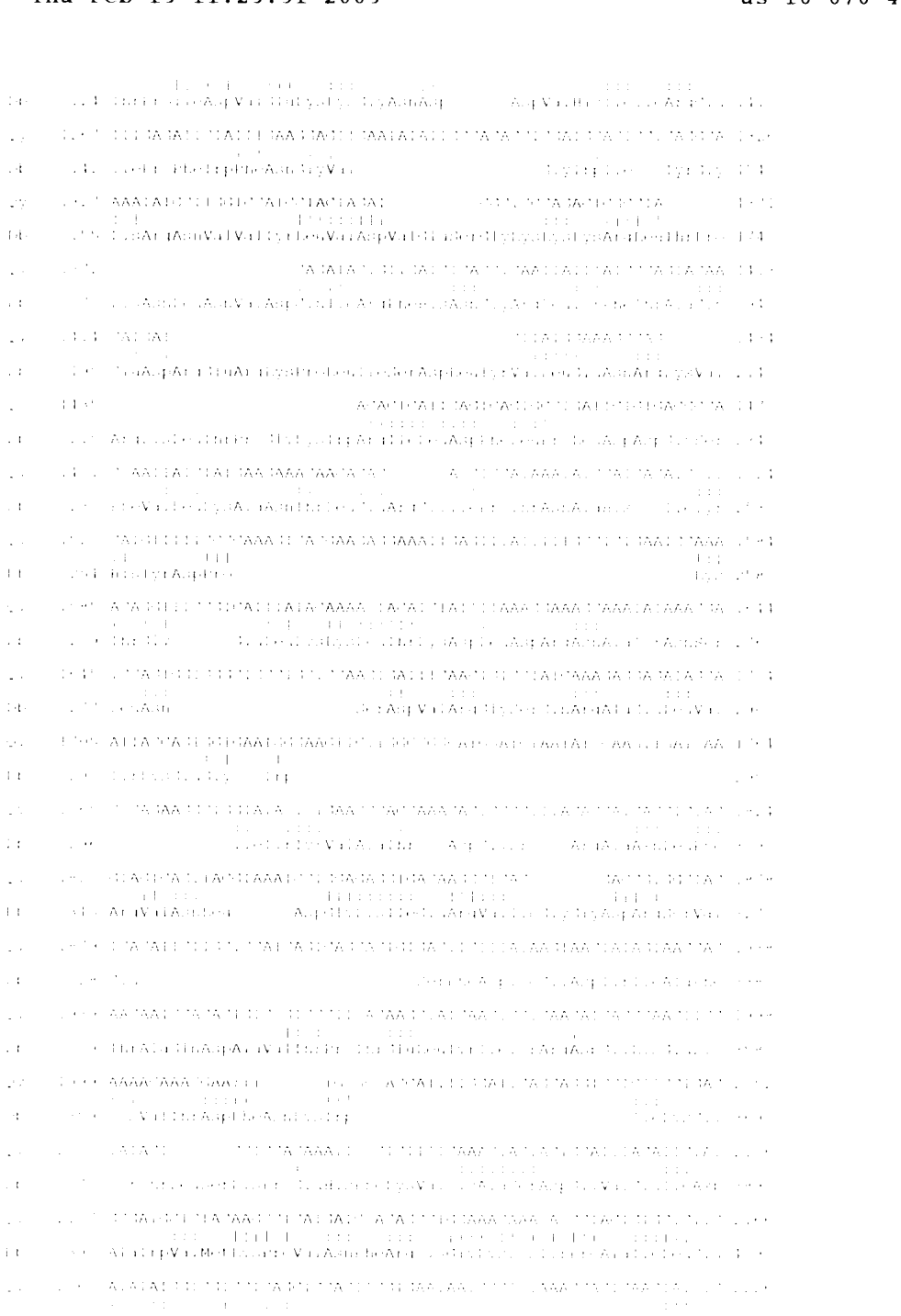


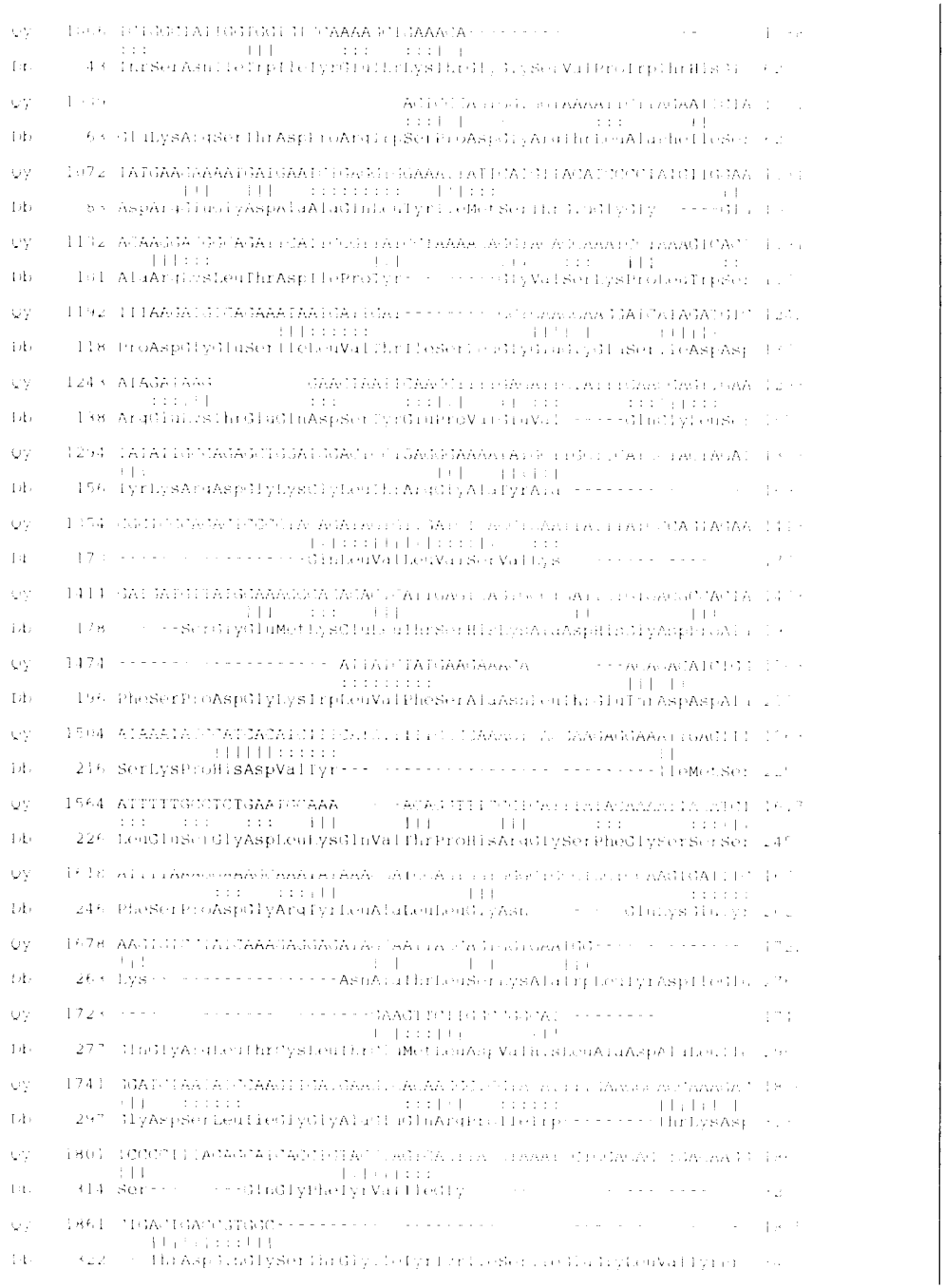


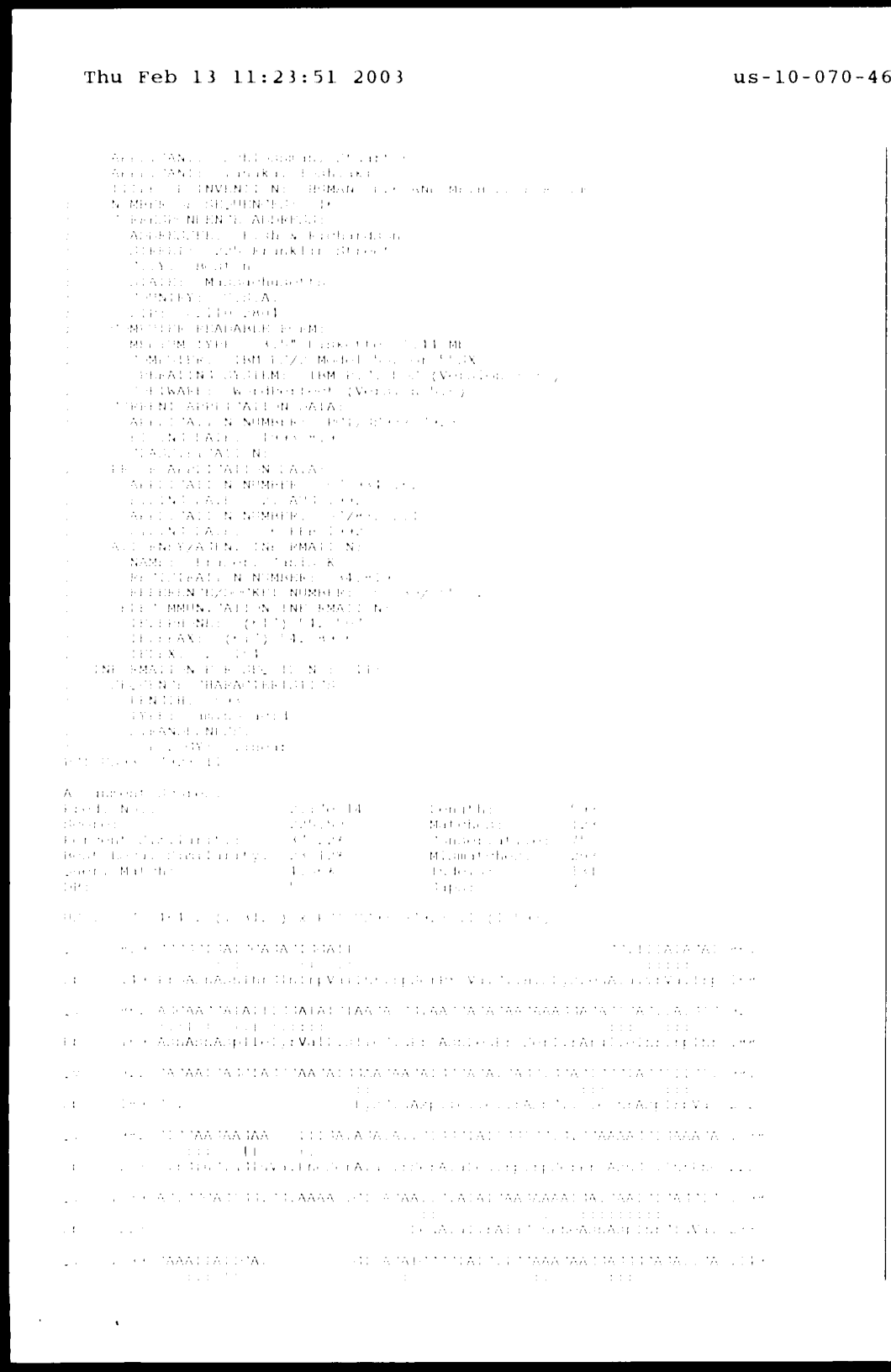


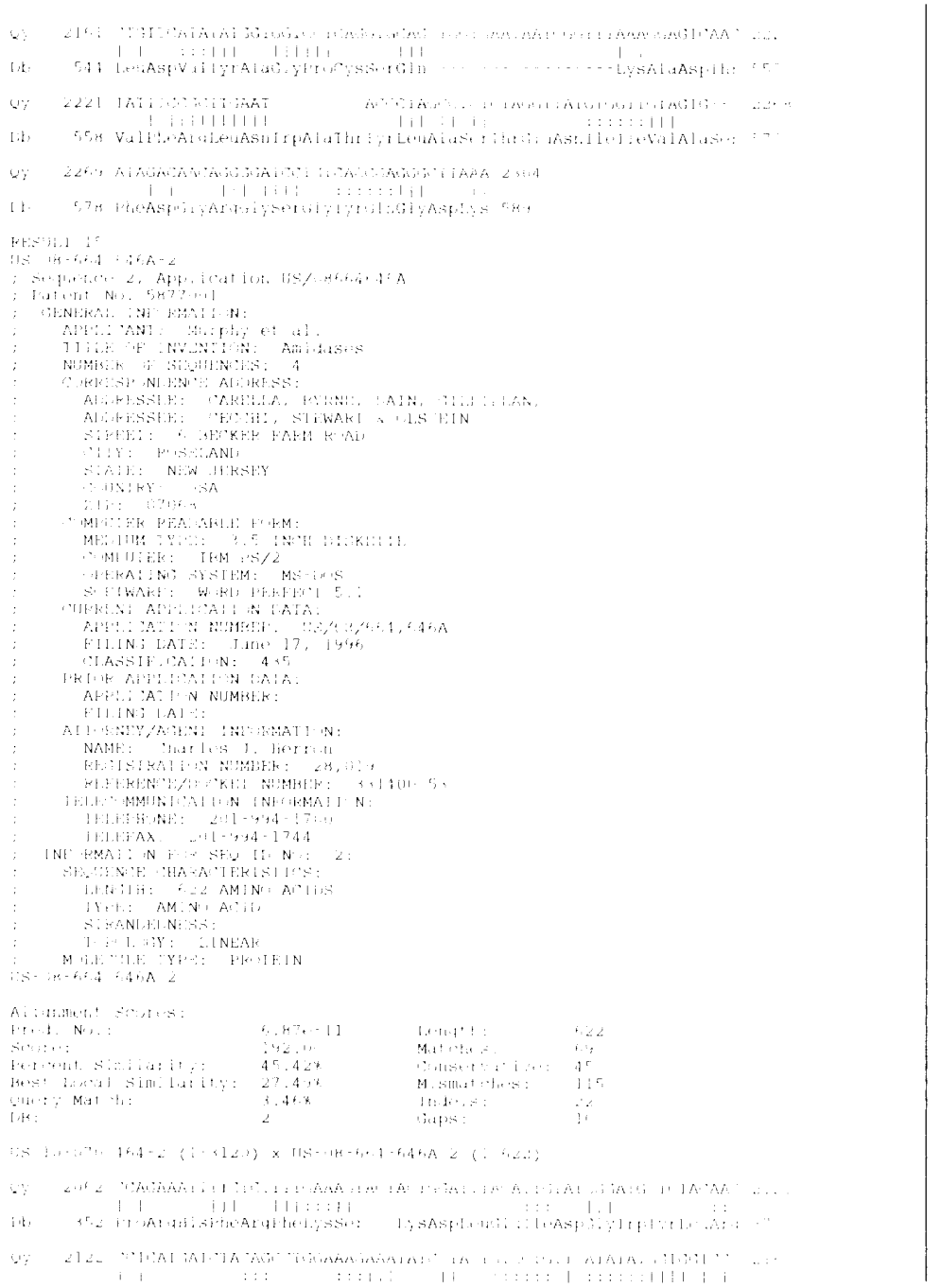












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; Patent No. 5872001
; GENERAL INFORMATION:
; APPLICANT: Murphy et al.
; TITLE OF INVENTION: Amidases
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
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; COMPUTER: IBM OS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/664,646A
; FILING DATE: June 17, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles J. Berman
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 3511US-5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-664-646A-2

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                        Copyright (c) 1993 - 2003  Compugen Ltd.

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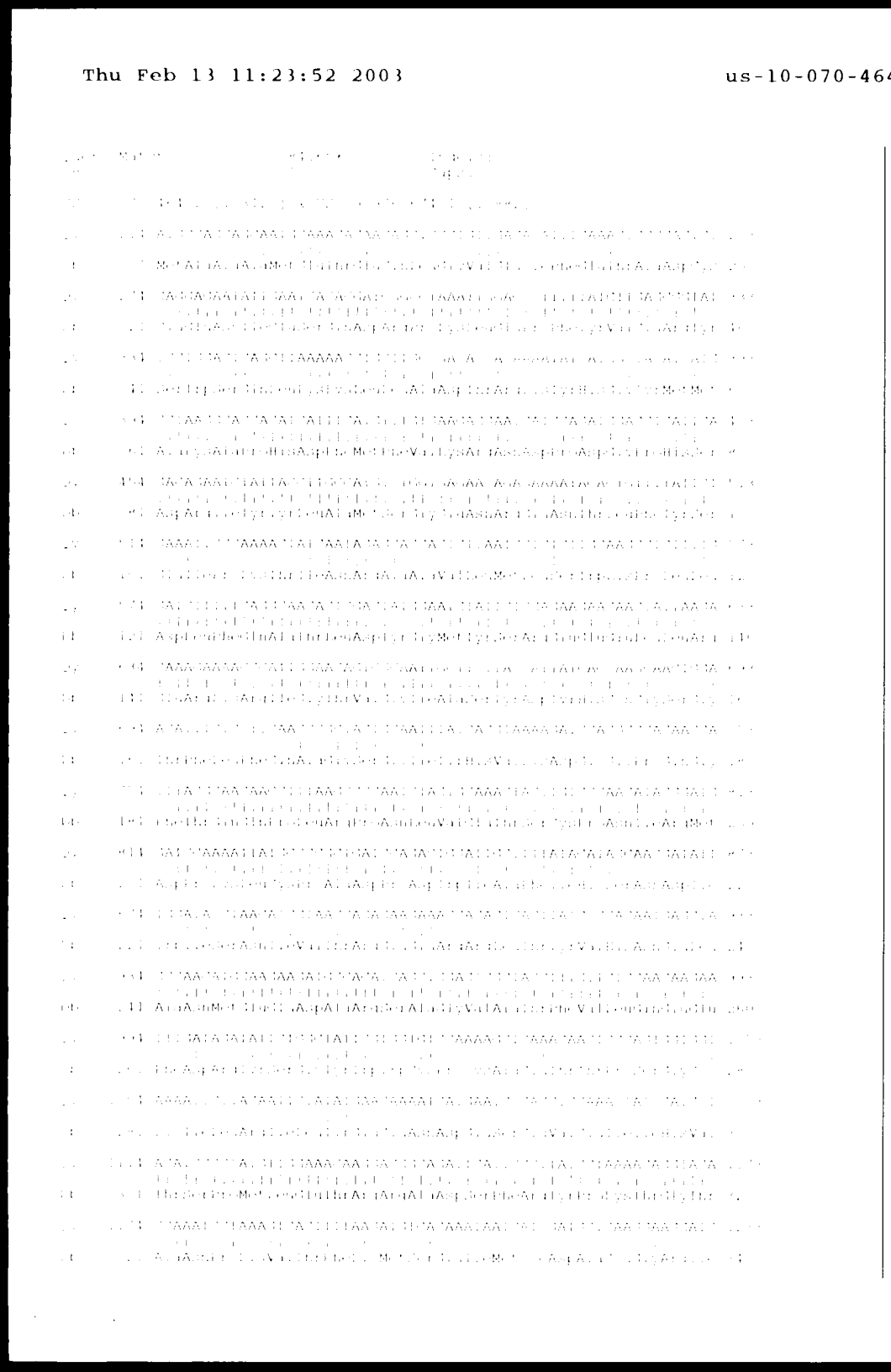
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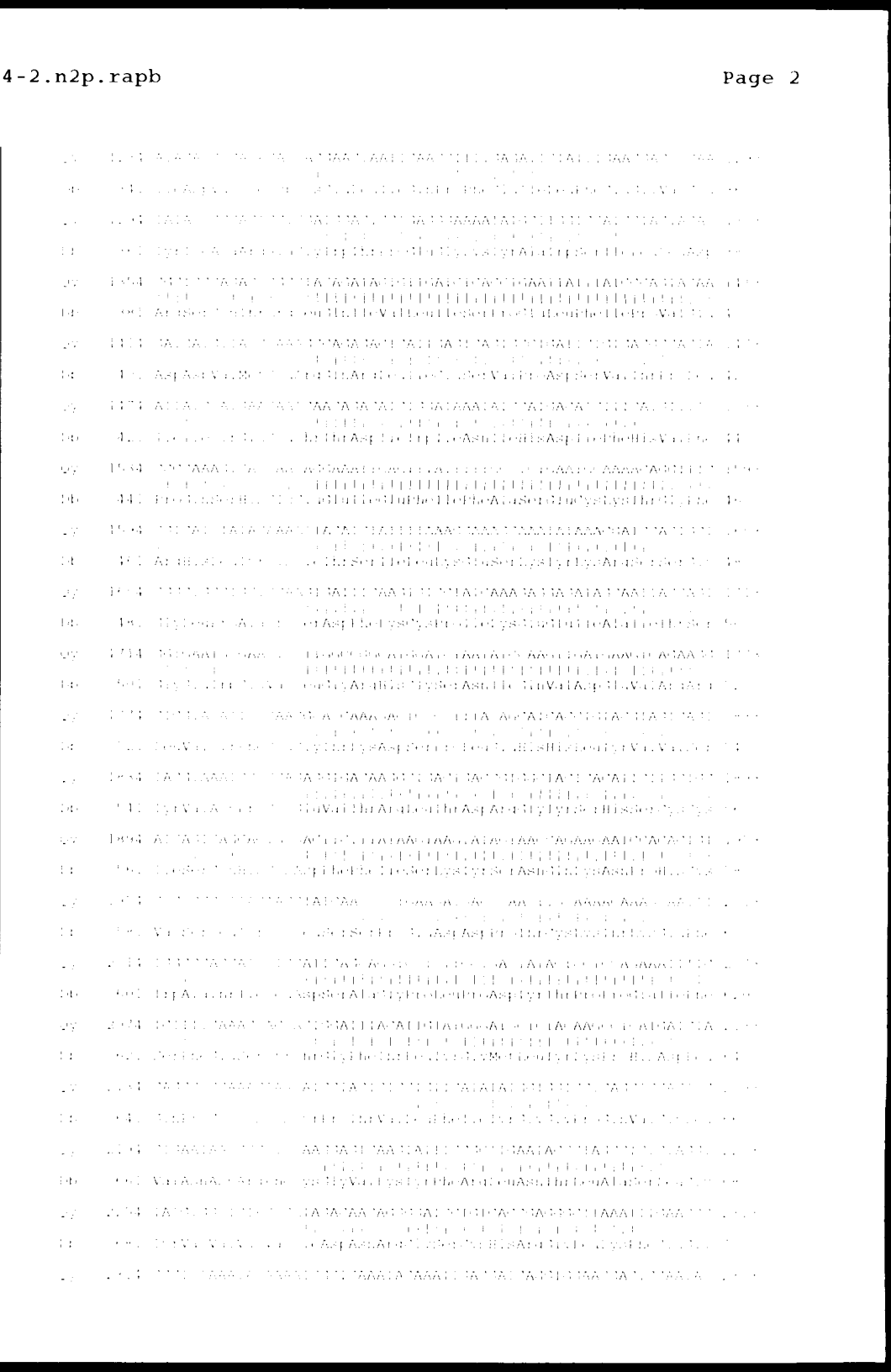
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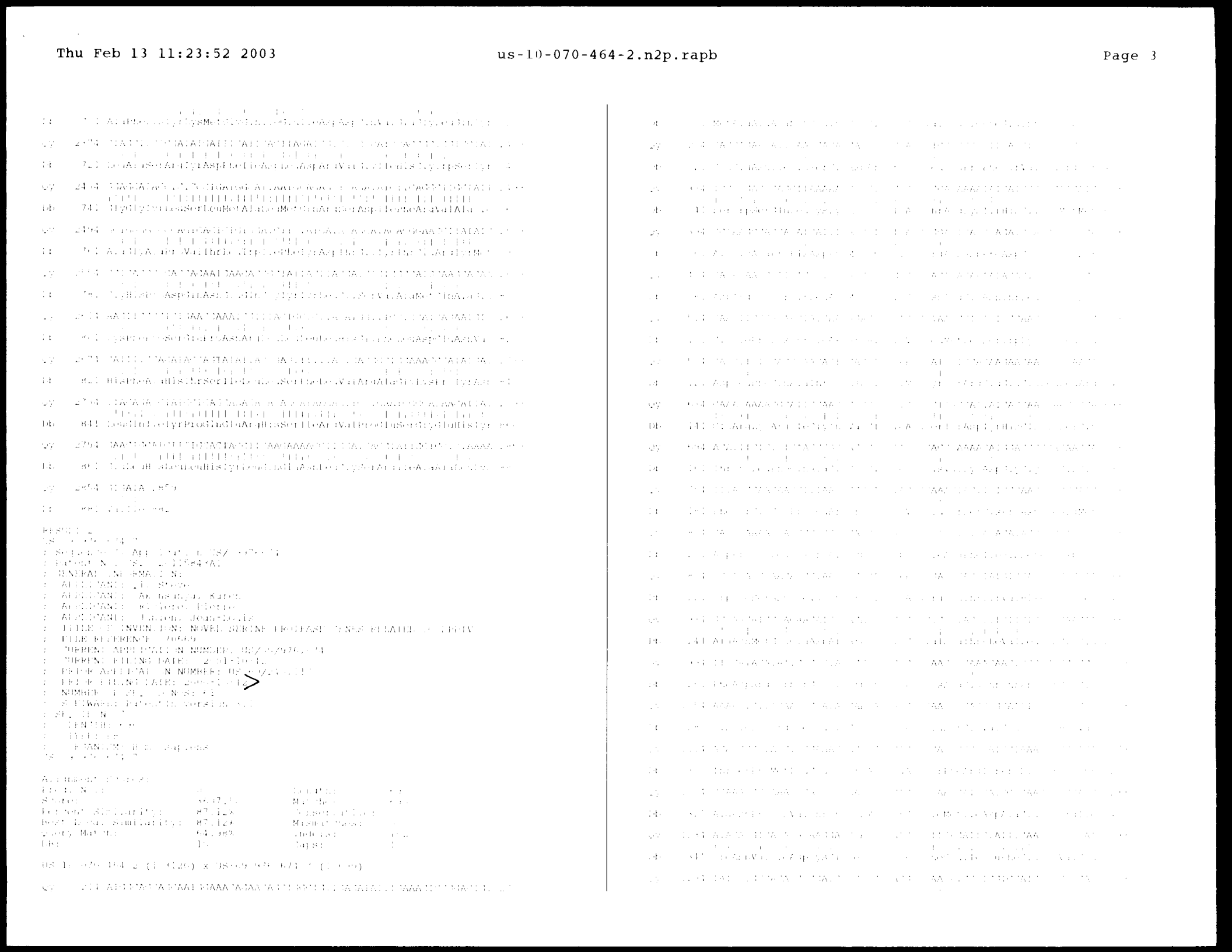
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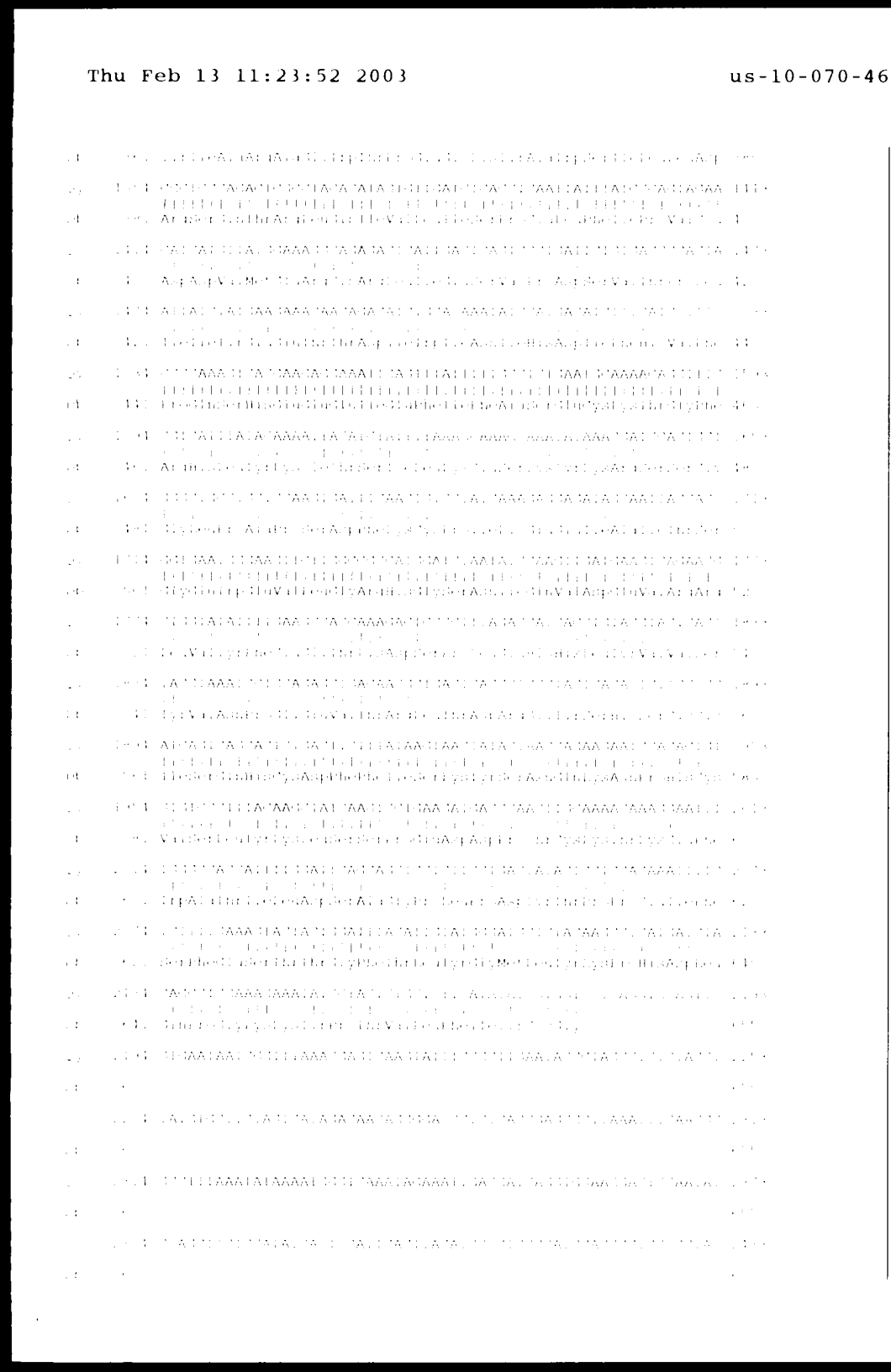
First processing: Minimum Match 0%
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                  Listing first 45 summaries

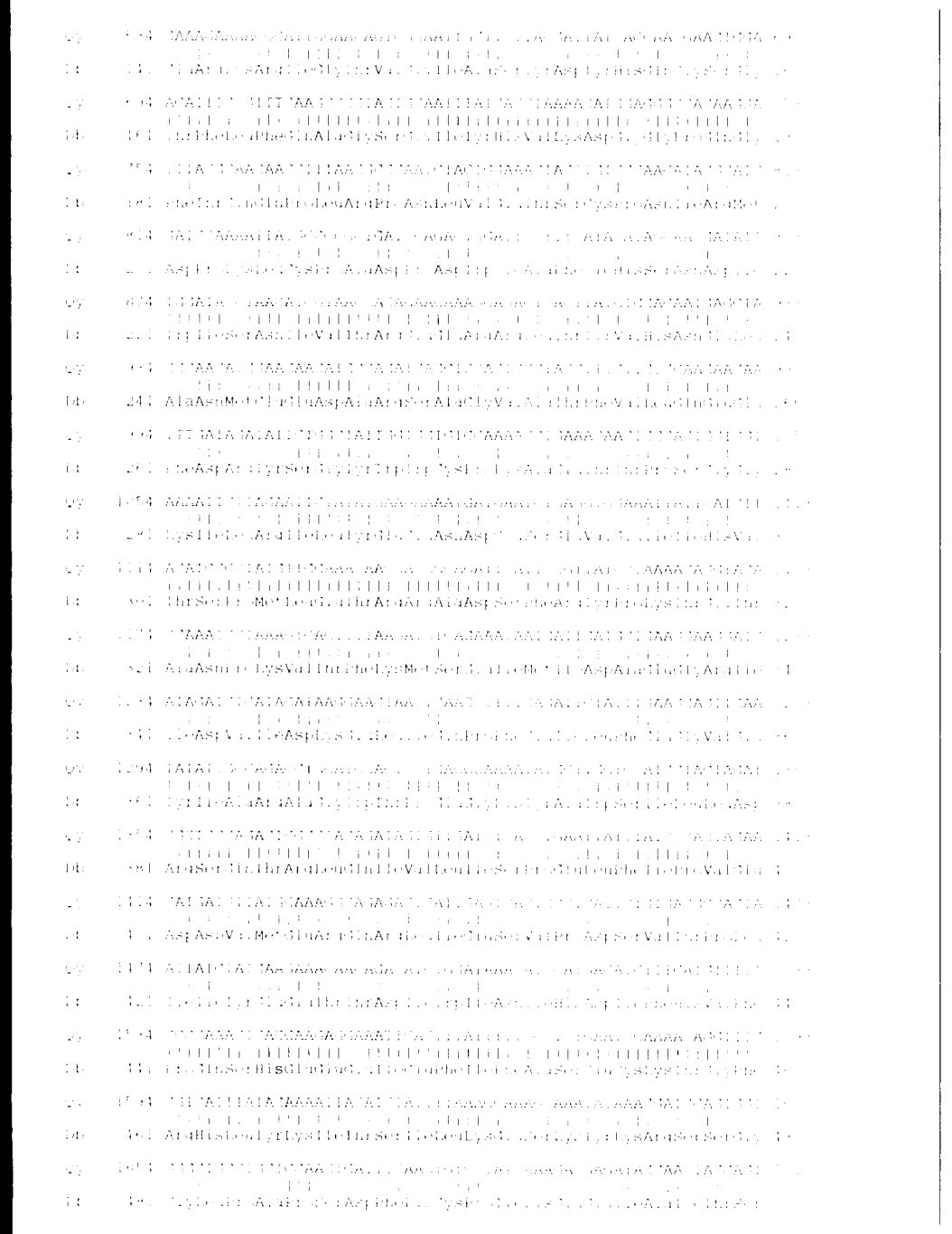
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-Q=/[illegible]/_p_4_US07_07363_5000_1_1_1_5000_1_5562_1426%/app_qpro_1.fas* -L=271
-DB Published_Applications_AA_*:PIR1 fasta* -SUFFIX n2p.rapb -MINMATCH 0...
-I=50PCL.0 -D=50PEX1.0 -UNITS=bits -START=1 -END=-1 -MATRIX blosum62
-TRANS human40.tbl -LIST 45 -ALIGN=200 -THR_SCORE pct -THR_MAX 100
-THR_MIN 0 -ALIGN 15 -MODE=SEMI_GLOBAL_SUBHMM-pro -NORM=xat -HEAPSIZE=50m -MINLEN
-MAXLEN=2000000000 -OUTFMT=/[illegible]/_1_1_1
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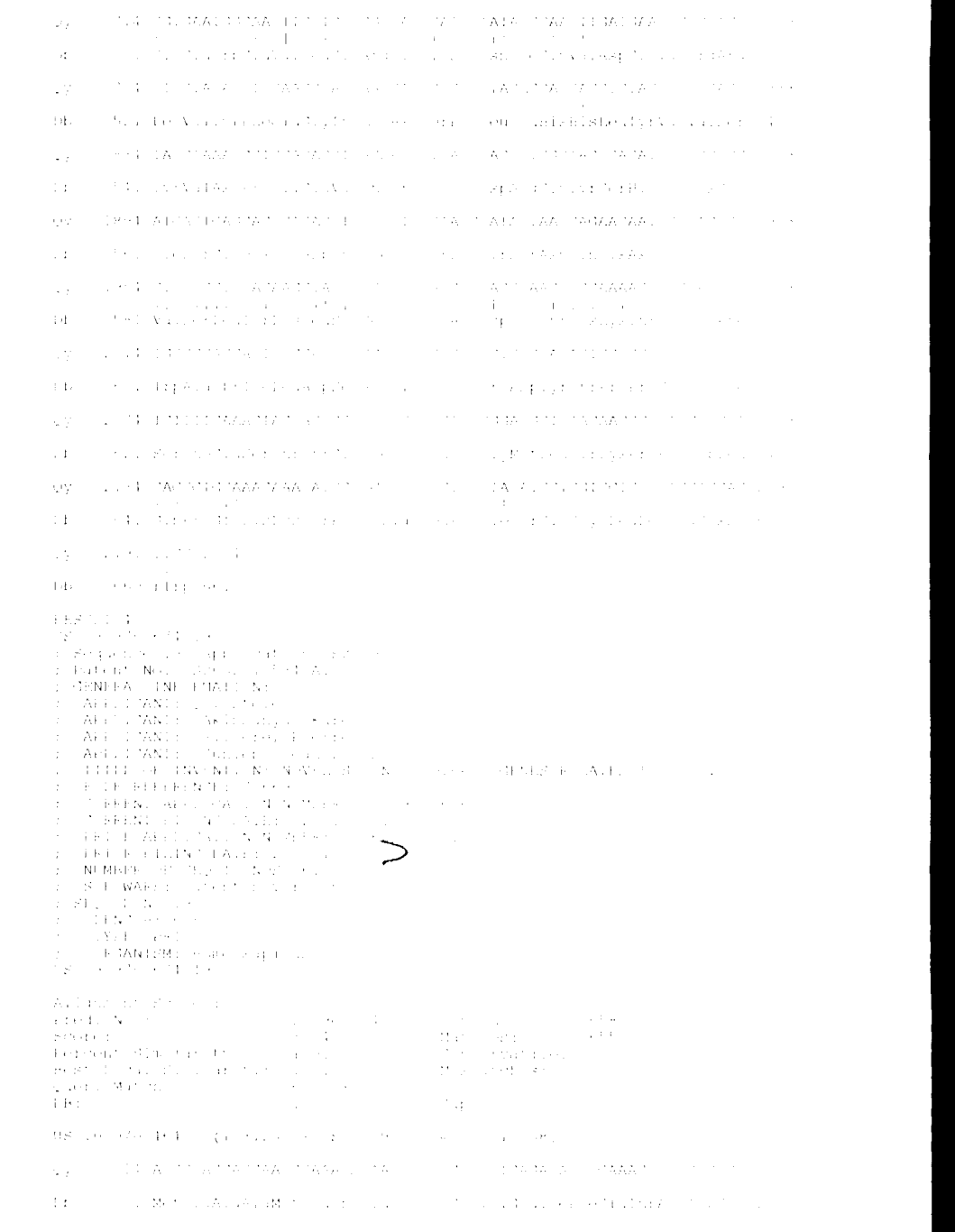


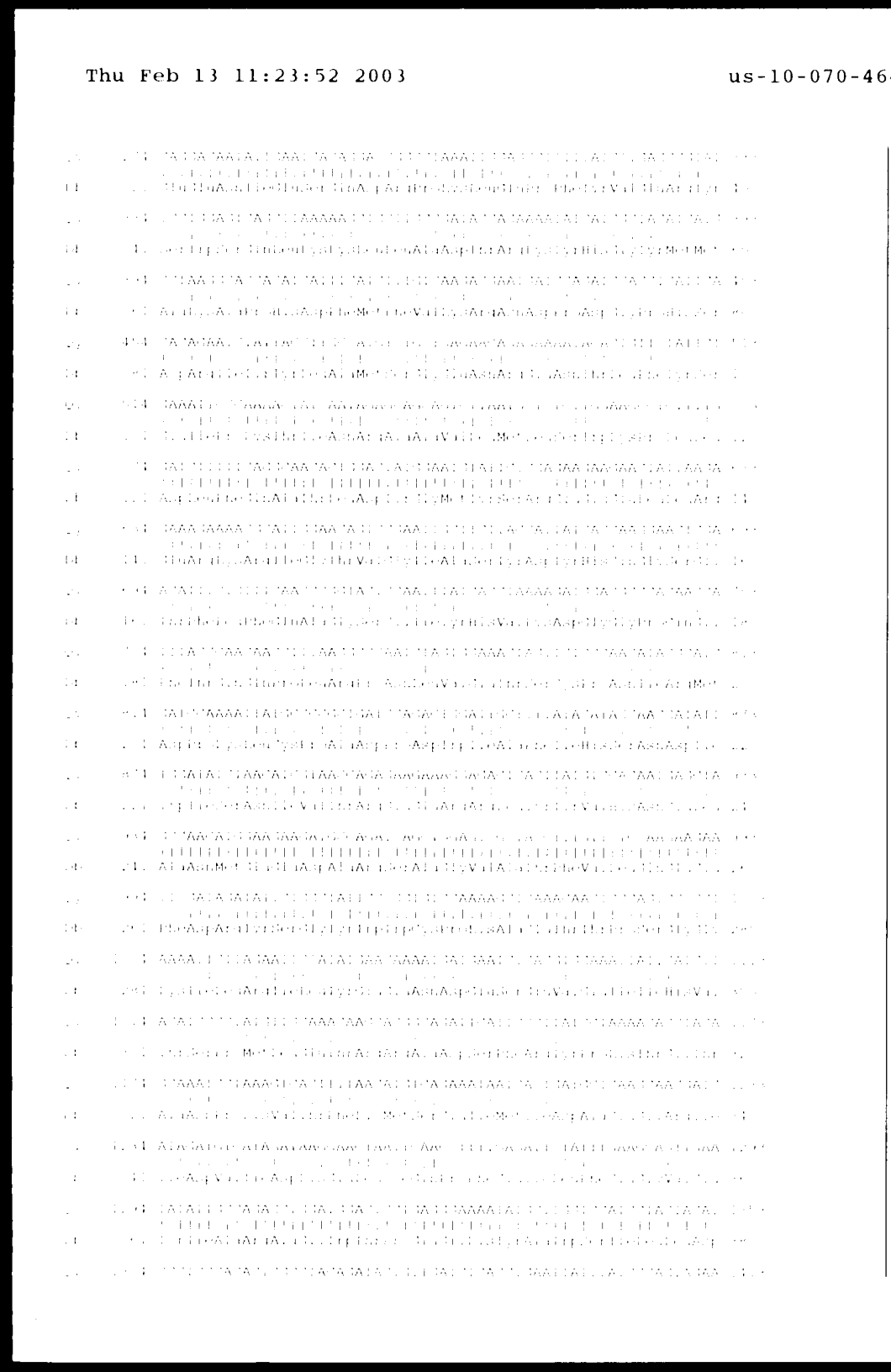


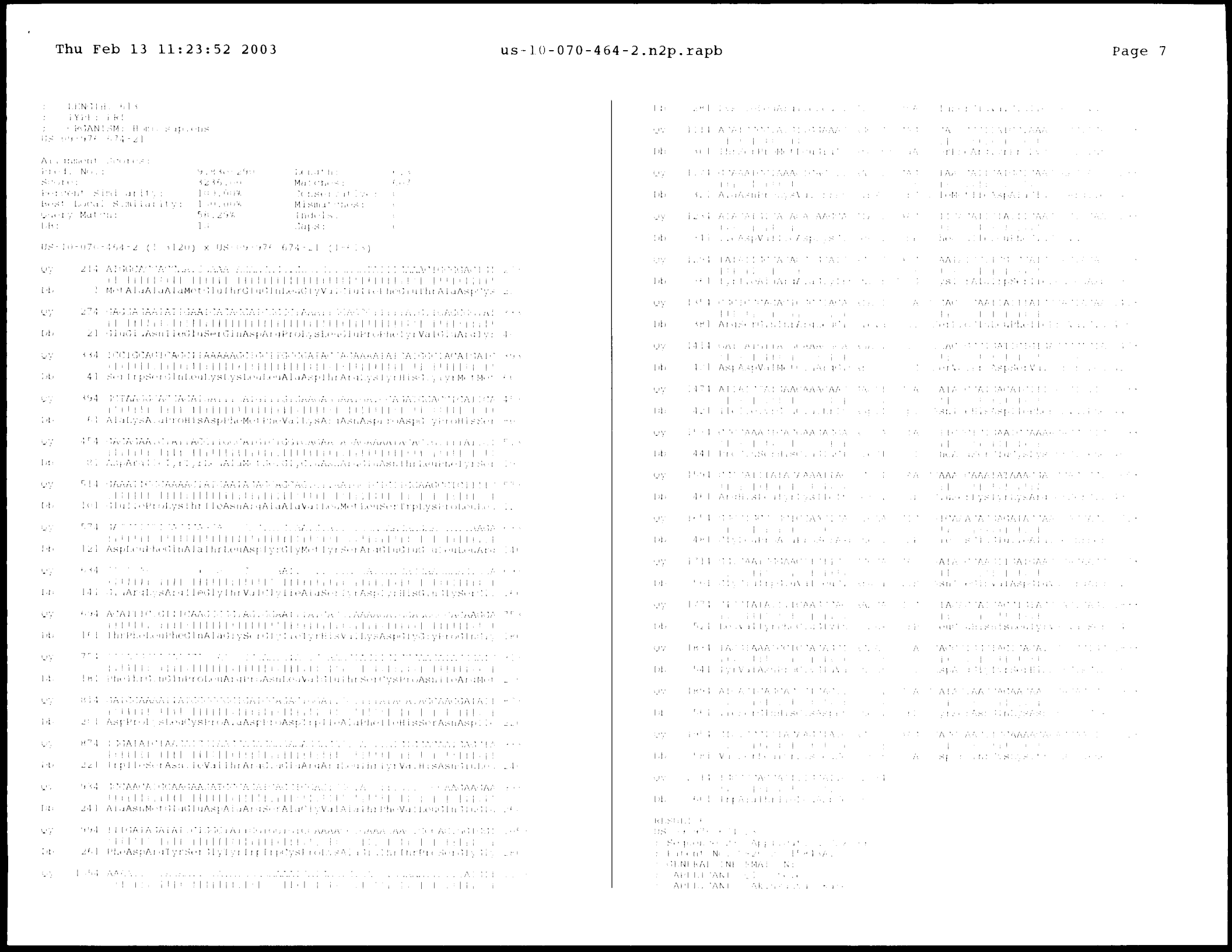


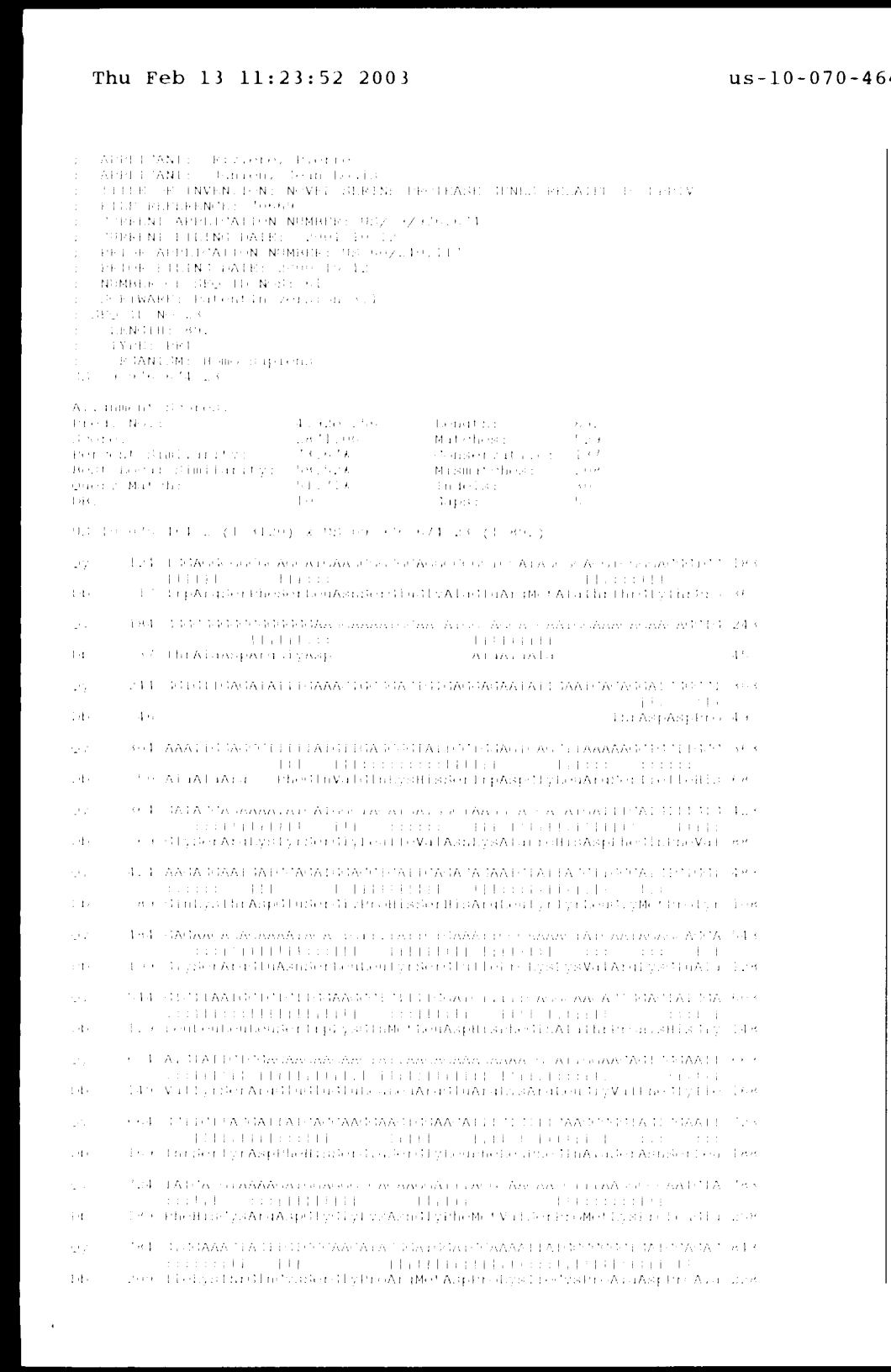


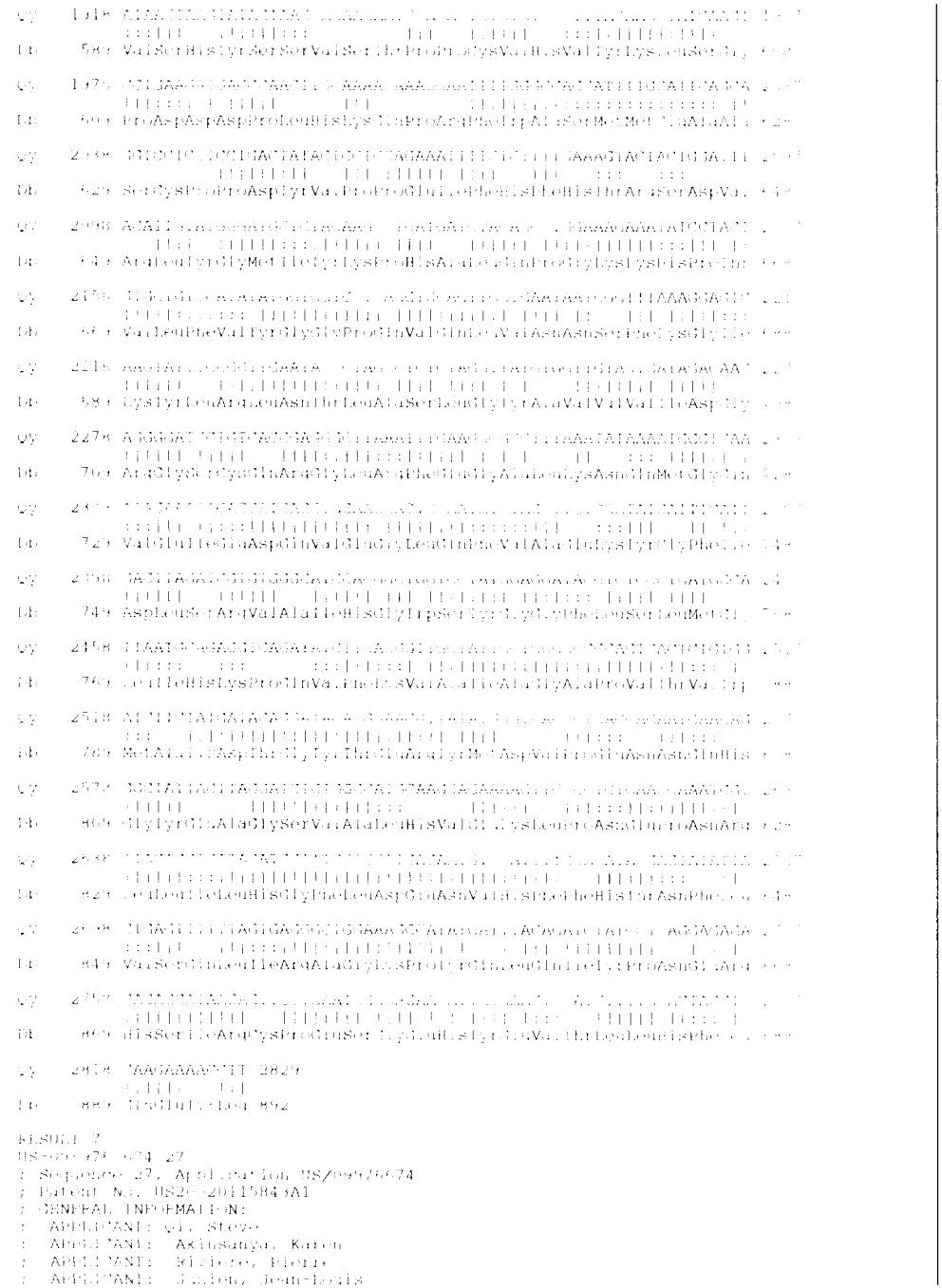


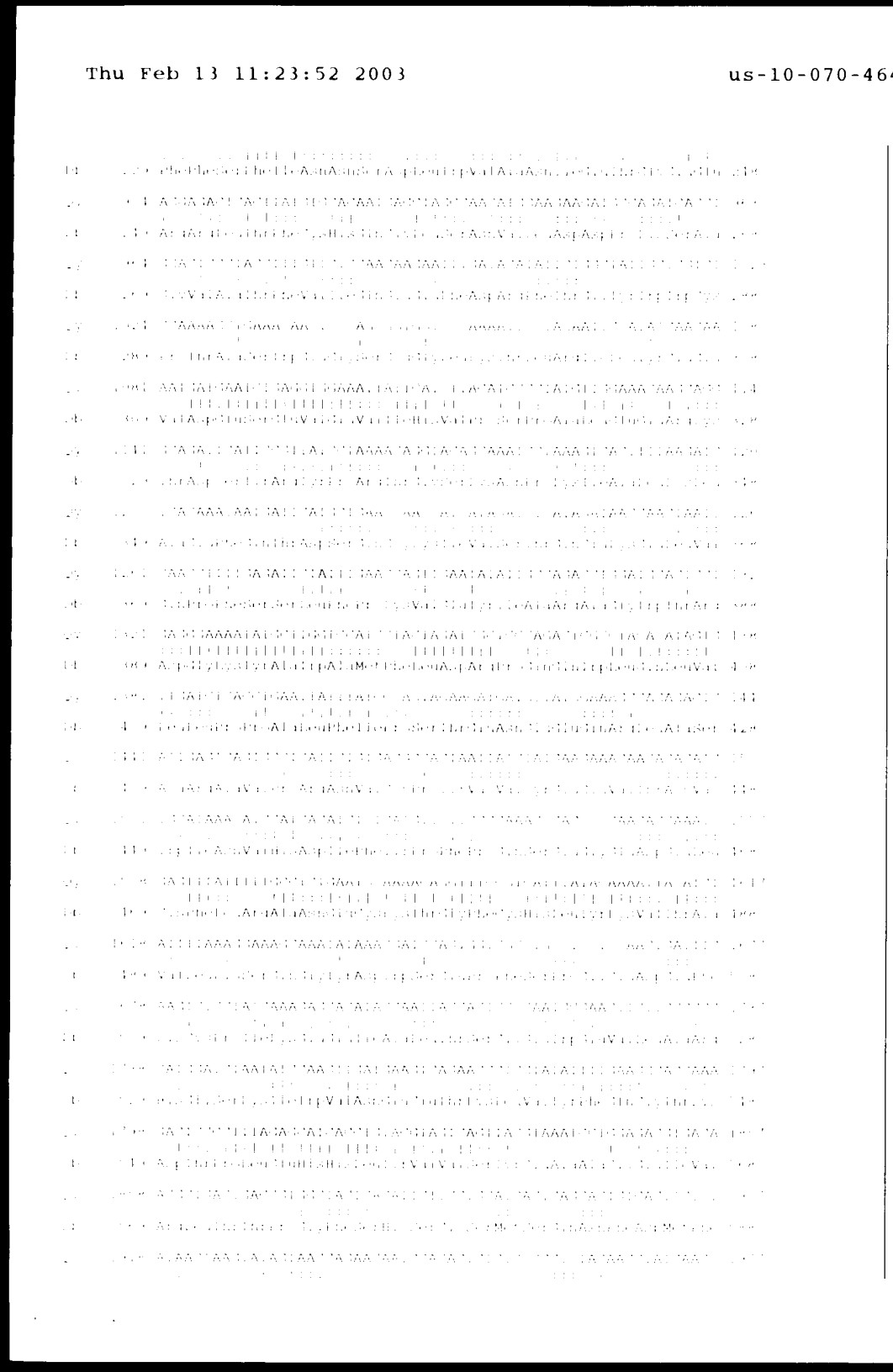


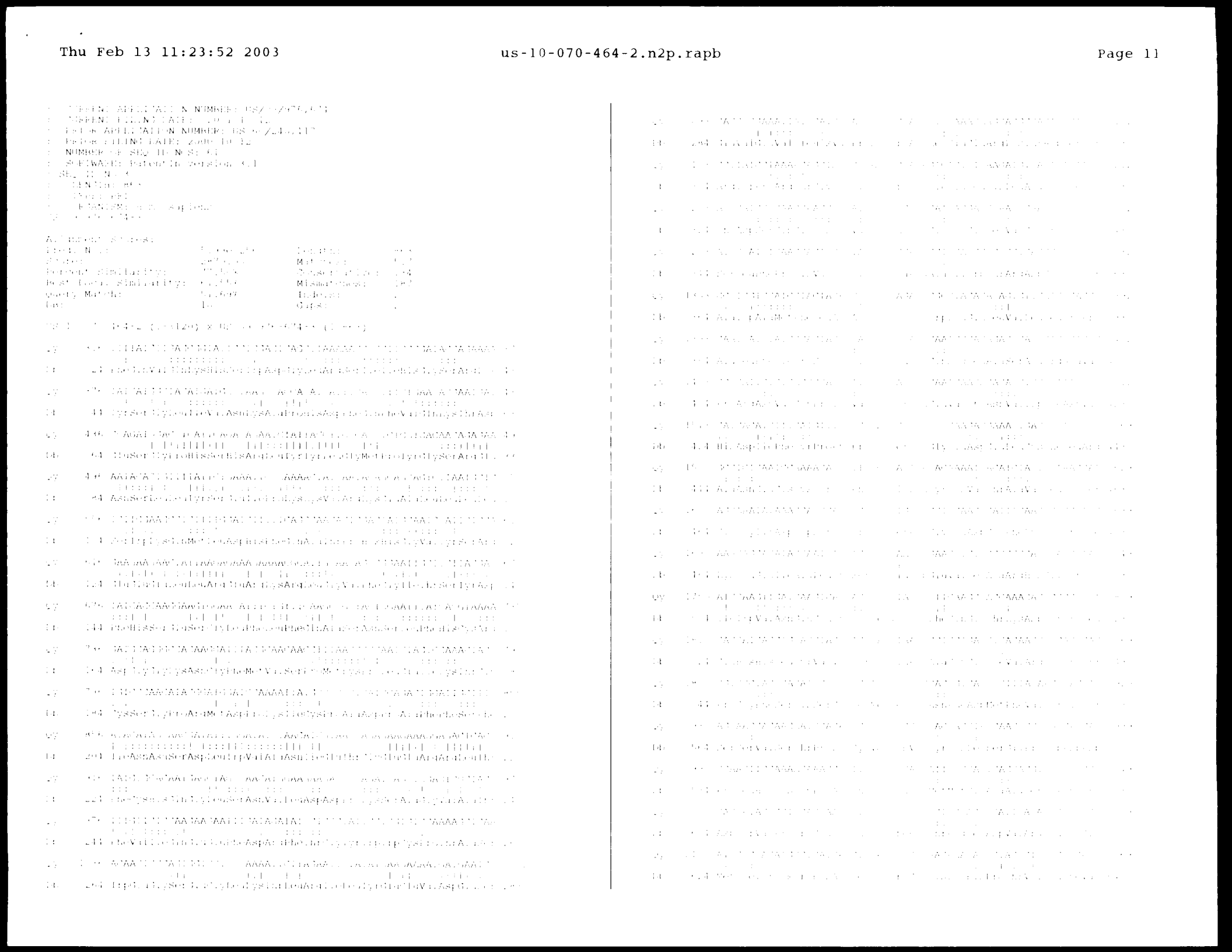


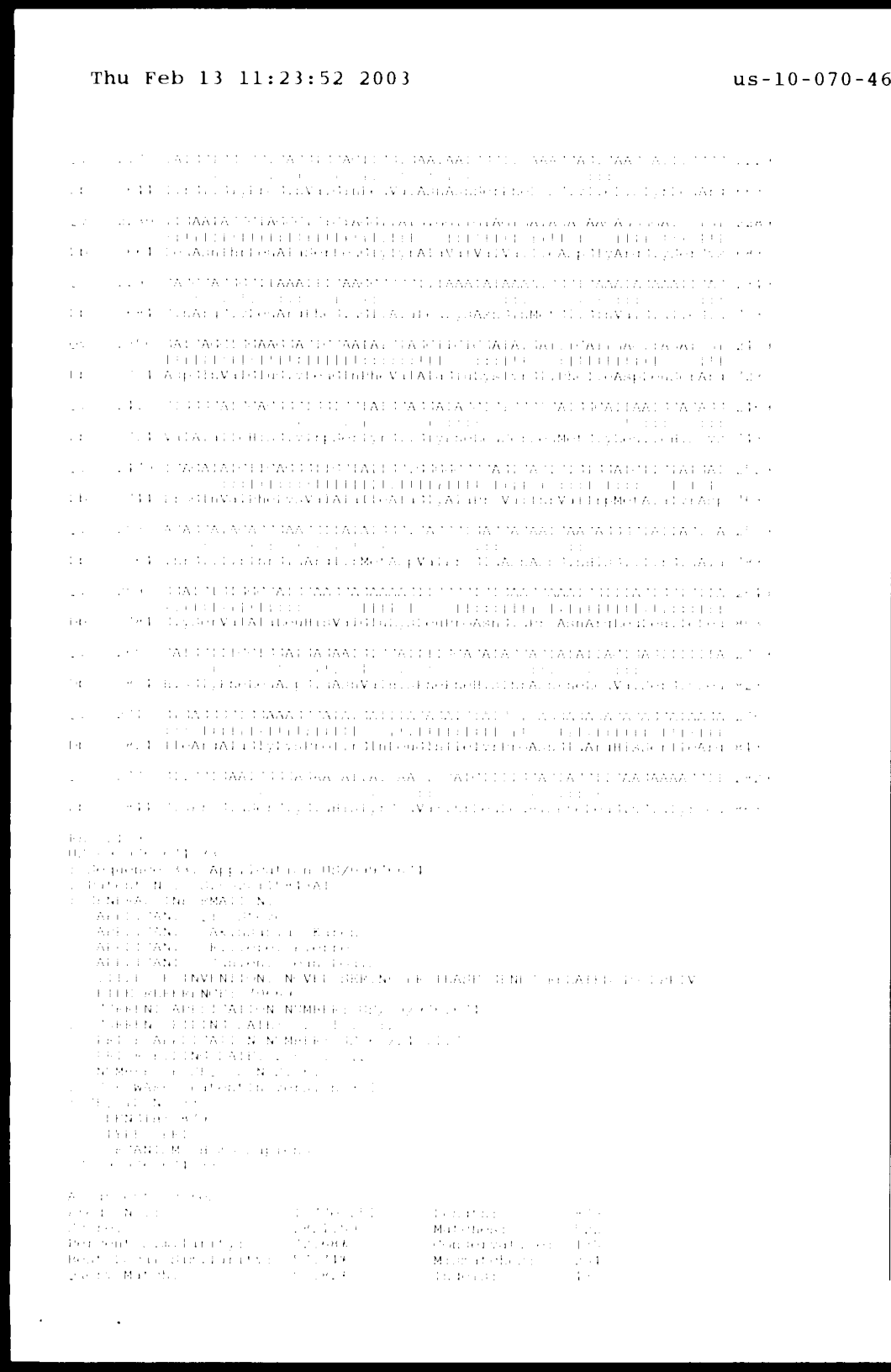


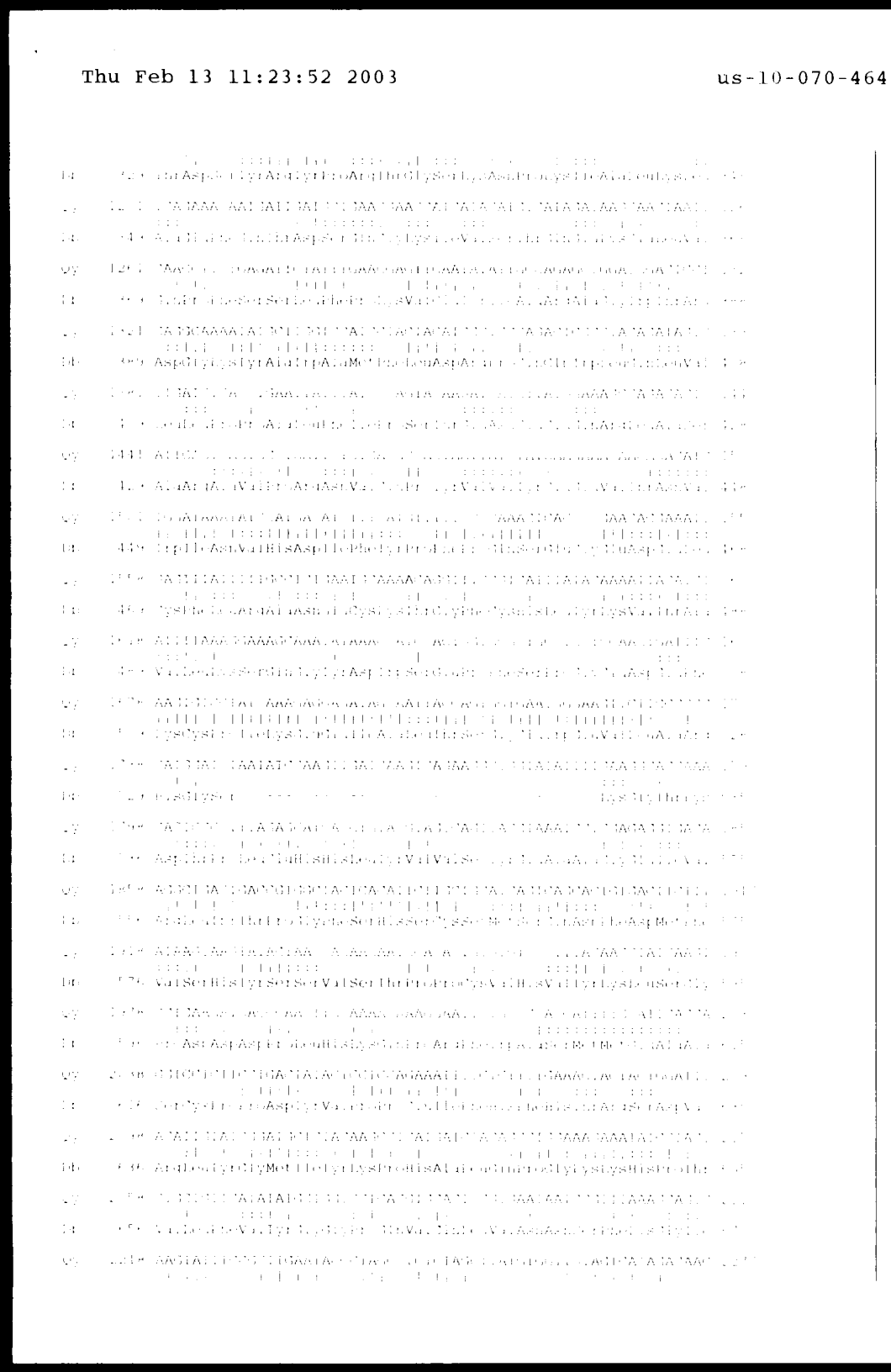


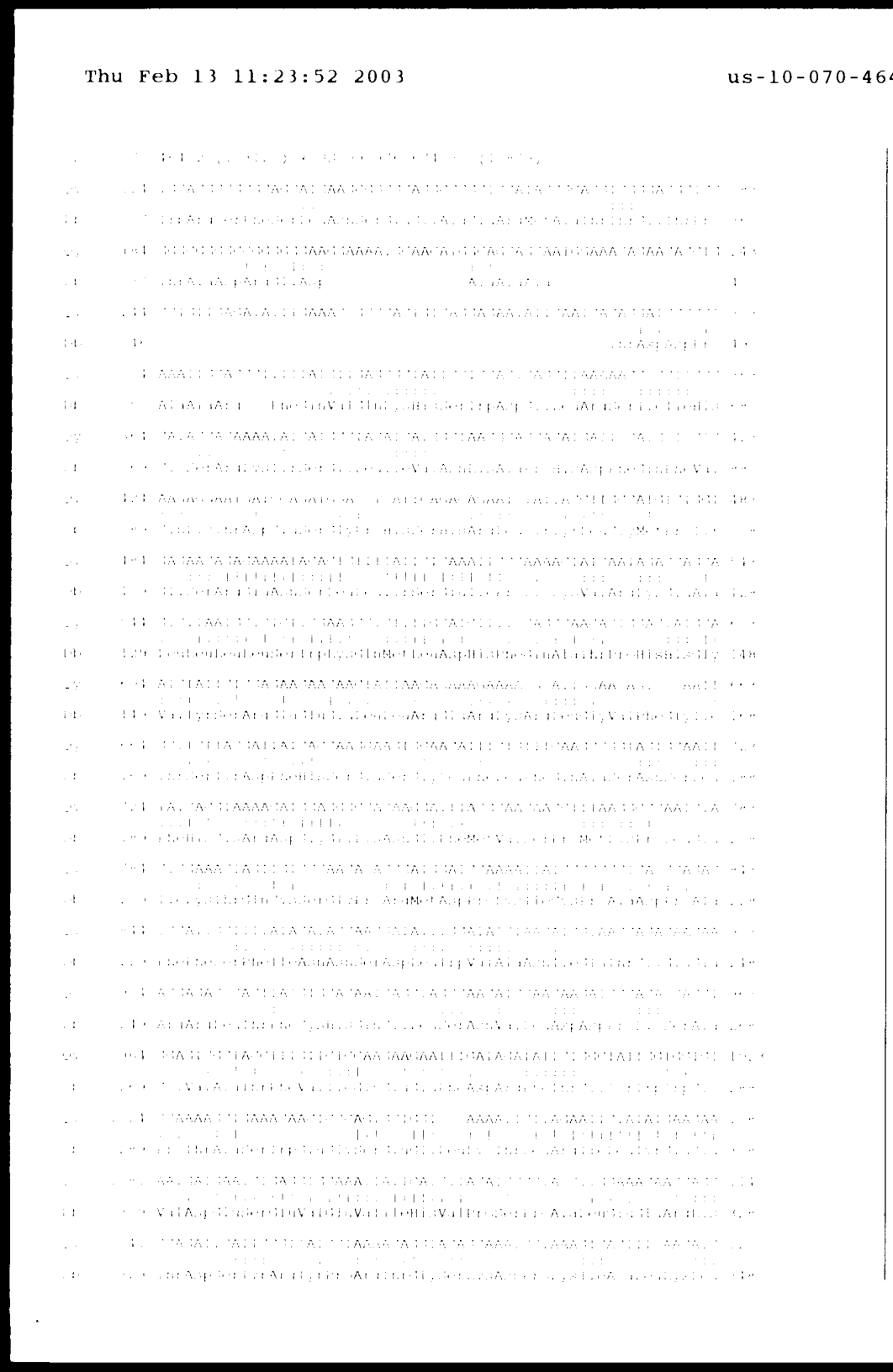


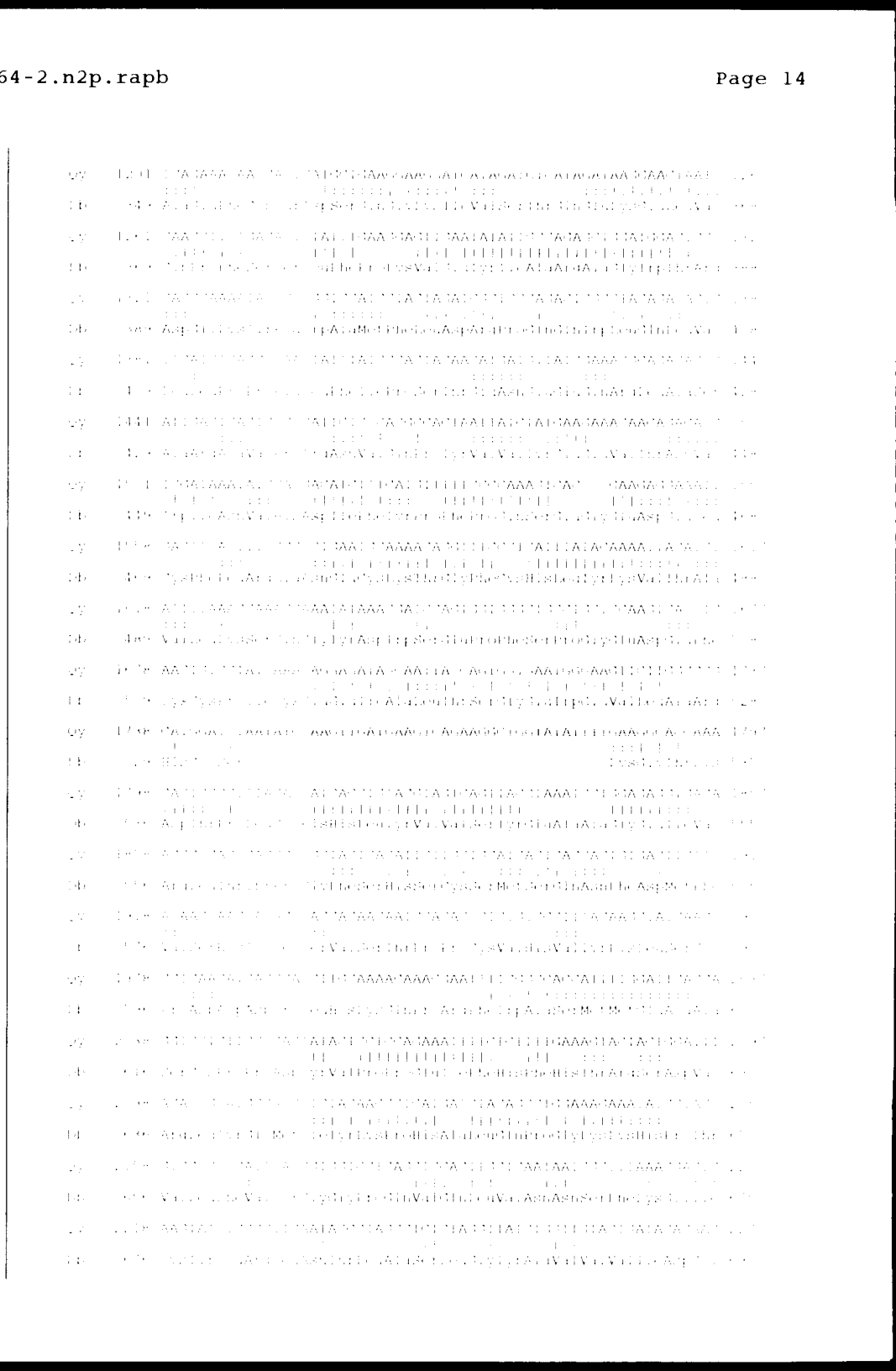


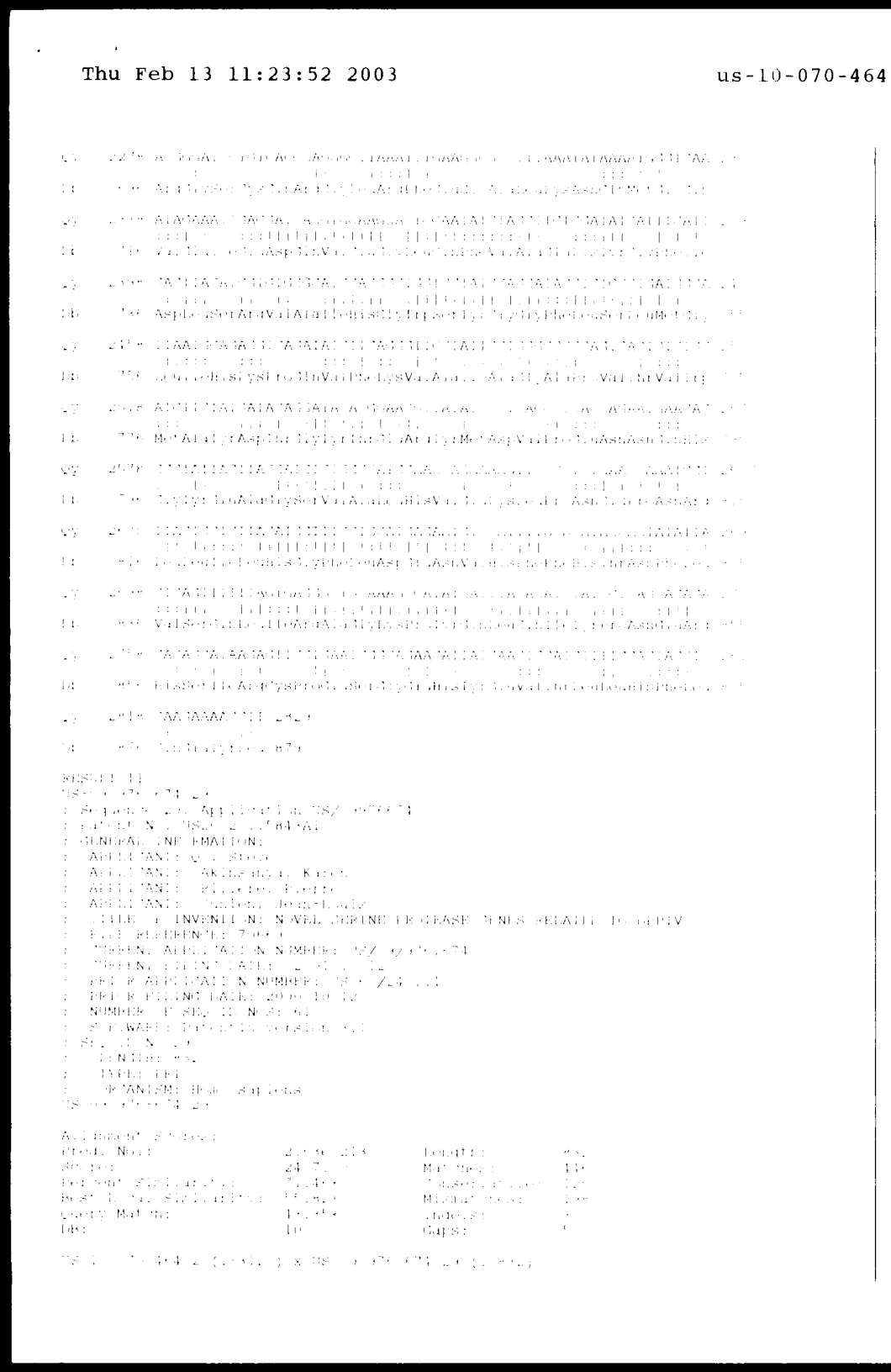


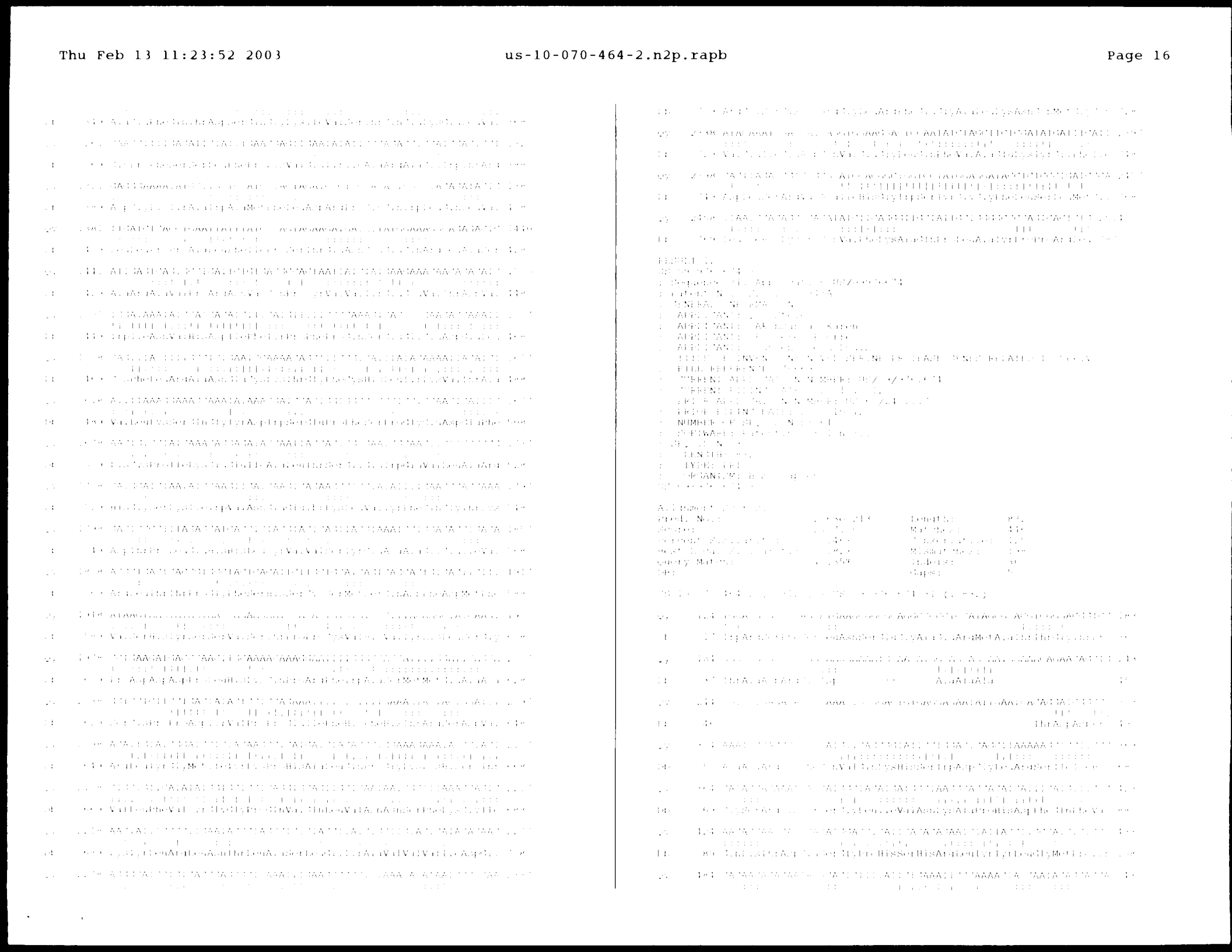


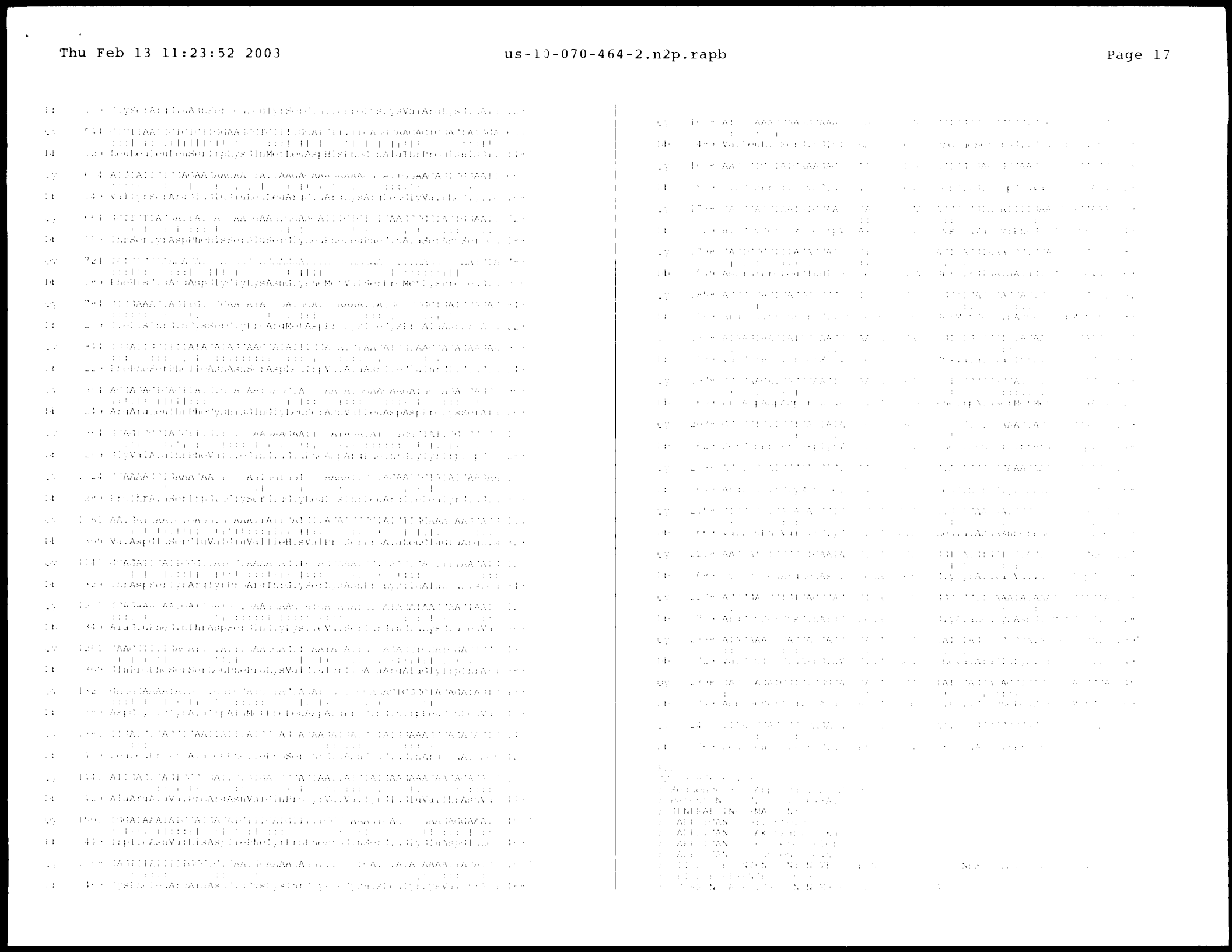


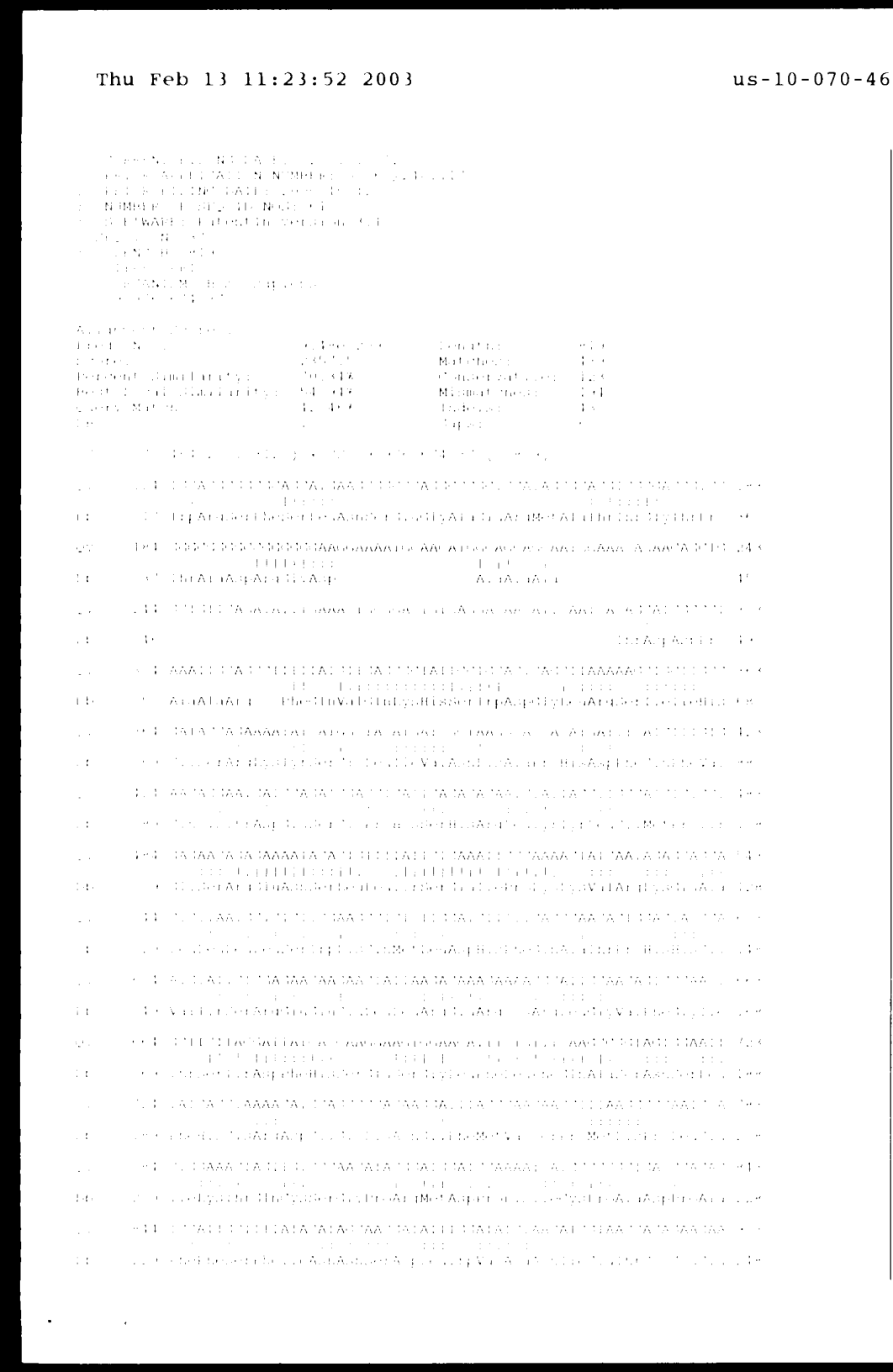


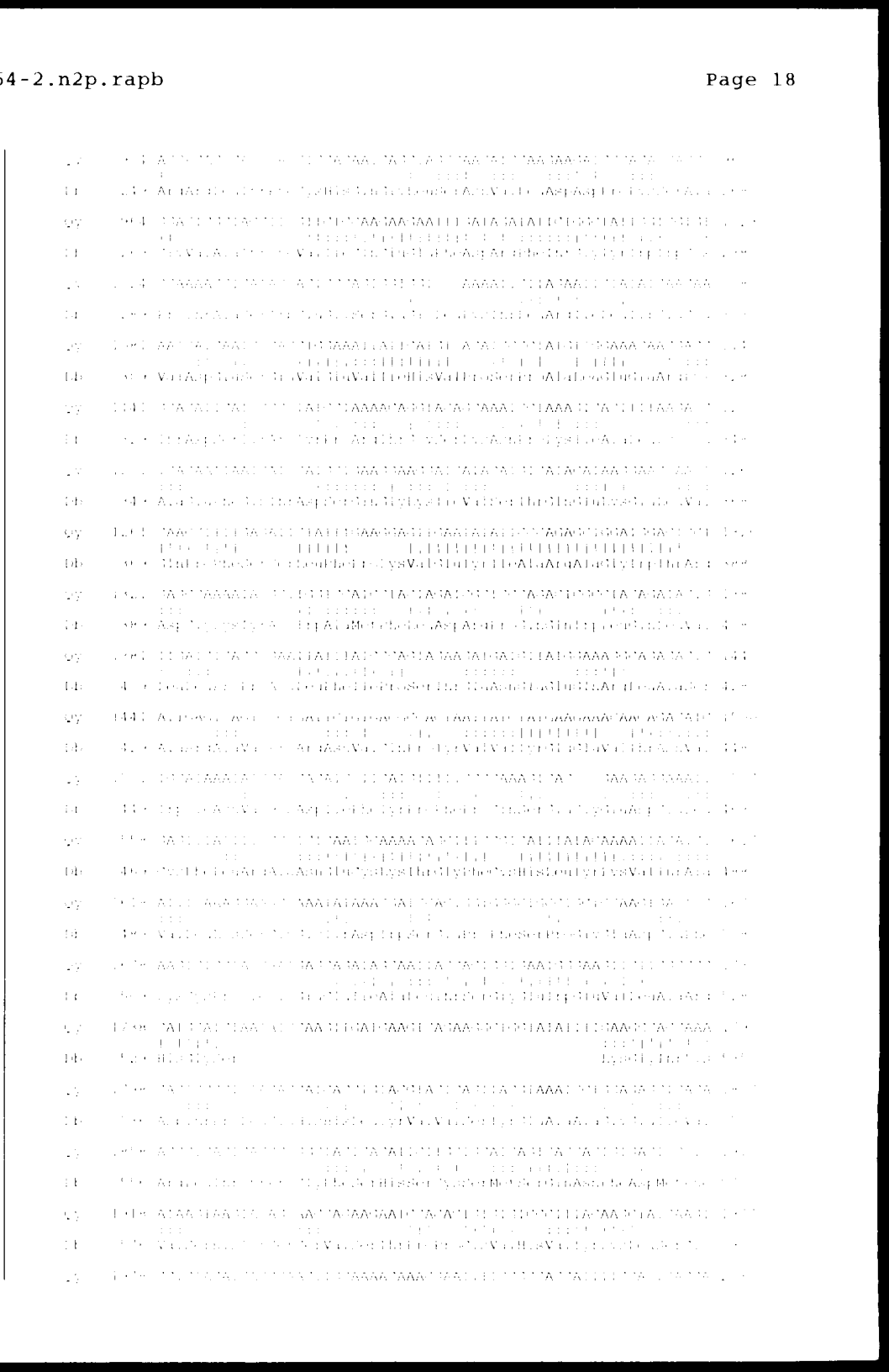


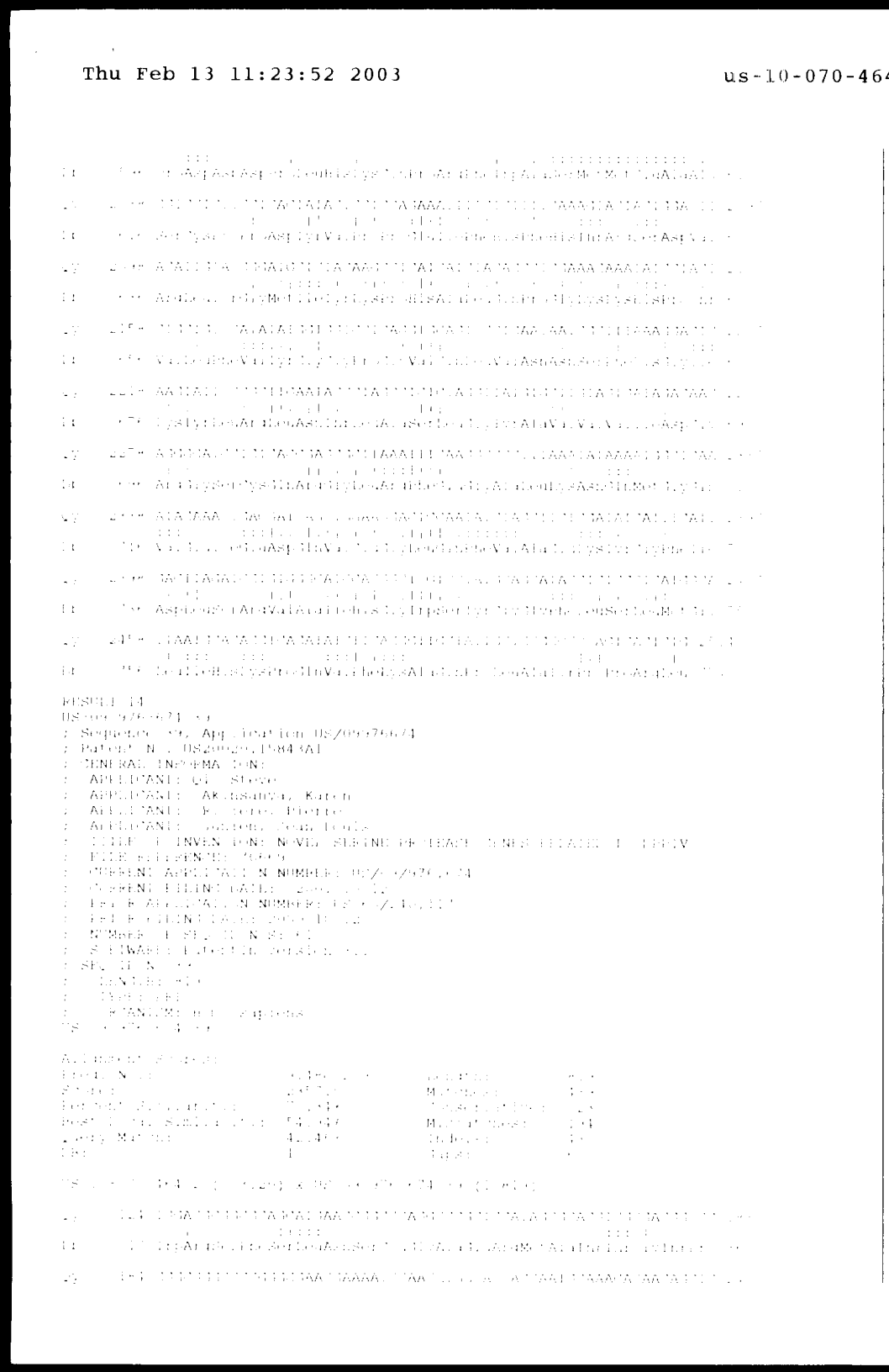


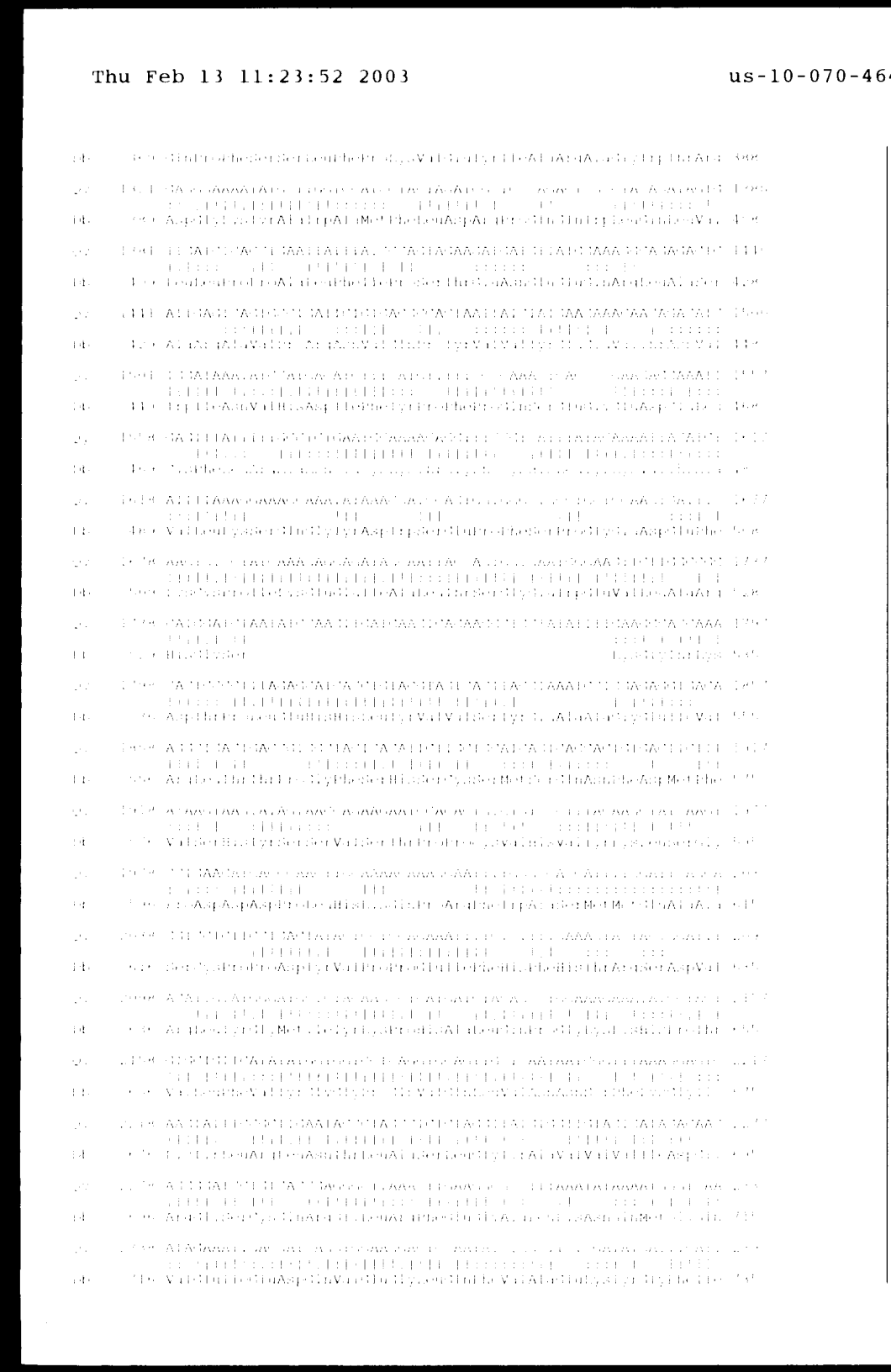












Geneseq Version 4.0
Copyright (c) 1998 - 2003 Compugen Ltd.

Published: February 6, 2003, 09:46:07 ; Search time 22 Seconds
(without alignments)
[illegible] Million cell updates/sec

Title: [illegible]
Perfect score: 4700
Sequence: 1 MAAAMCIIQEVVLIIIIAIF..... ...AAIIKVI 442

Scoring table: BLOSUM62
Xgap 10.0, Xext 1.0

Searched: 1853424 seqs, 501411210 residues

Total number of hits satisfying chosen parameters: 1853424

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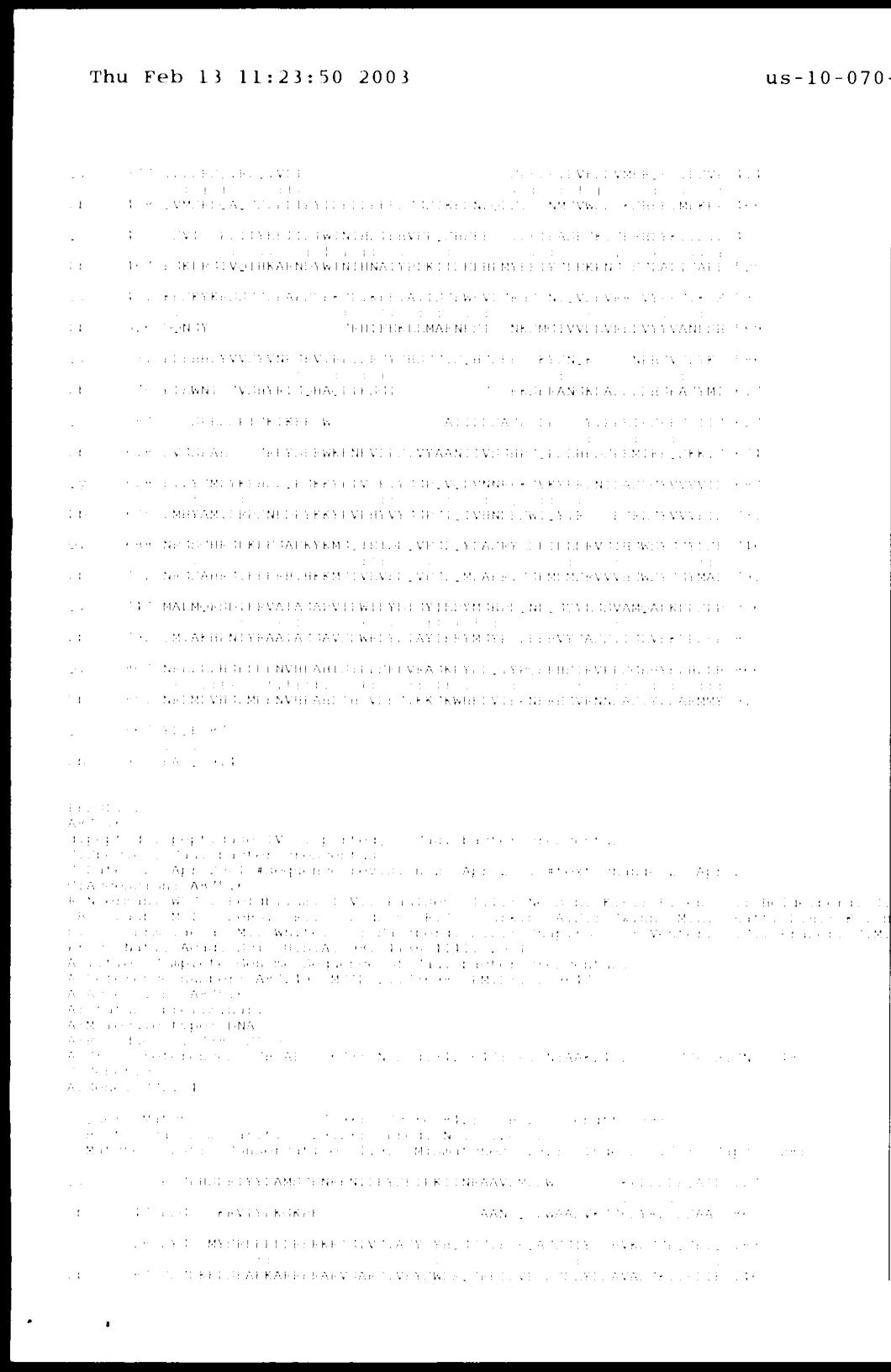
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

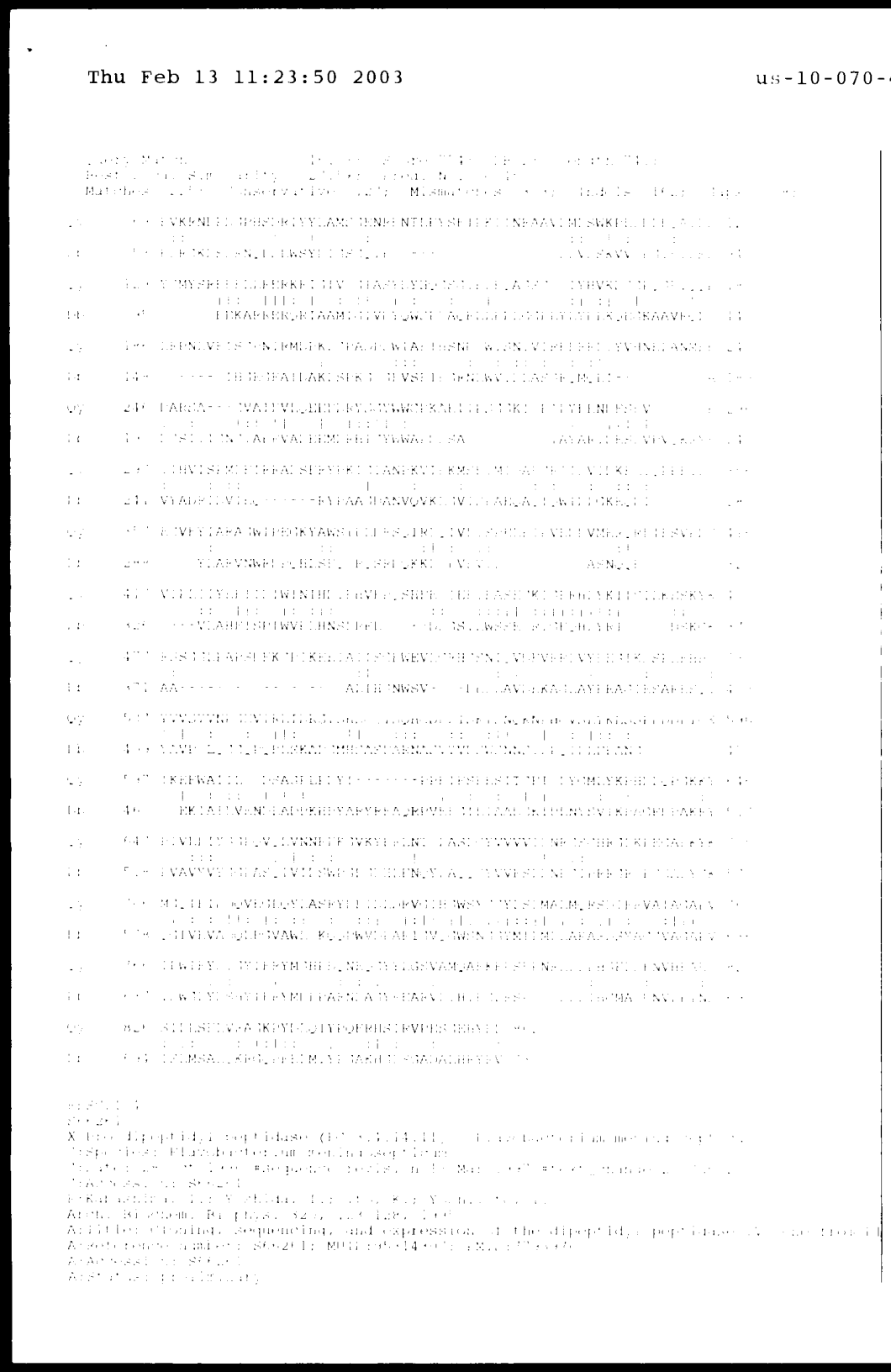
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2: geneseq2_pep:*
3: geneseq3_pep:*
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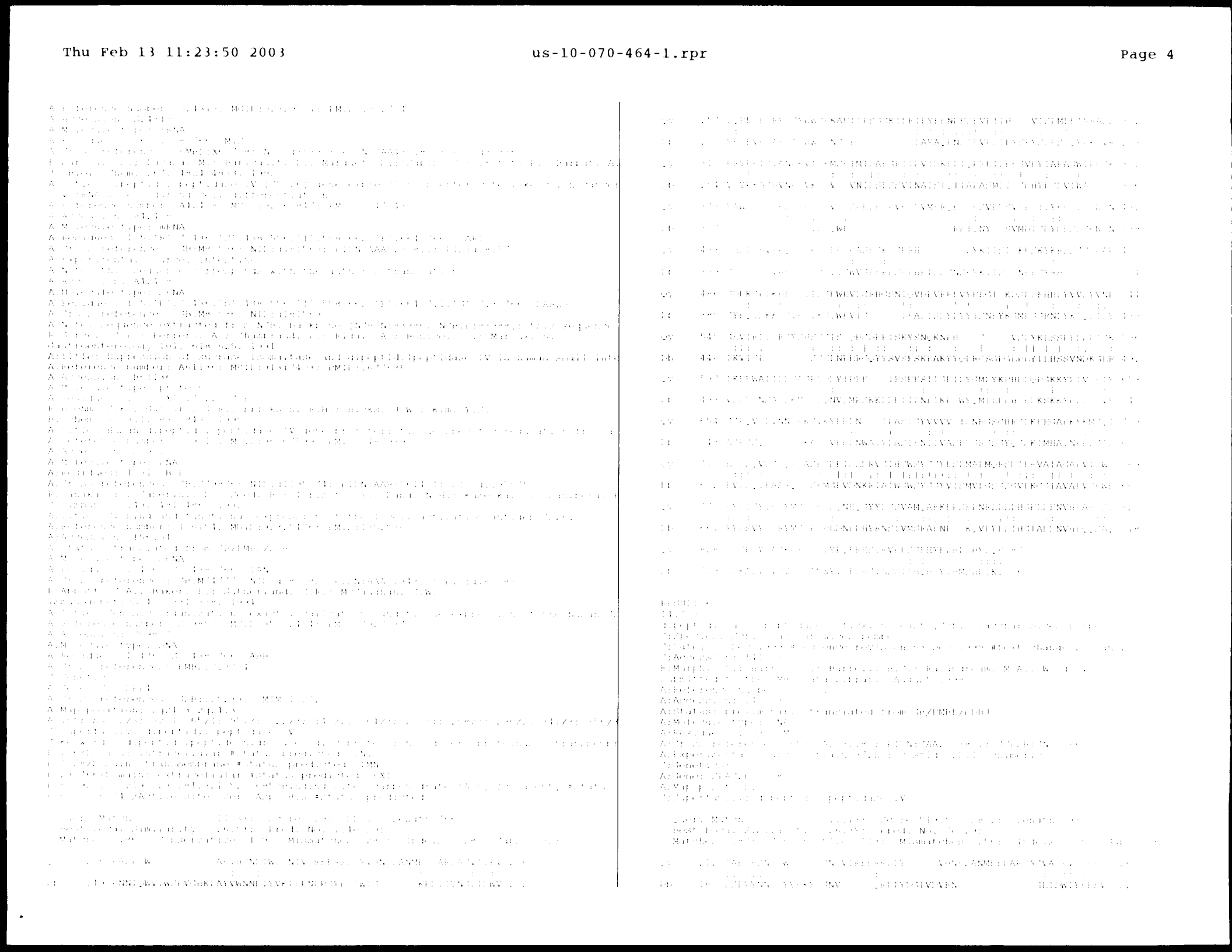
Post-processing: Of the [illegible] results processed, [illegible] scores greater than or equal to the score of the result being printed have been removed by analysis of the [illegible] score distribution.

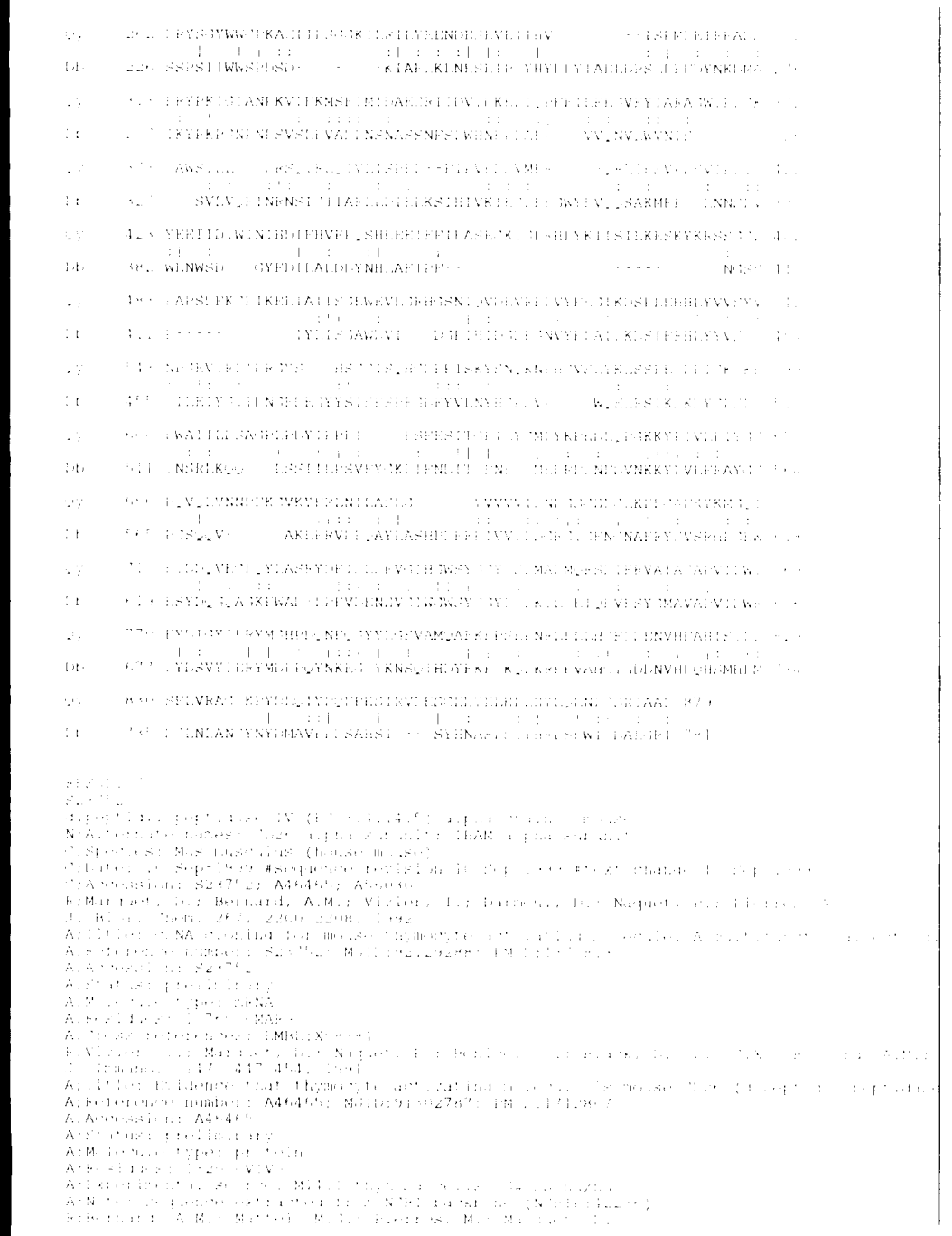
SUMMARIES

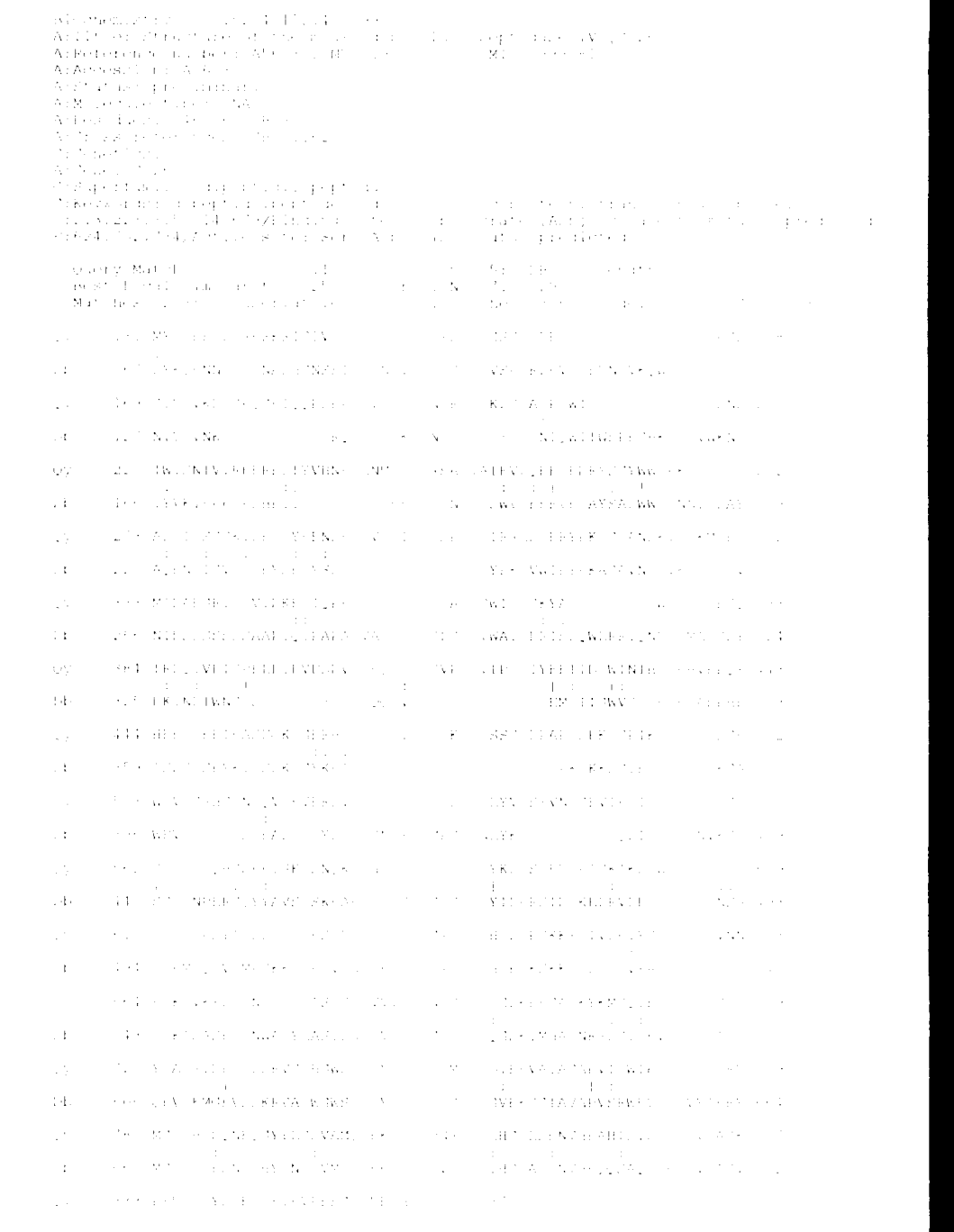
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3	754	16.0	734	2	AAY[illegible]	Xaa-Pro dipeptidase [illegible]
4	720	15.3	711	2	AAQ[illegible]	Xaa-Pro dipeptidase [illegible]
5	529	11.3	266	1	ABB[illegible]	dihydrofolate peptidase [illegible]
6	[illegible]	[illegible]	744	2	[illegible]	dipeptidase [illegible]
7	[illegible]	[illegible]	[illegible]	2	[illegible]	dipeptidase [illegible]
8	[illegible]	[illegible]	734	2	AAY[illegible]	dipeptidase [illegible]
9	464	9.9	418	1	ABB[illegible]	dipeptidase [illegible]
10	465	9.9	441	2	AAQ[illegible]	dipeptidase [illegible]
11	[illegible]	[illegible]	744	2	[illegible]	Xaa-Pro dipeptidase [illegible]
12	[illegible]	[illegible]	[illegible]	2	[illegible]	[illegible]
13	44	0.9	[illegible]	2	AAL[illegible]	dipeptidase [illegible]
14	42	0.9	[illegible]	2	[illegible]	dipeptidase [illegible]
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16	[illegible]	[illegible]	[illegible]	2	[illegible]	hypothetical protein [illegible]
17	[illegible]	[illegible]	[illegible]	2	[illegible]	dipeptidase [illegible]
18	[illegible]	[illegible]	[illegible]	2	[illegible]	[illegible]
19	[illegible]	[illegible]	[illegible]	2	[illegible]	protease [illegible]
20	[illegible]	[illegible]	[illegible]	2	[illegible]	[illegible]
21	[illegible]	[illegible]	[illegible]	2	[illegible]	[illegible]
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27	[illegible]	[illegible]	[illegible]	2	[illegible]	[illegible]
28	[illegible]	[illegible]	[illegible]	2	[illegible]	[illegible]
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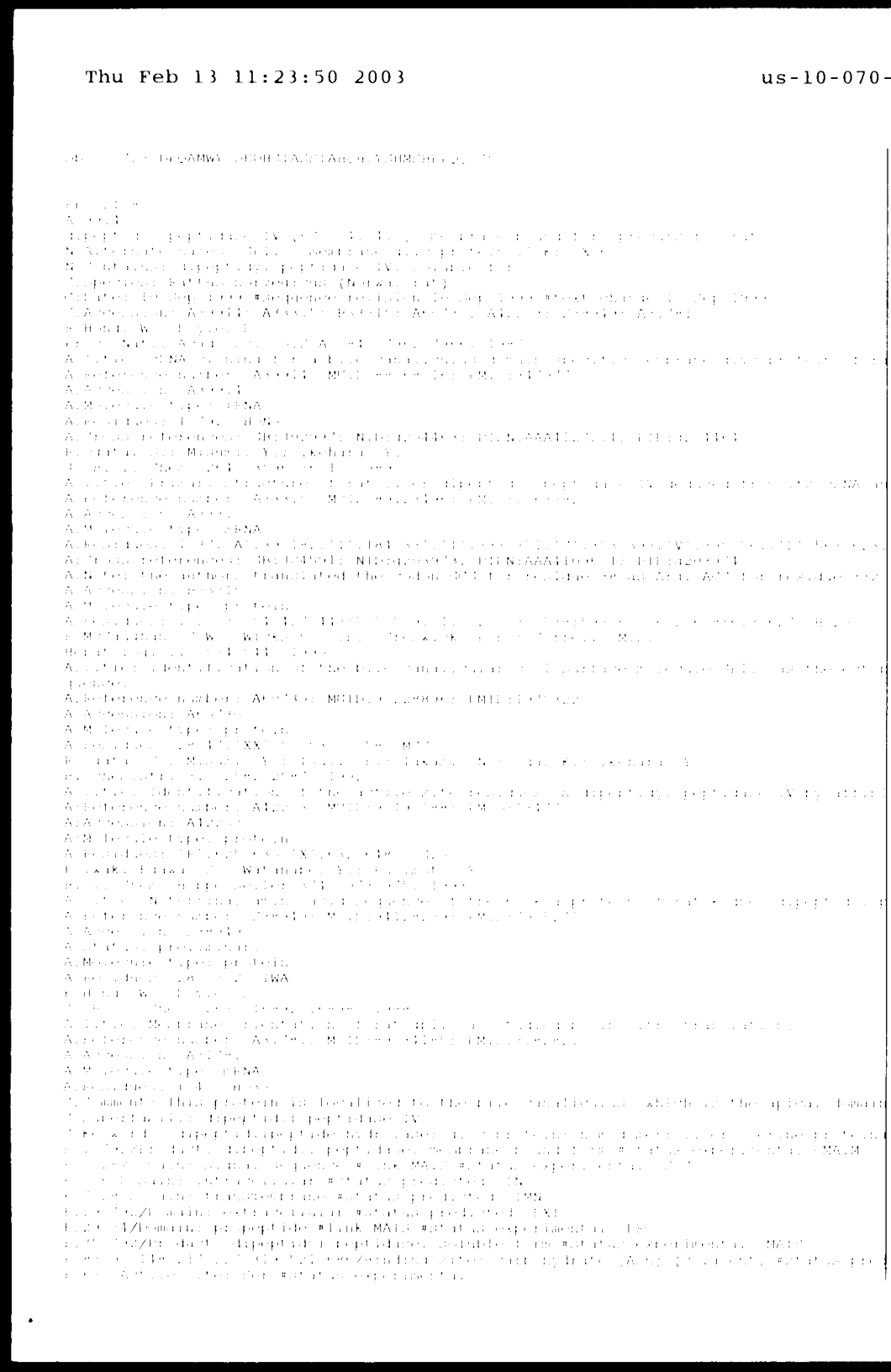


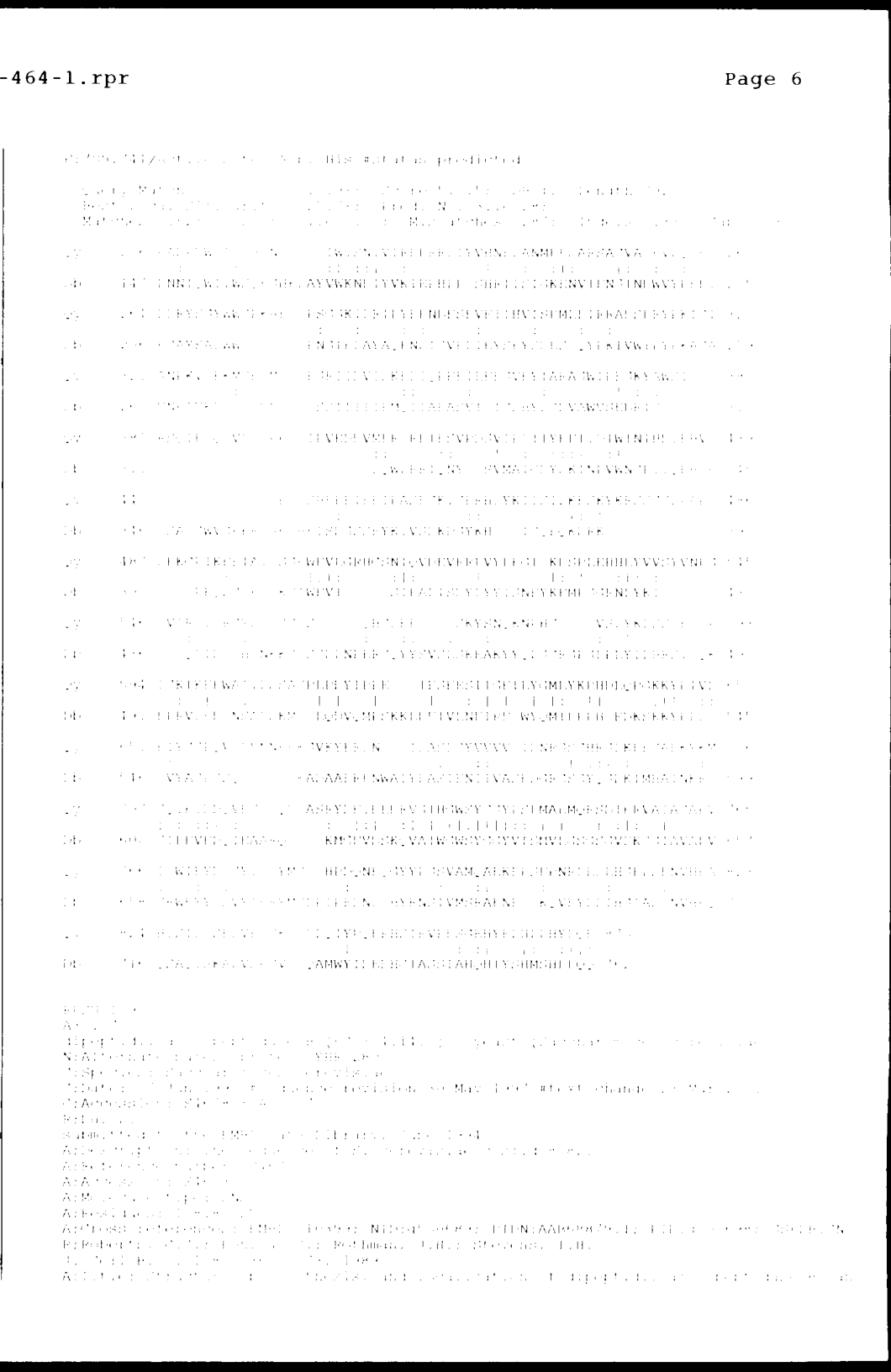


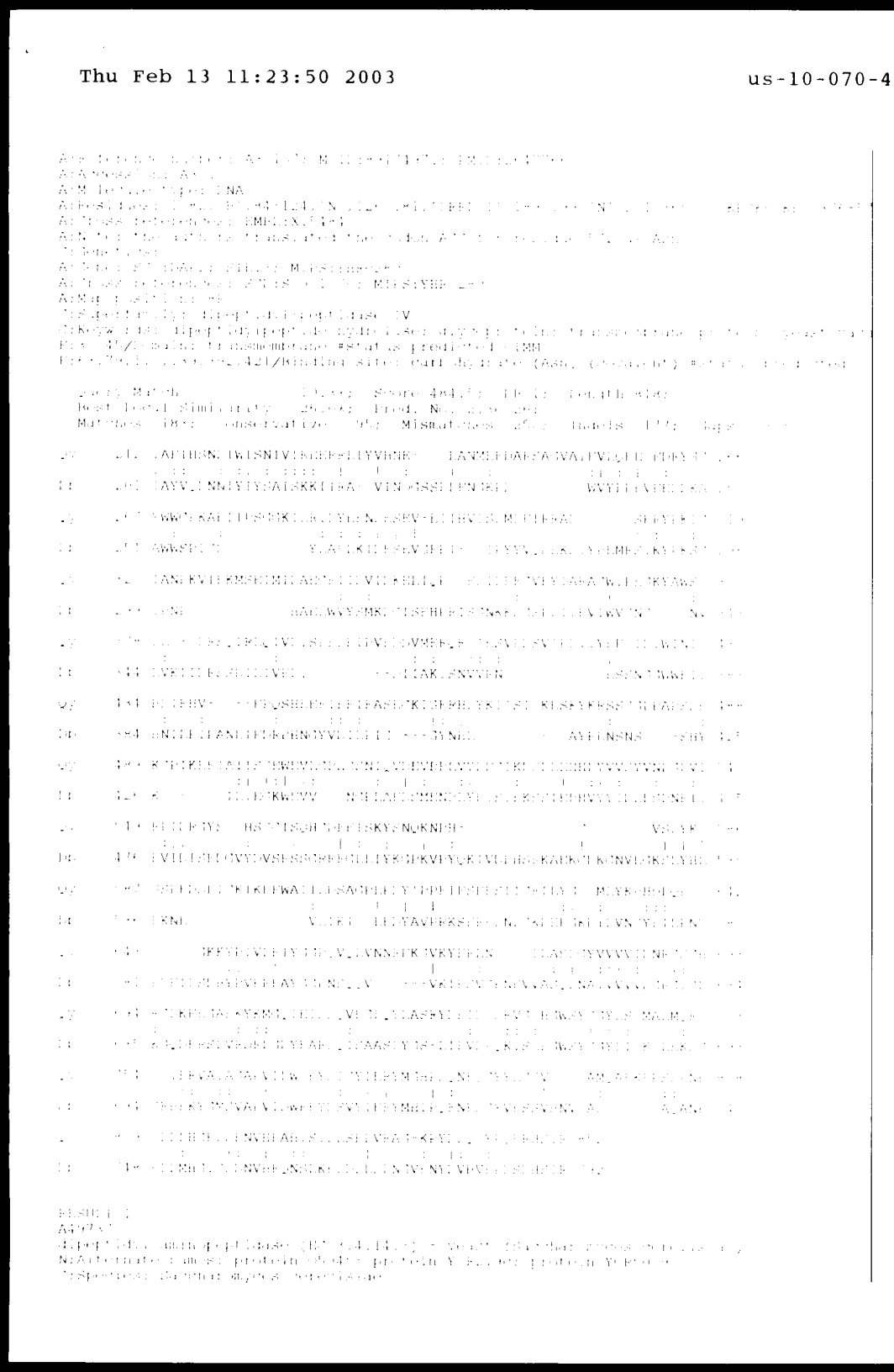


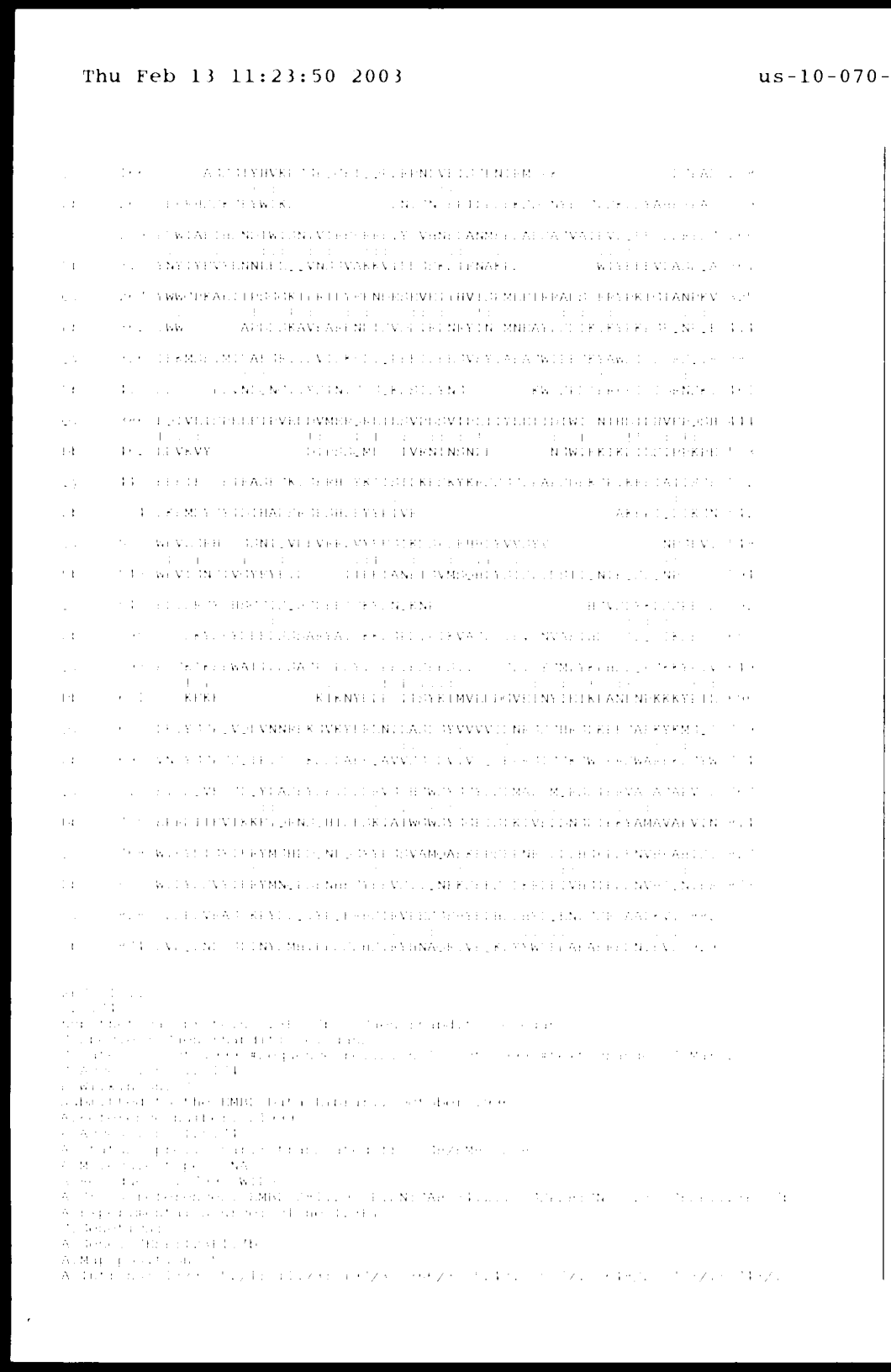


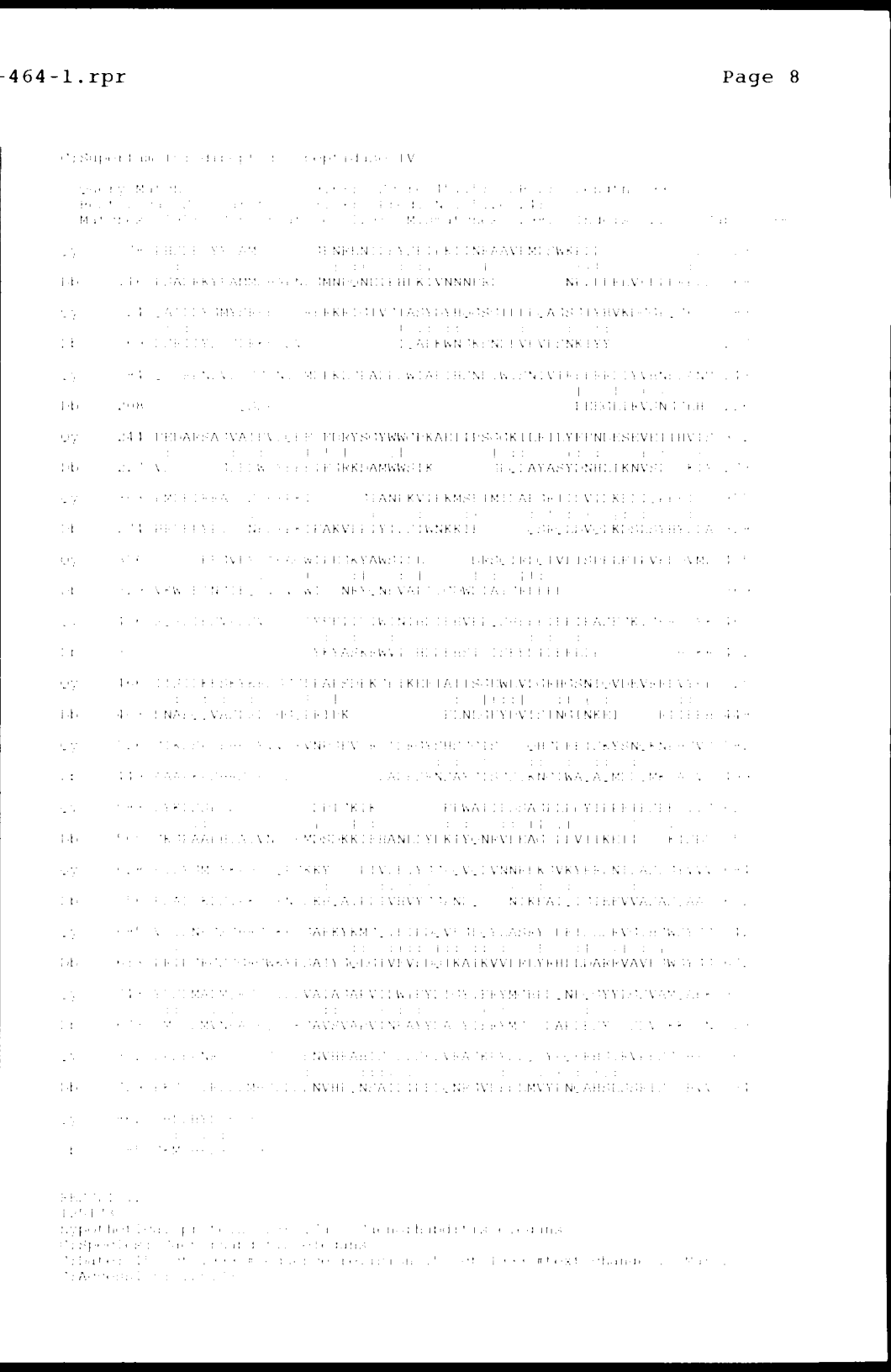


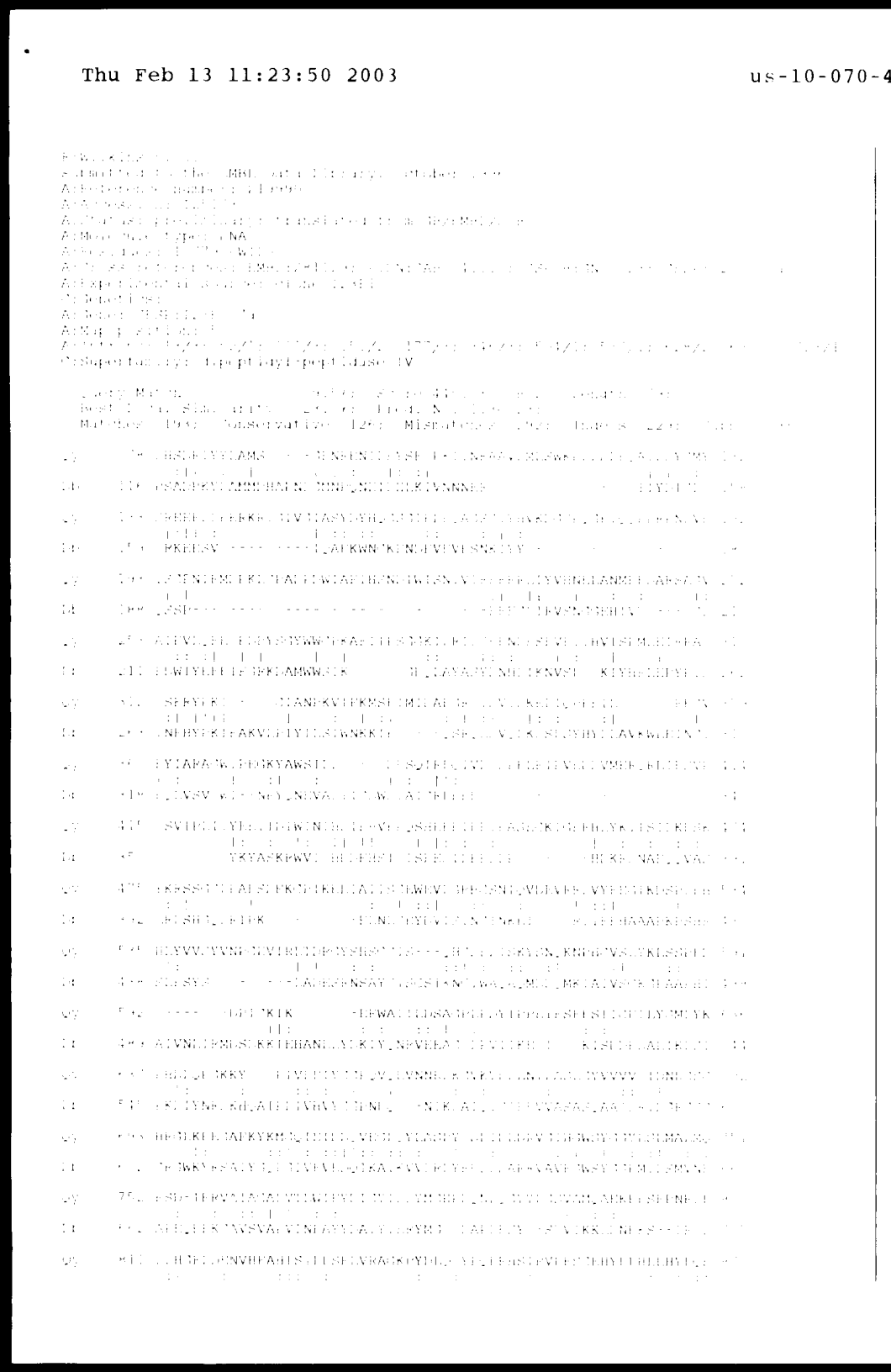


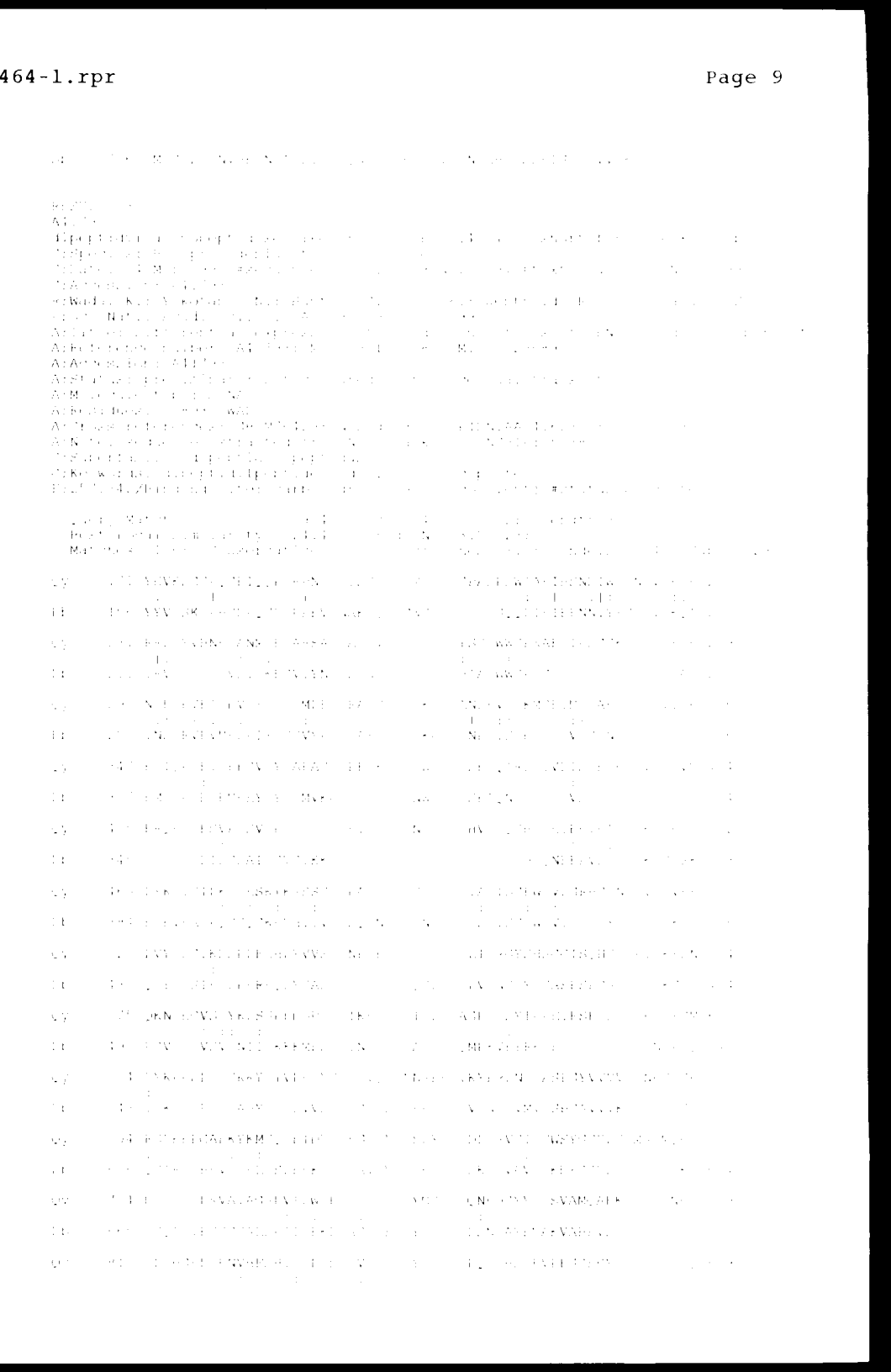


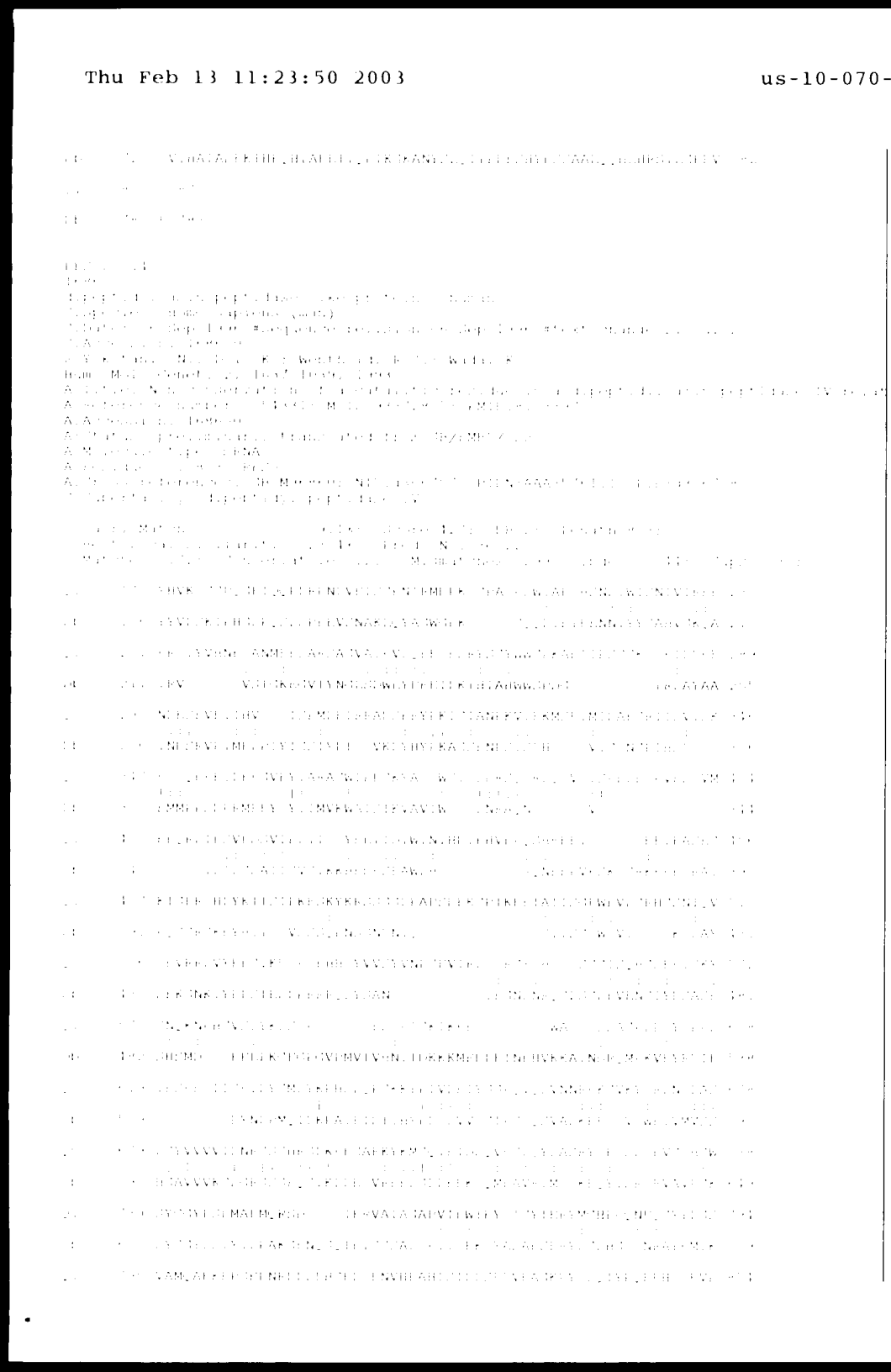


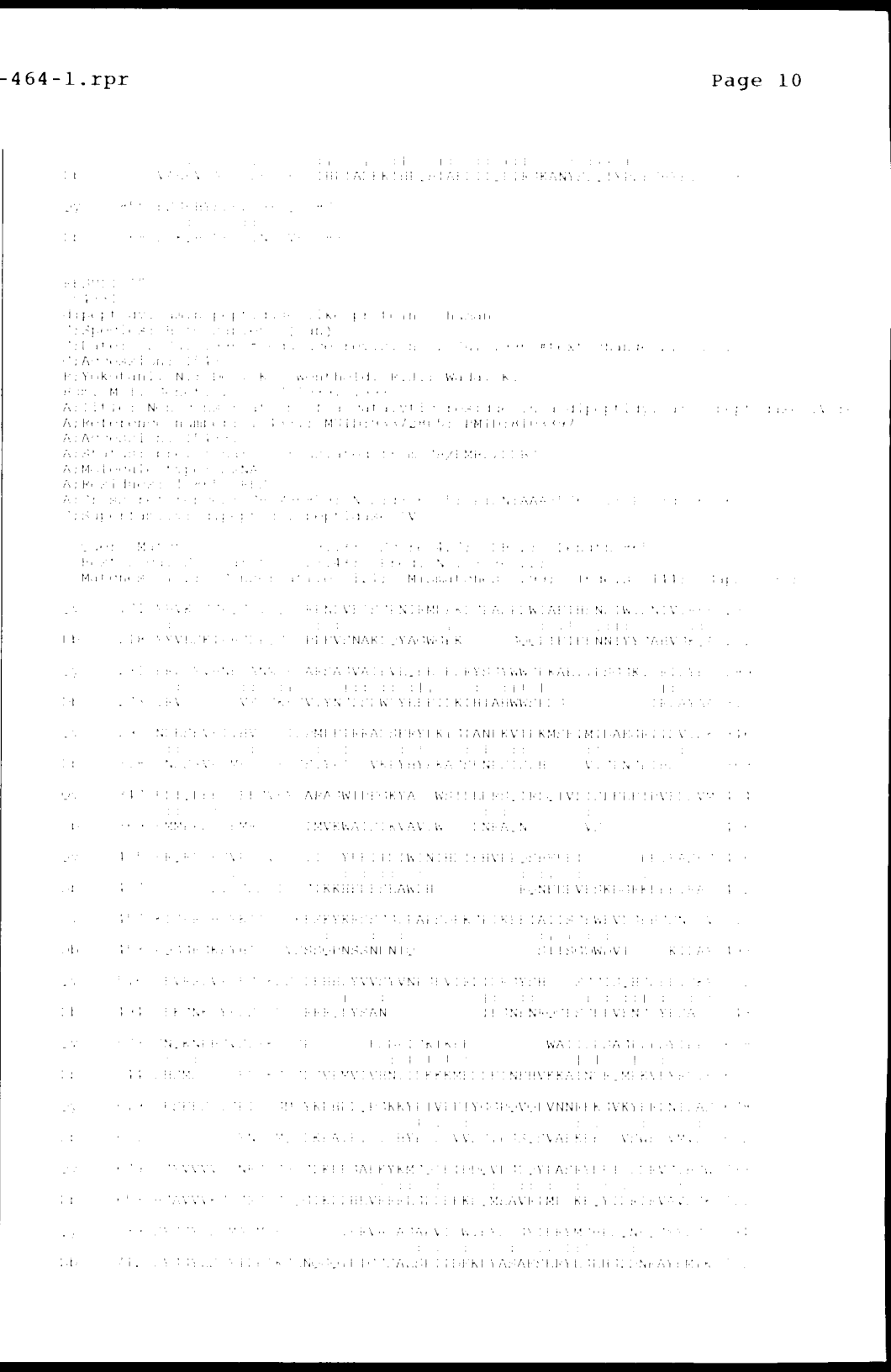












Version version[illegible]
Copyright (c) 1993 - 2003 Compugen Ltd.

Method: prot_a Search, [illegible] model

Run on: February 5, 2003, [illegible] Search [illegible] seconds
([illegible] connects)
[illegible] Million cell [illegible]

Title: US-10-070-464-1
Perfect score: 4700
Sequence: 1 MAAAMETEGLSVGIFFLAC[illegible]HLEHYLQRNLQSKIAALKV 92

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 72802 seqs, 44478528 residues

Total number of hits satisfying chosen parameters: 72802

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

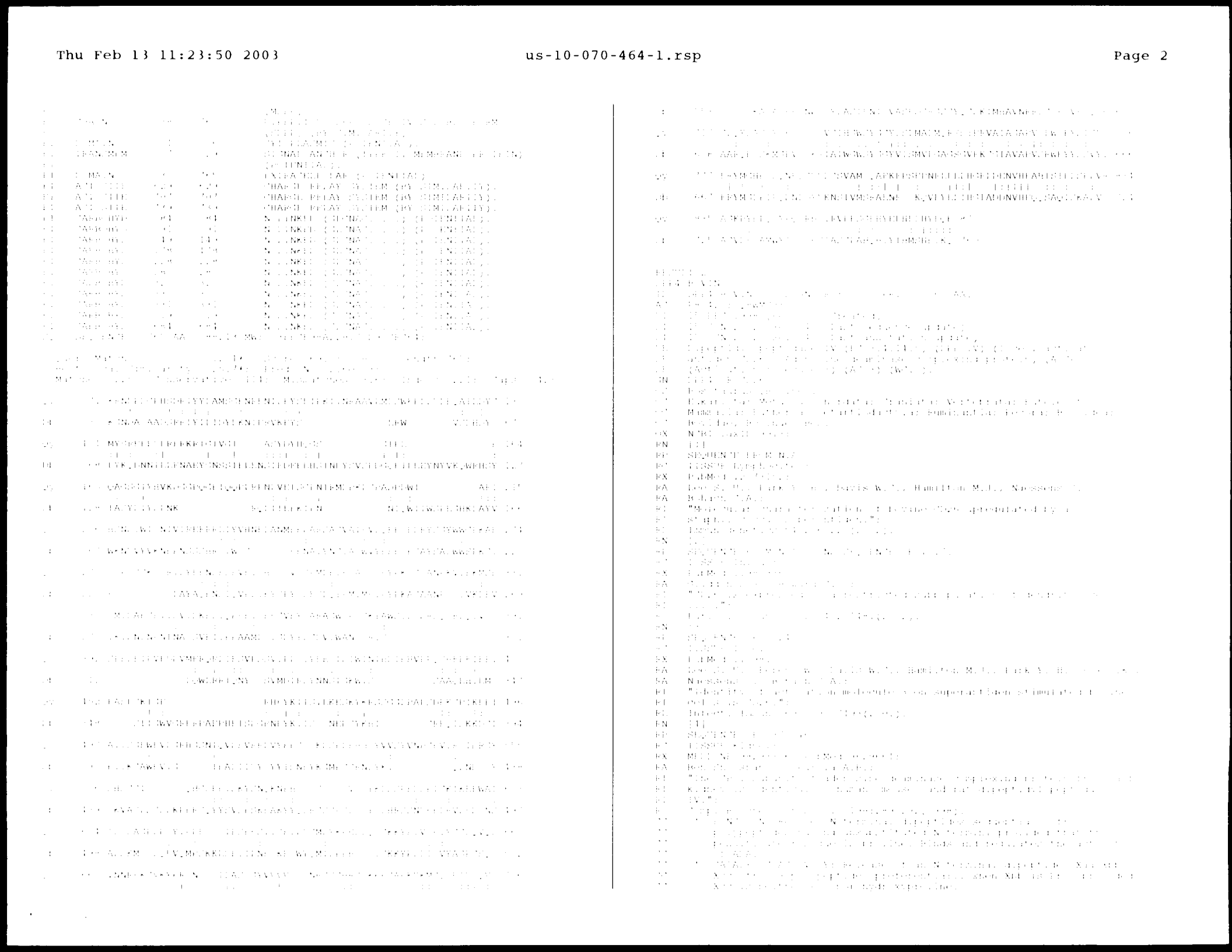
Prob. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

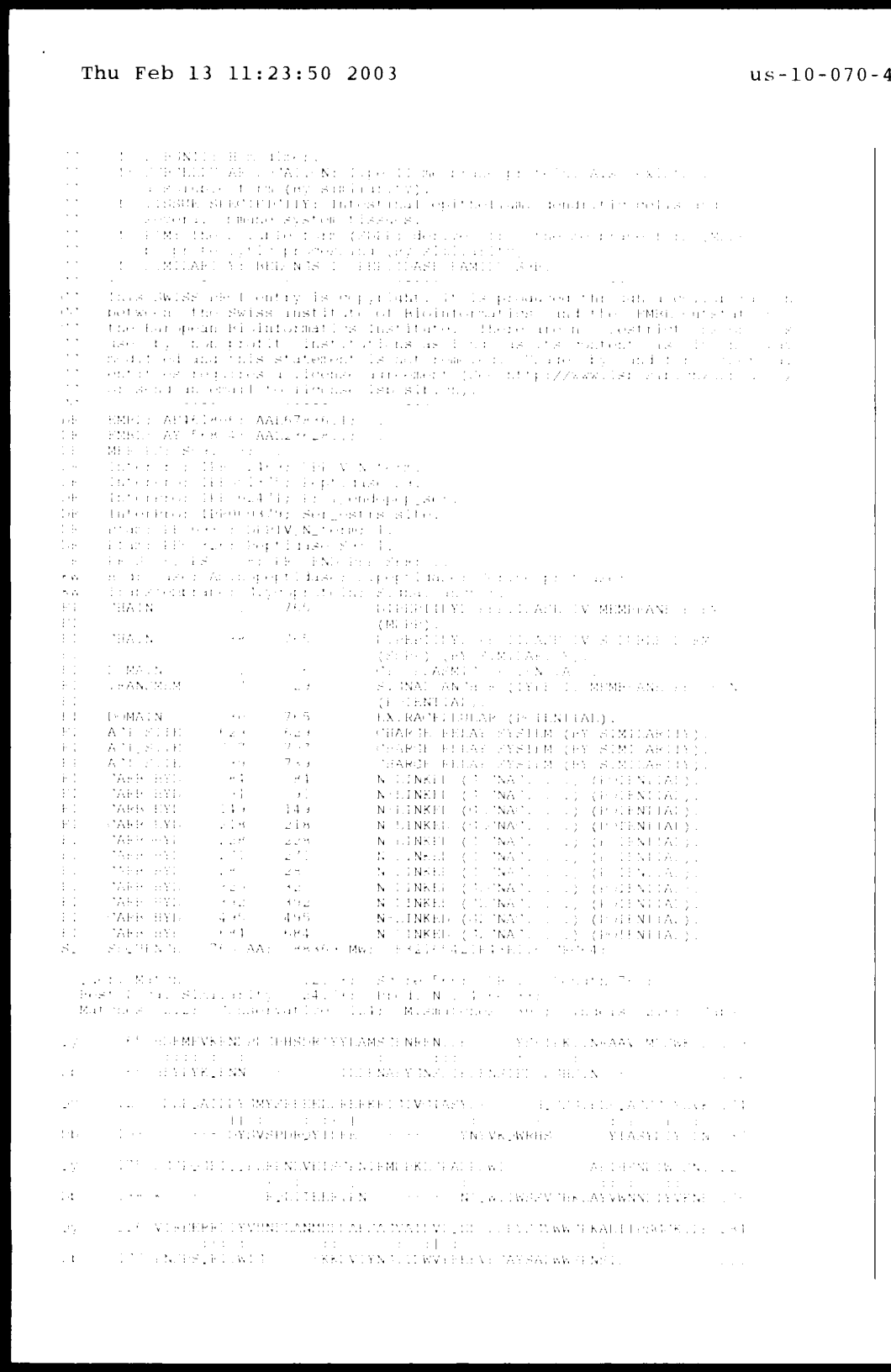
SUMMARIES

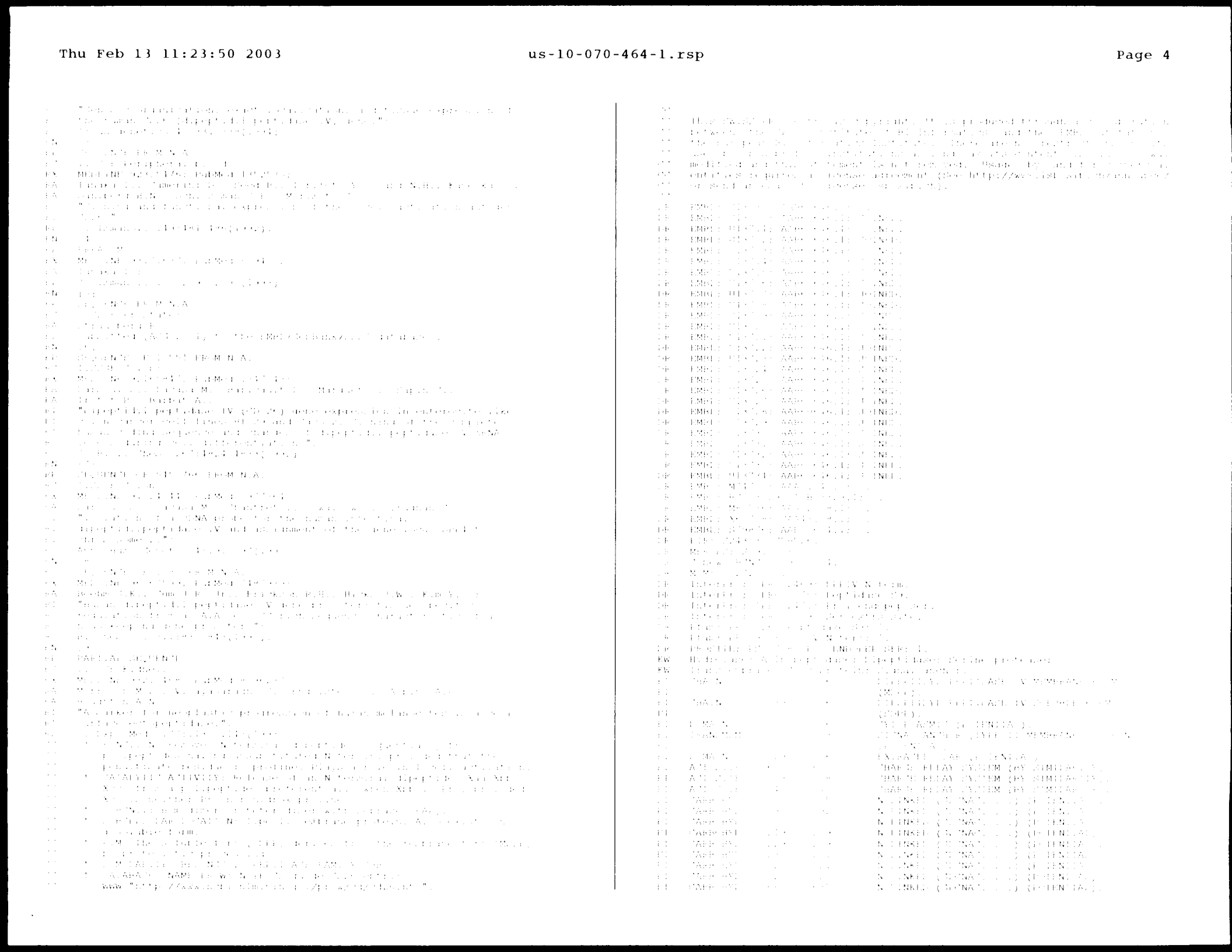
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3	525	11.2	766	1	DPP4_HUMAN	P27487 homo sapi[illegible]
4	523.5	11.1	767	1	DPP4_RAT	P14740 rattus no[illegible]
5	517.5	11.0	760	1	DPP4_MOUSE	P28843 mus musc[illegible]
6	484.5	10.3	818	2	DAP2_YEAST	P18962 saccharom[illegible]
7	478.5	10.2	761	1	SEPR_MOUSE	P97321 mus musc[illegible]
8	465	9.9	941	2	DAP1_YEAST	P36894 saccharom[illegible]
9	454	9.7	760	1	SEPR_HUMAN	Q12884 homo sapi[illegible]
10	440	9.4	863	1	DPP6_BOVIN	P42669 bos taurus
11	431	9.2	859	1	DPP6_RAT	P48201 rattus no[illegible]
12	427	9.1	865	1	DPP6_HUMAN	P42658 homo sapi[illegible]
13	245.5	5.2	657	1	YUX1_BACSU	P54539 bacillus [illegible]
14	172	3.7	742	1	ACPH_HUMAN	P13798 homo sapi[illegible]
15	171	3.6	732	1	ACPH_RAT	P16676 rattus no[illegible]
16	161	3.4	732	1	ACPH_PIG	P14235 sus scrof[illegible]
17	156	3.2	741	1	YL4_CAEEL	P34422 caenorhab[illegible]
18	149	3.1	696	1	PPCS_AERHY	Q59053 aeromonas [illegible]
19	136	2.9	722	1	YI71_PICPA	P42171 pichia pa[illegible]
20	134	2.9	1014	1	BGAL_BACCE	Q65CS9 bacillus [illegible]
21	125.5	2.7	136	1	PAPA_CAVPO	P27693 cavia por[illegible]
22	124.5	2.6	1855	1	AGE1_YEAST	P32526 saccharom[illegible]
23	123.5	2.6	736	1	PPCP_FLAME	P27105 flavobact[illegible]
24	123	2.6	1762	2	DAP4_EMENI	P27617 emericell[illegible]
25	122	2.6	735	1	Y439_FRIPS	P55656 frigidoba[illegible]
26	119.5	2.5	1018	1	CAZ5_HUMAN	P21110 homo sapi[illegible]
27	118.5	2.5	735	1	PPCP_FLAME	P27628 flavobact[illegible]
28	118.5	2.5	710	1	PPCP_HUMAN	P14234 homo sapi[illegible]
29	118.5	2.5	1436	1	SPO3_STAAW	Q5HGF5 staphylo[illegible]
30	118.5	2.5	1436	1	SPO3_STAAM	Q6GA66 staphylo[illegible]
31	118	2.5	1285	1	DXA_PASMU	P17452 pasteurel[illegible]
32	115	2.4	1047	1	PCL_SIVAI	P12974 simian i[illegible]
33	115	2.4	3114	1	VPS1_YEAST	Q12028 saccharom[illegible]
34	114.5	2.4	1436	1	SPO3_STAAS	Q6GIL7 staphylo[illegible]
35	114	2.4	1436	1	SPO3_STAAN	P63400 staphylo[illegible]
36	113.5	2.4	1436	1	SPO3_STAAR	Q6GEB7 staphylo[illegible]
37	113.5	2.4	1436	1	SPO3_STAAU	Q6G8Y1 staphylo[illegible]
38	113.5	2.4	1436	1	SPO3_STAAB	Q6GCT1 staphylo[illegible]
39	113.5	2.4	1436	1	SPO3_STAAE	Q6GAT1 staphylo[illegible]
40	113.5	2.4	1436	1	SPO3_STAAS	Q6GJ73 staphylo[illegible]
41	113.5	2.4	1436	1	SPO3_STAAM	Q6GA66 staphylo[illegible]
42	113.5	2.4	1436	1	SPO3_STAAW	Q5HGF5 staphylo[illegible]
43	113.5	2.4	1436	1	SPO3_STAAN	P63400 staphylo[illegible]
44	113.5	2.4	1436	1	SPO3_STAAR	Q6GEB7 staphylo[illegible]
45	113.5	2.4	1436	1	SPO3_STAAU	Q6G8Y1 staphylo[illegible]

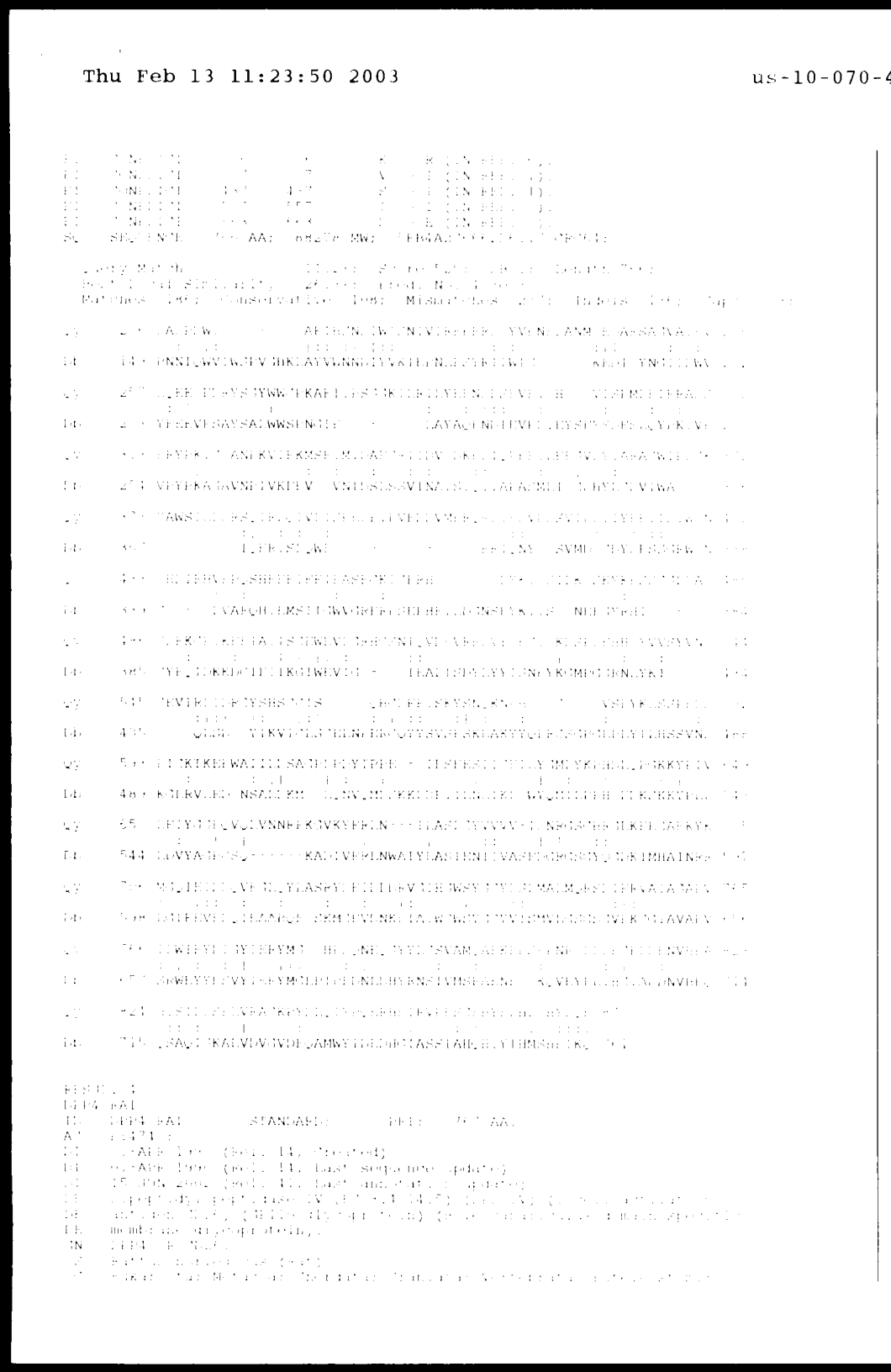
ALIGNMENTS

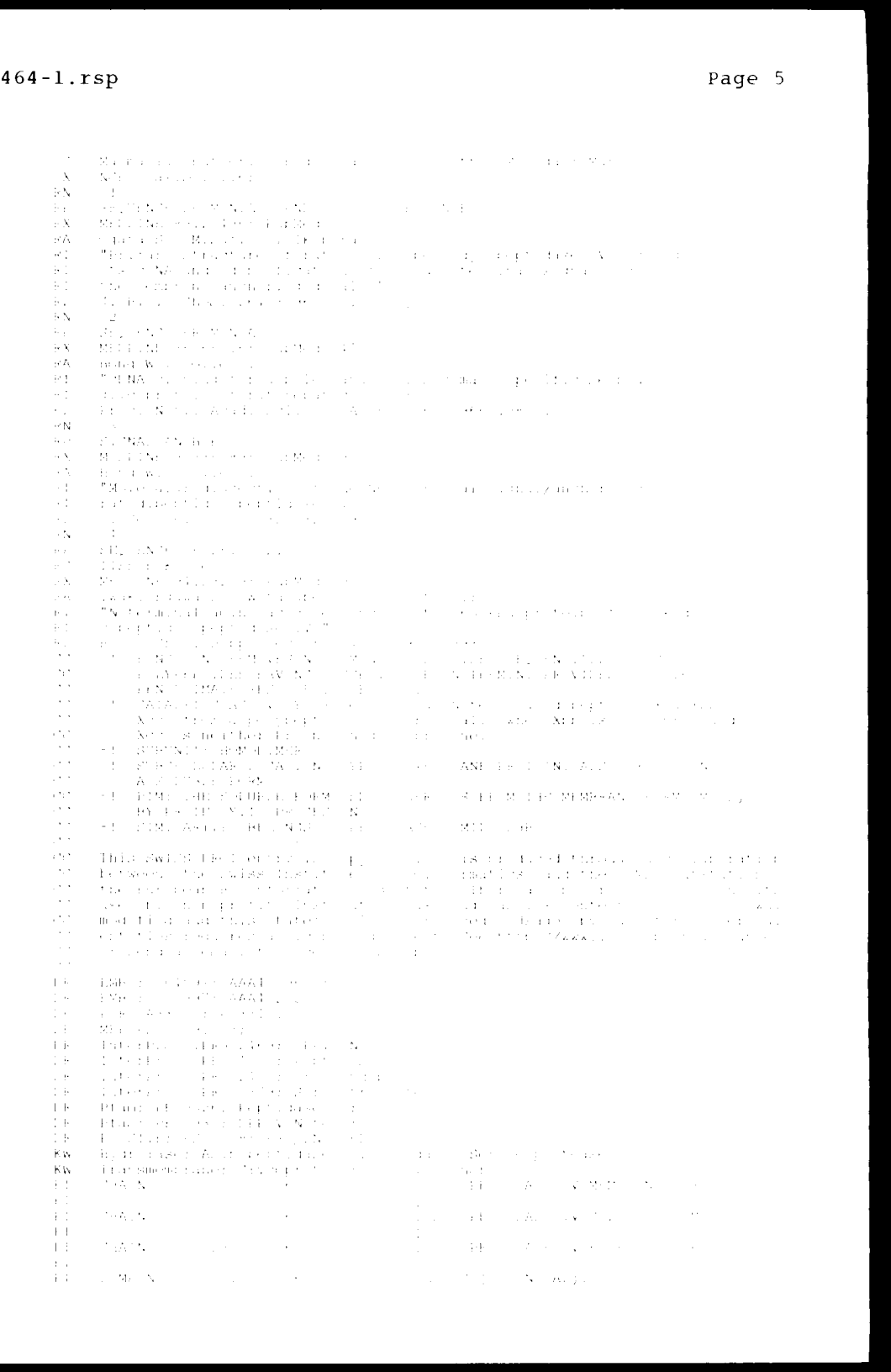
RESULT 1
DPP4_FELCA
ID DPP4_FELCA STANDARD; PRT; 765 AA.
AC Q9N217;
DT 15-JUN-[illegible] (Rel. 39, Created)
DT 15-JUN-[illegible] (Rel. 39, Last sequence update)
DT 15-JUN-[illegible] (Rel. 39, Last annotation update)
DE Dipeptidyl peptidase IV (CD26) (DPP IV) (EC 3.4.14.5).
GN Name=DPP4;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Feliformia; Felidae; Felinae;
OC Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis;
RX MEDLINE=99[illegible]; PubMed=[illegible];
RA Niedermeier W., Steinke W.;
RA Kikkawa Y., Sokolowska-Kohler W., Hartmann G.D., Klein H.W.;
RT "Mammalian dipeptidyl-peptidase IV (CD26): glycosylation, [illegible]
RT and [illegible] analysis.";
RL Int. J. Exp. Clin. Chemother. Res. 1:[illegible] (1999).
CC -!- FUNCTION: Dipeptidyl peptidase IV (DPP IV) [illegible]
CC peptides from [illegible] (Xaa-Pro or Xaa-Ala) [illegible]
CC [illegible] (Xaa = [illegible]; Yaa = Pro or Ala). Also [illegible]
CC [illegible] from polypeptides [illegible] also [illegible] Xaa-Pro
CC [illegible] Xaa is [illegible] Ile, Leu, Met, Phe, Trp or Tyr.
CC -!- SUBUNIT: [illegible] homodimer [illegible].
CC -!- SUBCELLULAR LOCATION: [illegible] membrane protein [illegible]
CC [illegible] short [illegible] tail [illegible] a [illegible] region
CC [illegible] [illegible] [illegible].
CC -!- SIMILARITY: [illegible] [illegible] [illegible].
CC -!- [illegible]
CC This SWISS-PROT [illegible] is [illegible] [illegible] and
CC between the Swiss Institute [illegible] and the [illegible].
CC The [illegible] and [illegible] [illegible] [illegible] [illegible]
CC use by [illegible] [illegible] [illegible] [illegible] [illegible]
CC modified [illegible] [illegible] [illegible] [illegible] [illegible]
CC [illegible] [illegible] [illegible] See http://www.[illegible]
CC or send an [illegible] [illegible].
CC
DR EMBL; AF[illegible]; [illegible].
DR MEROPS; [illegible].
DR [illegible]; [illegible].
DR [illegible]; [illegible].
DR [illegible]; [illegible].
DR [illegible]; [illegible].
DR [illegible]; [illegible].
DR [illegible]; [illegible].
KW [illegible]; Multigene [illegible]; Secreted; [illegible].
KW [illegible]; Transmembrane; [illegible].
FT [illegible]

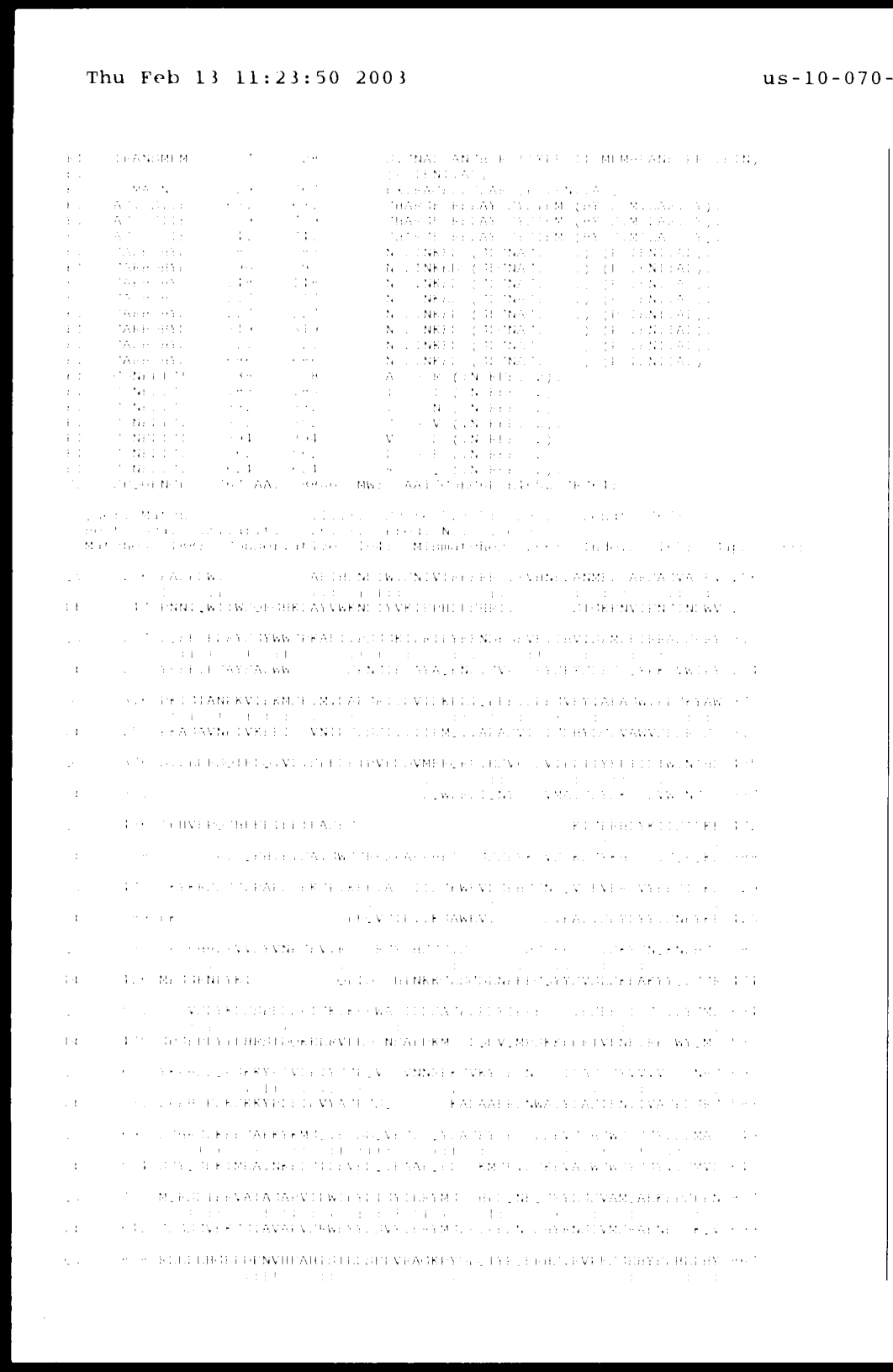


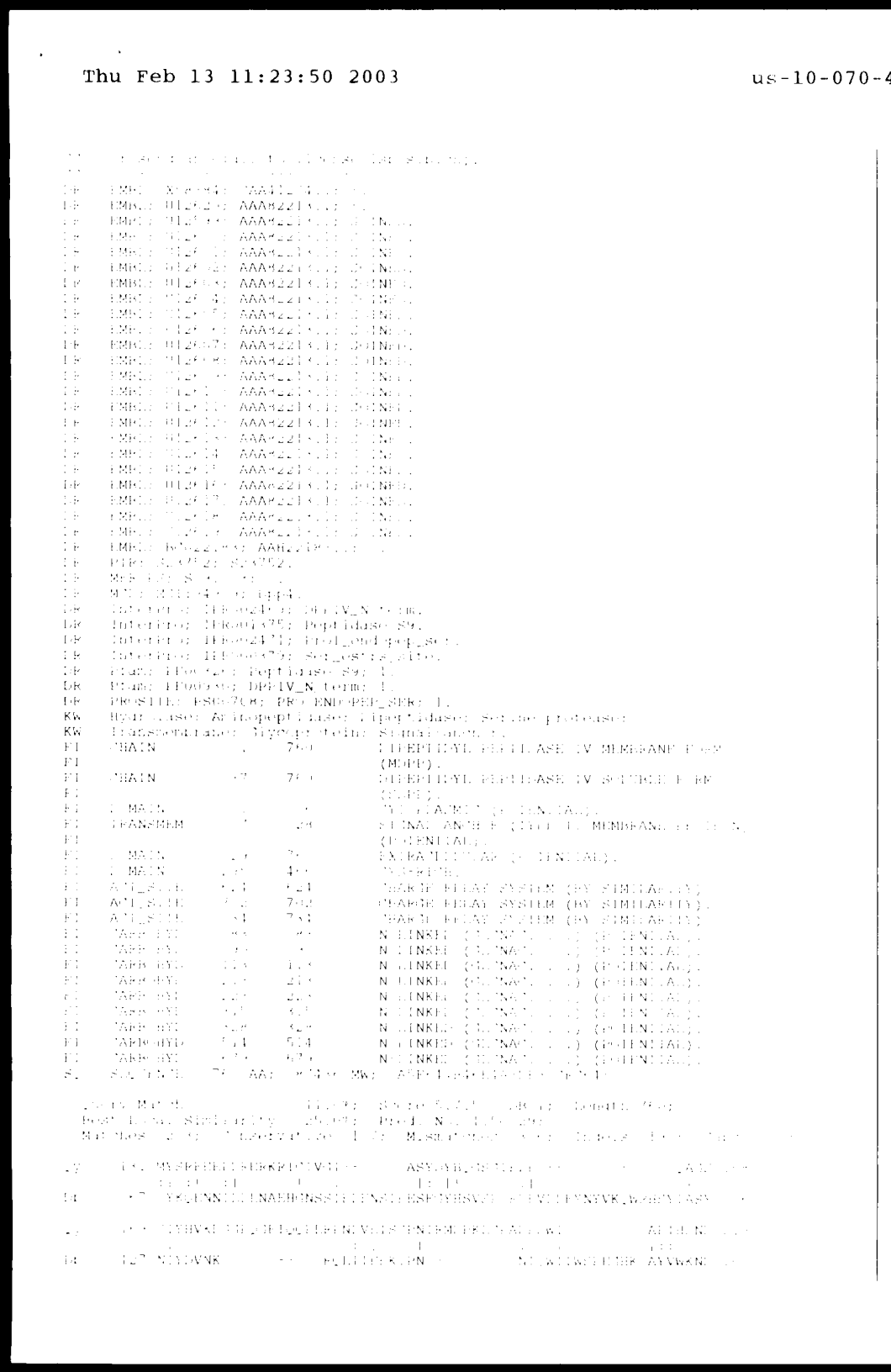


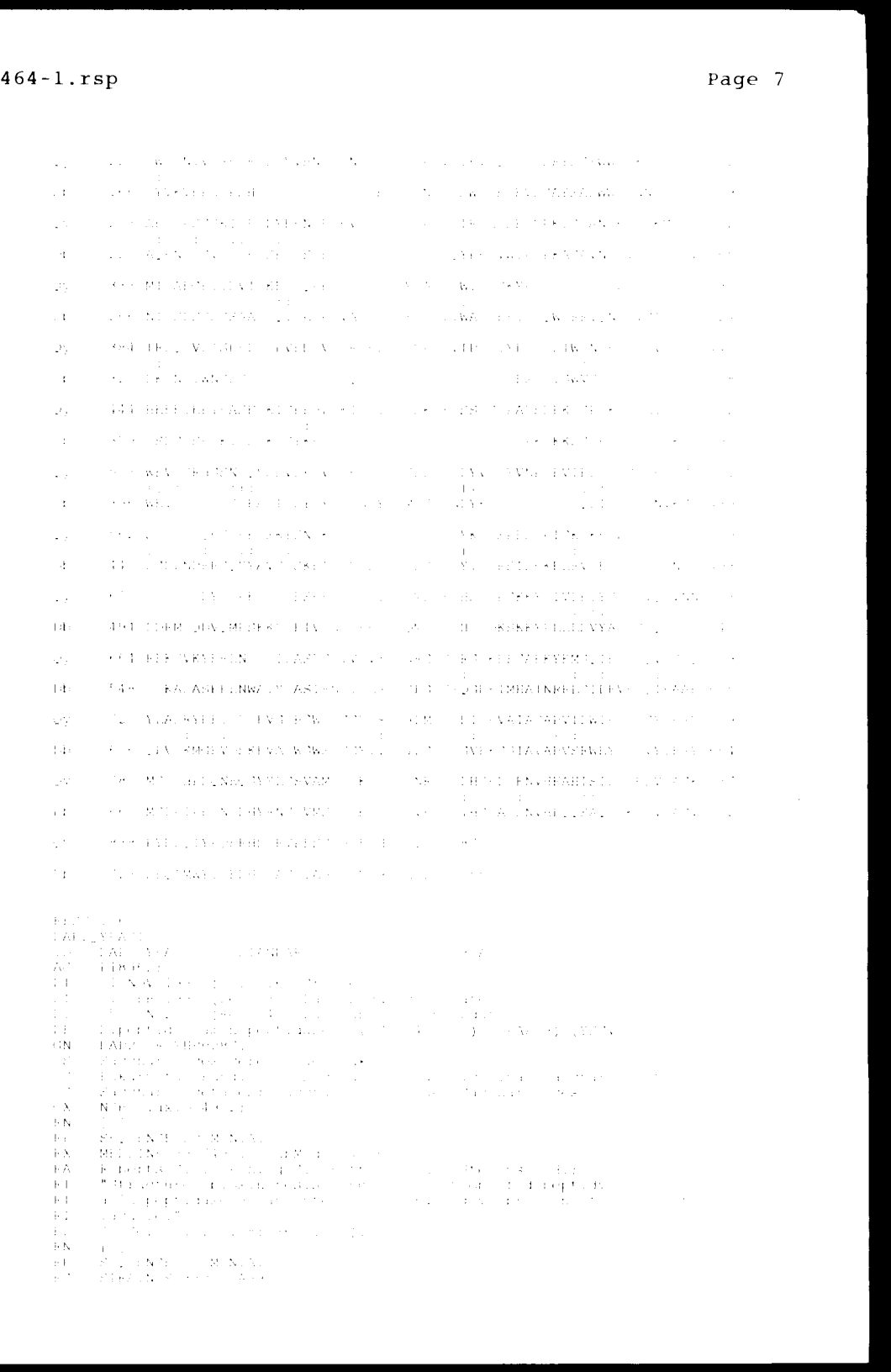


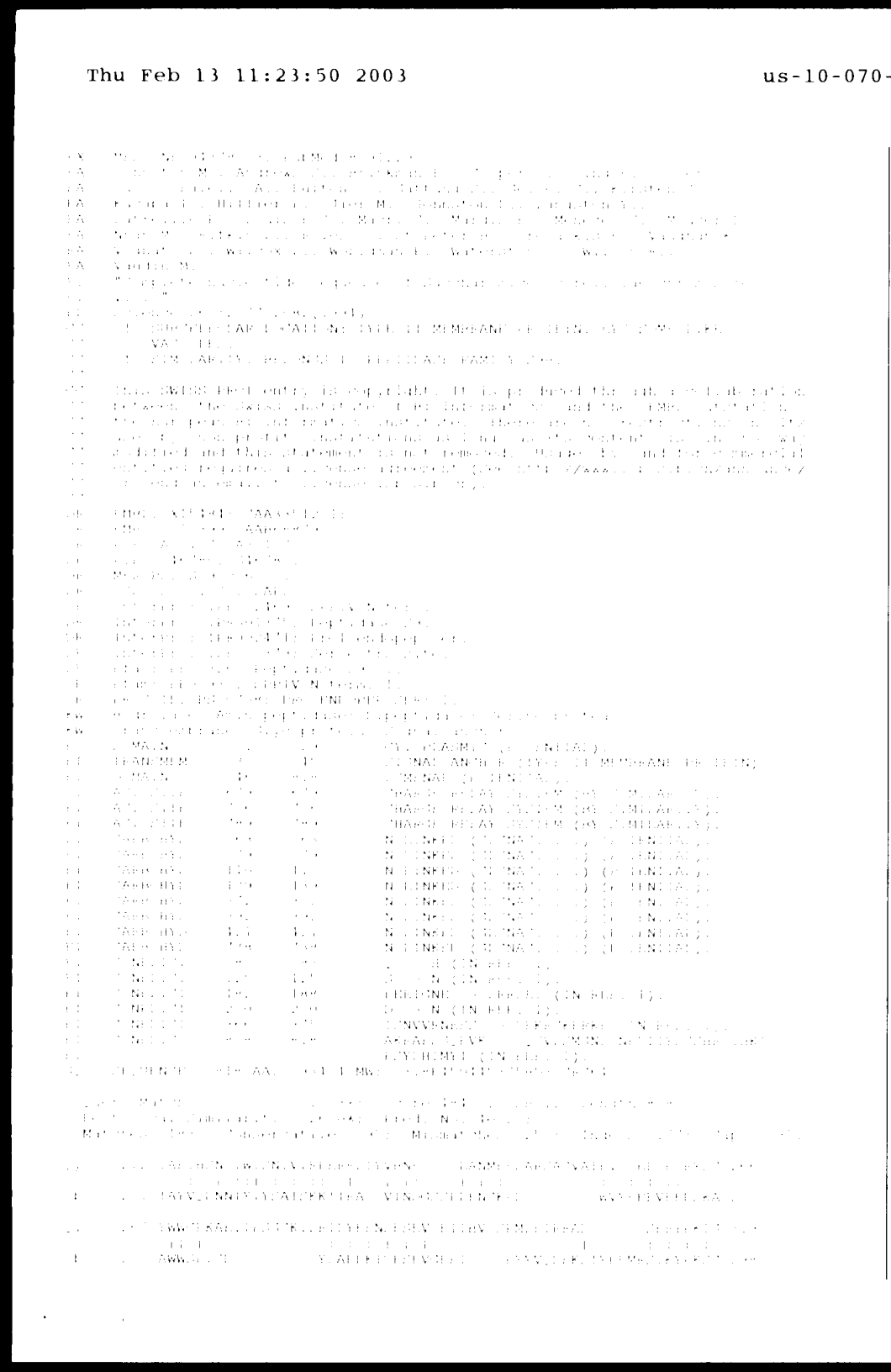


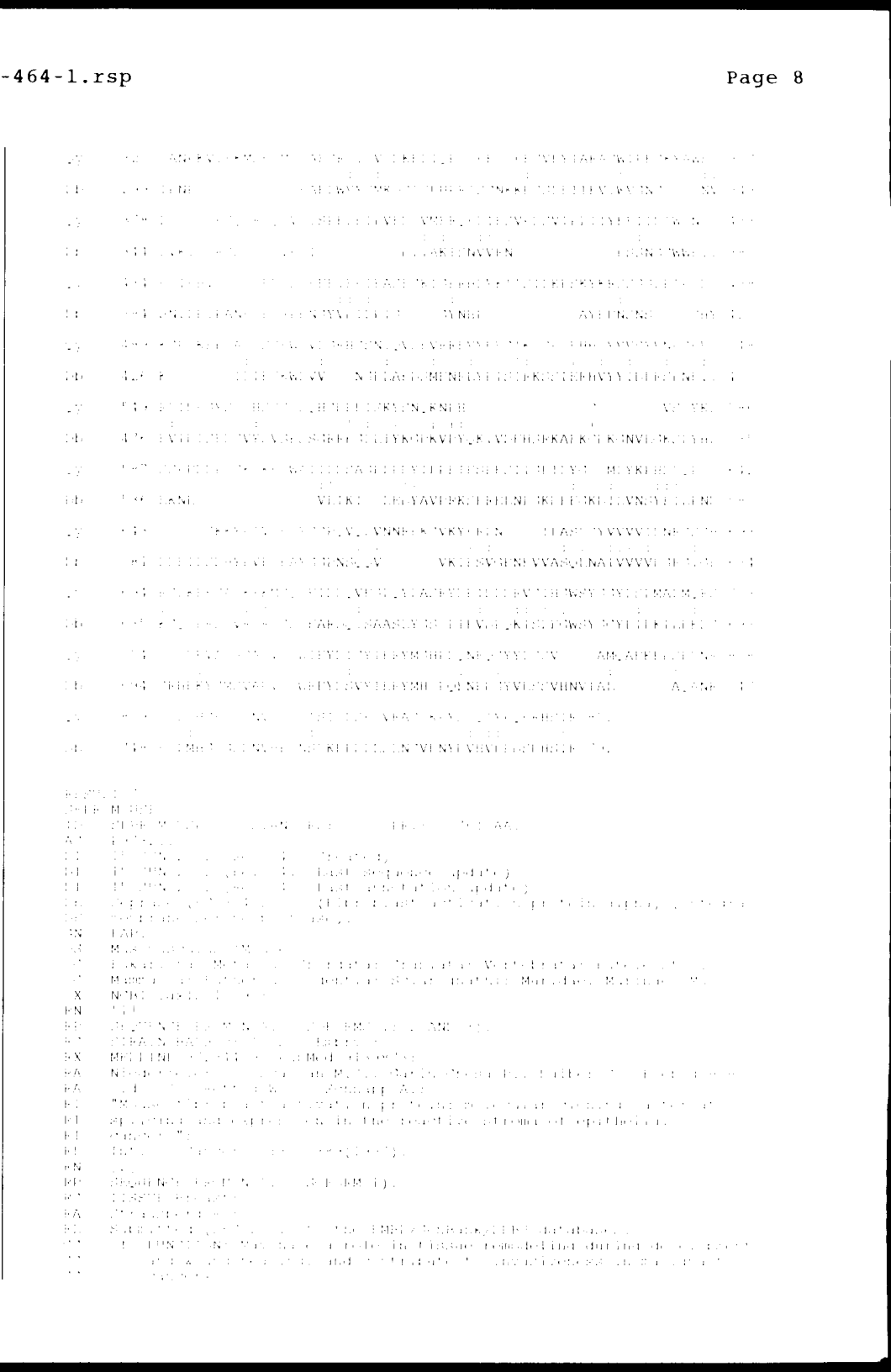


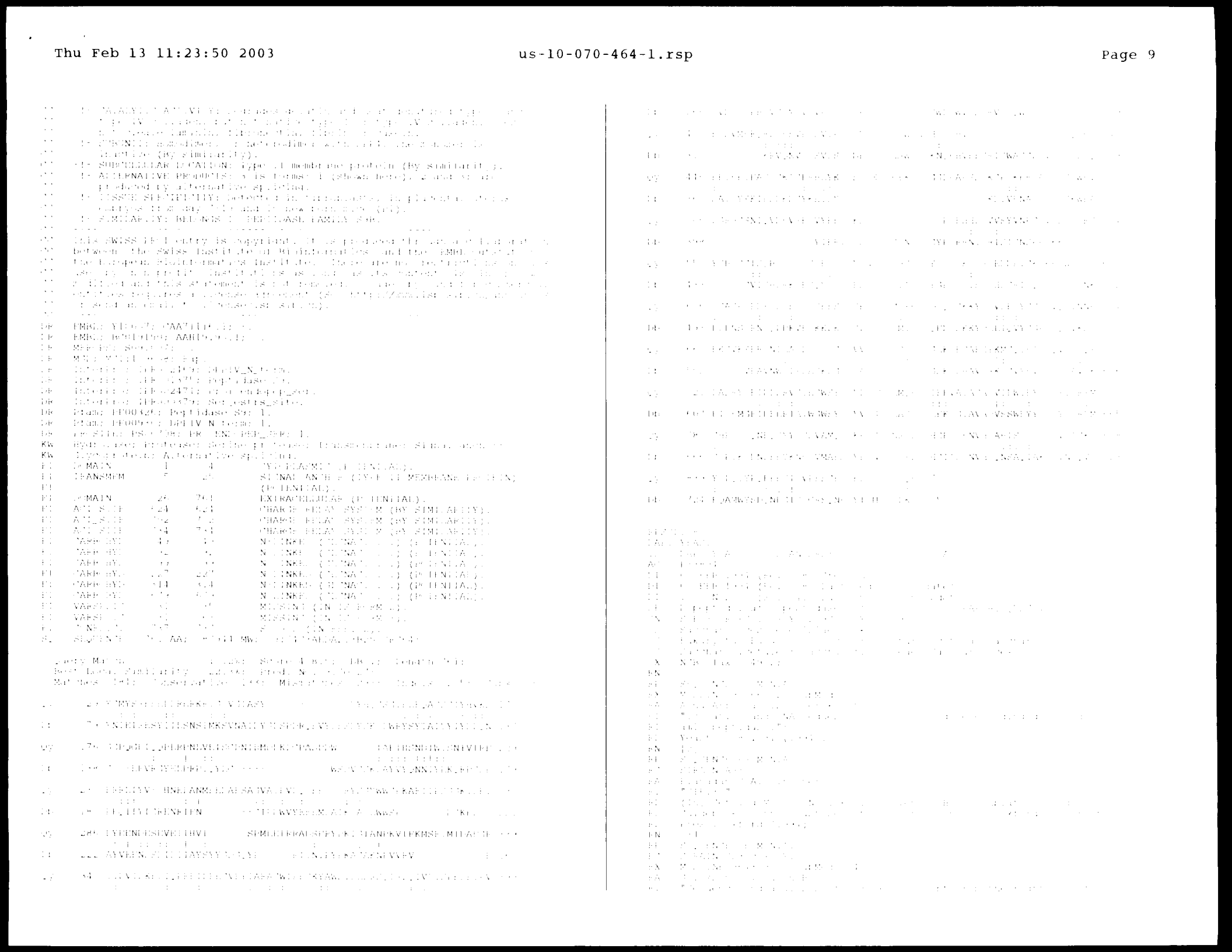


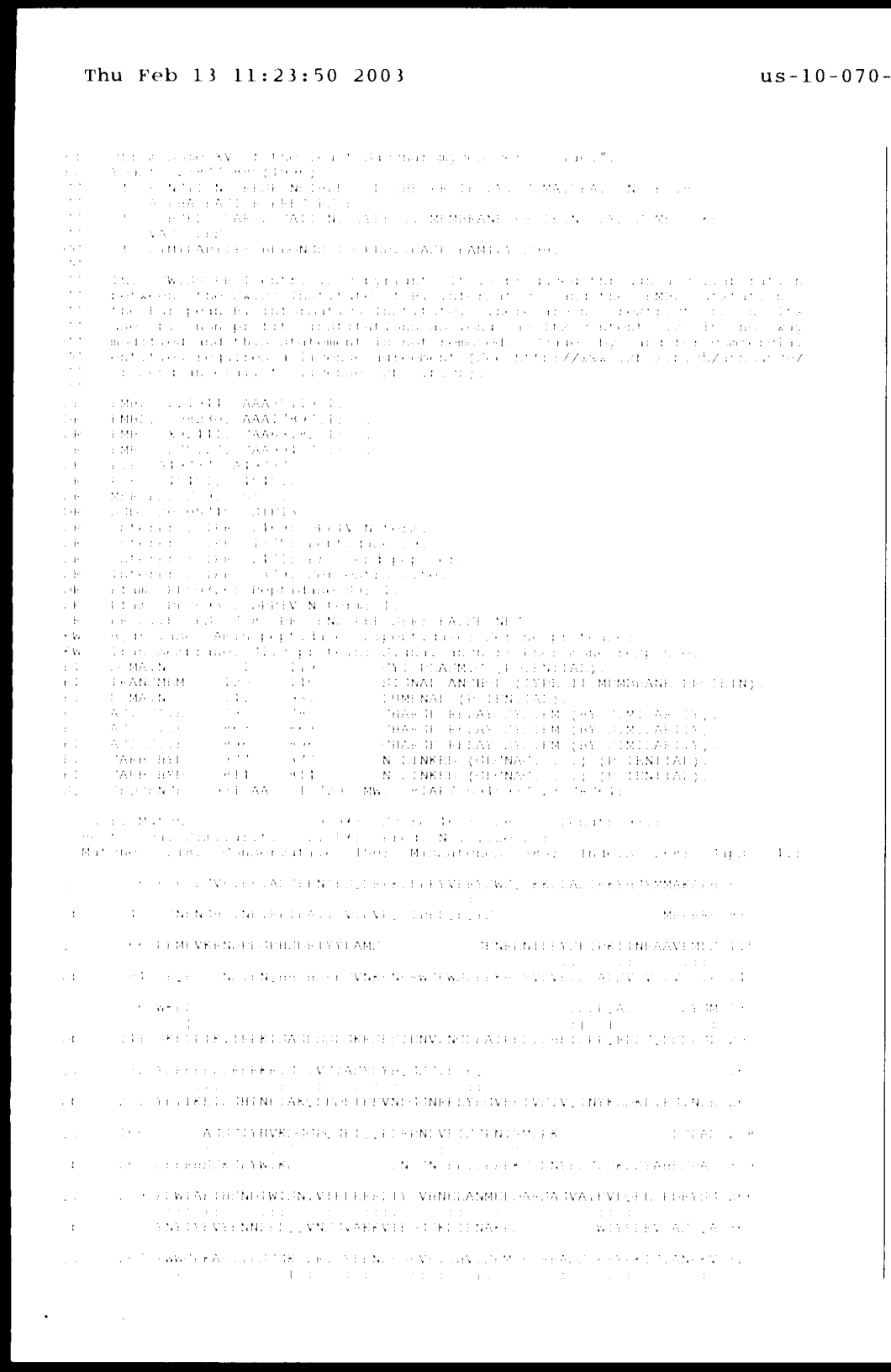


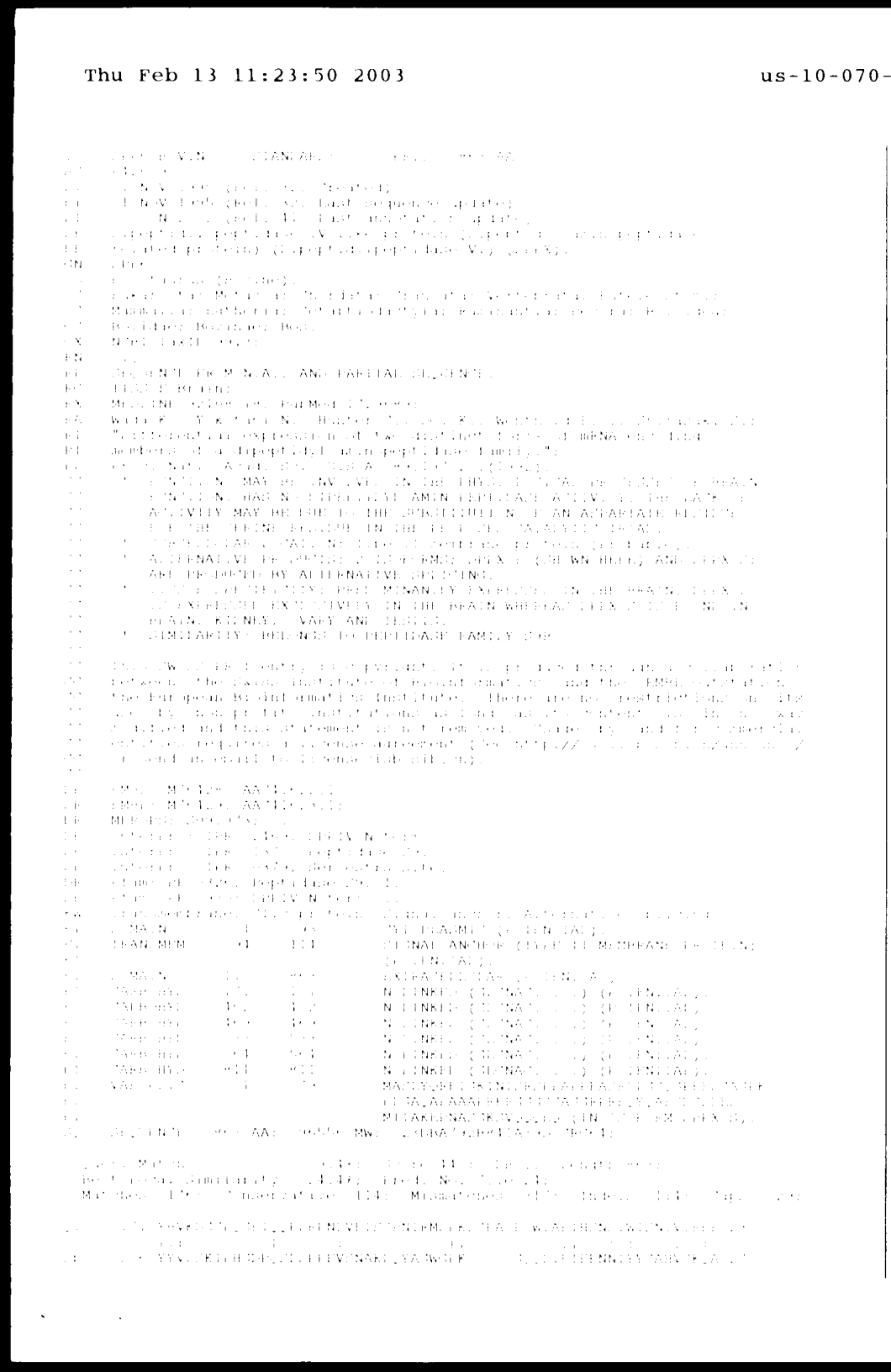


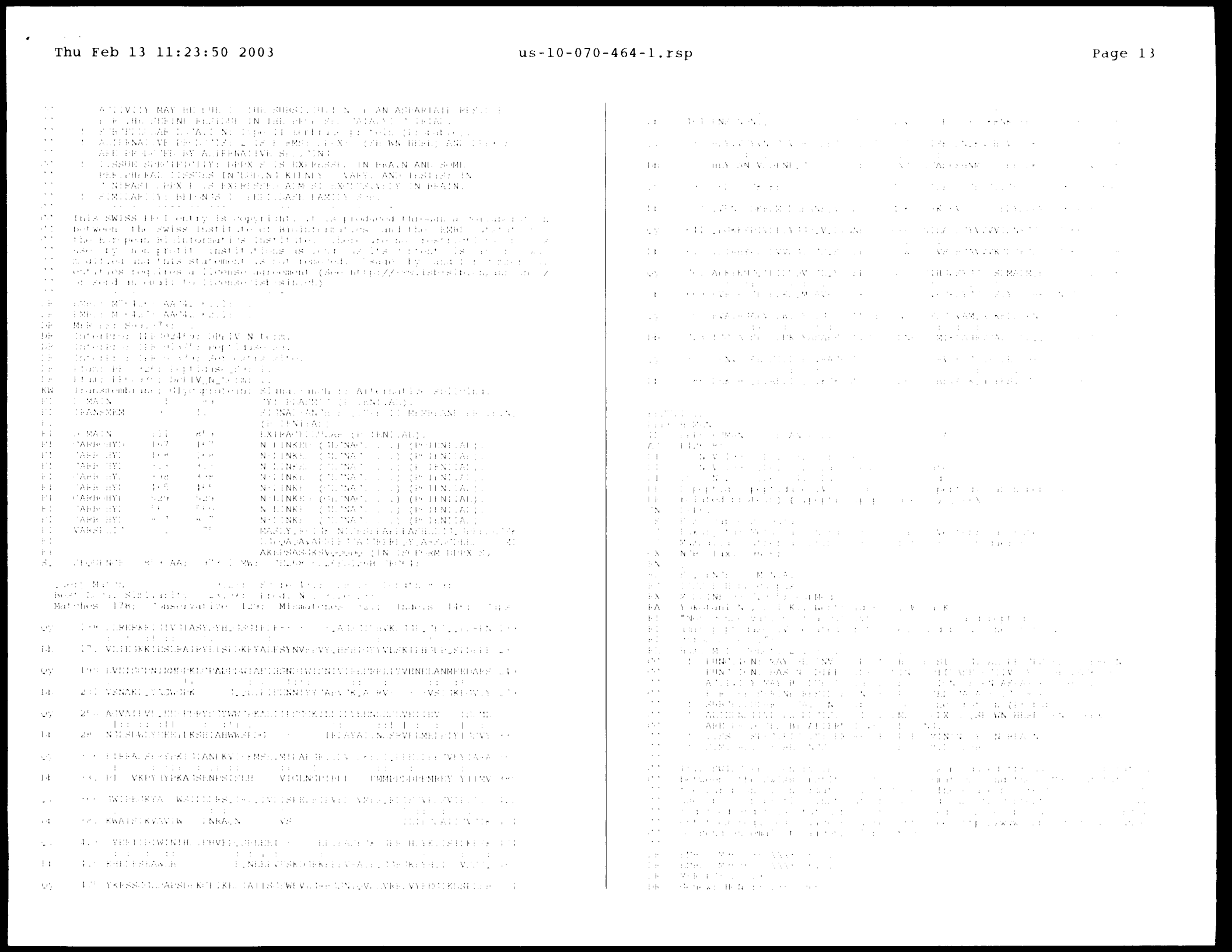


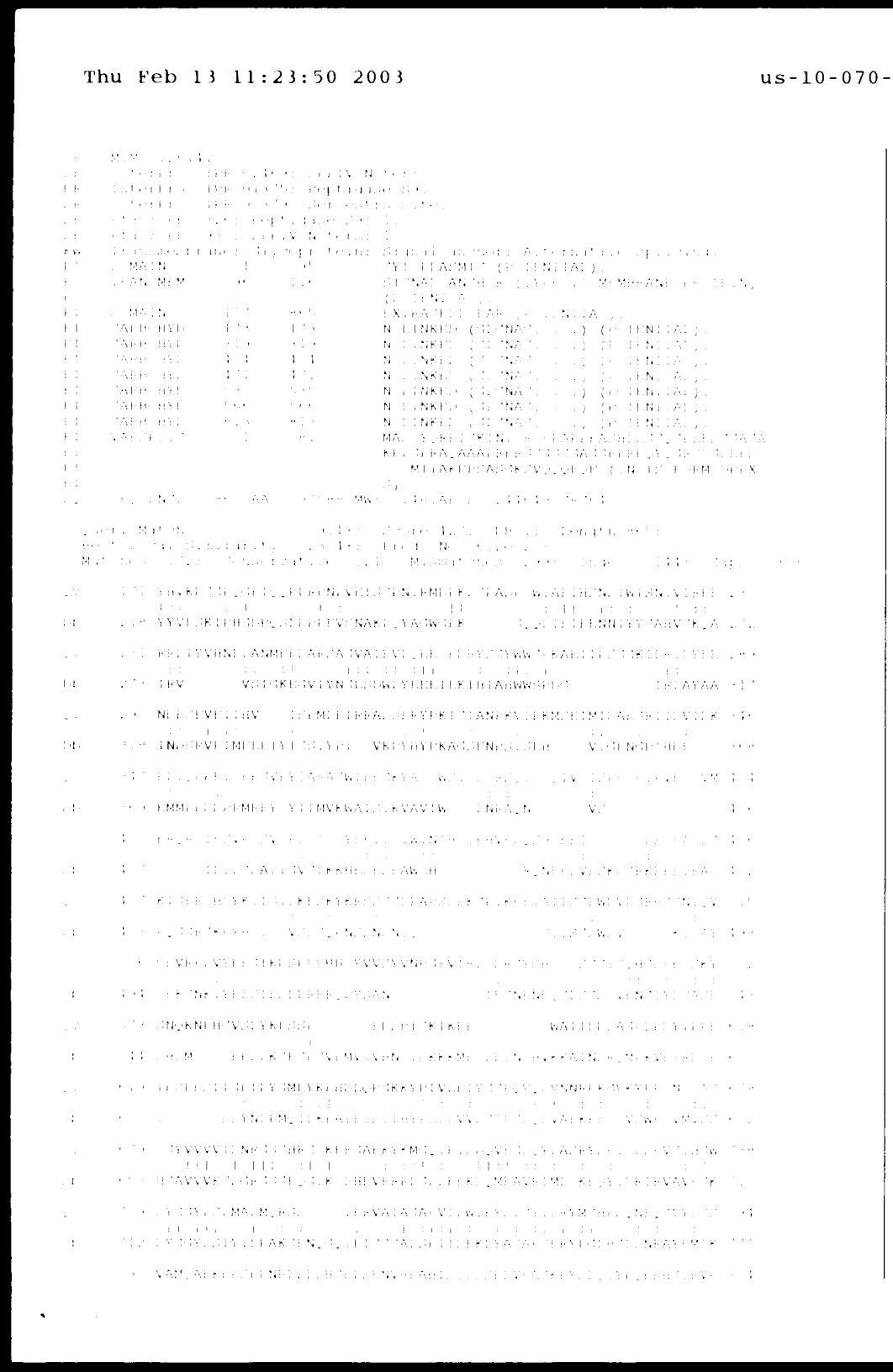


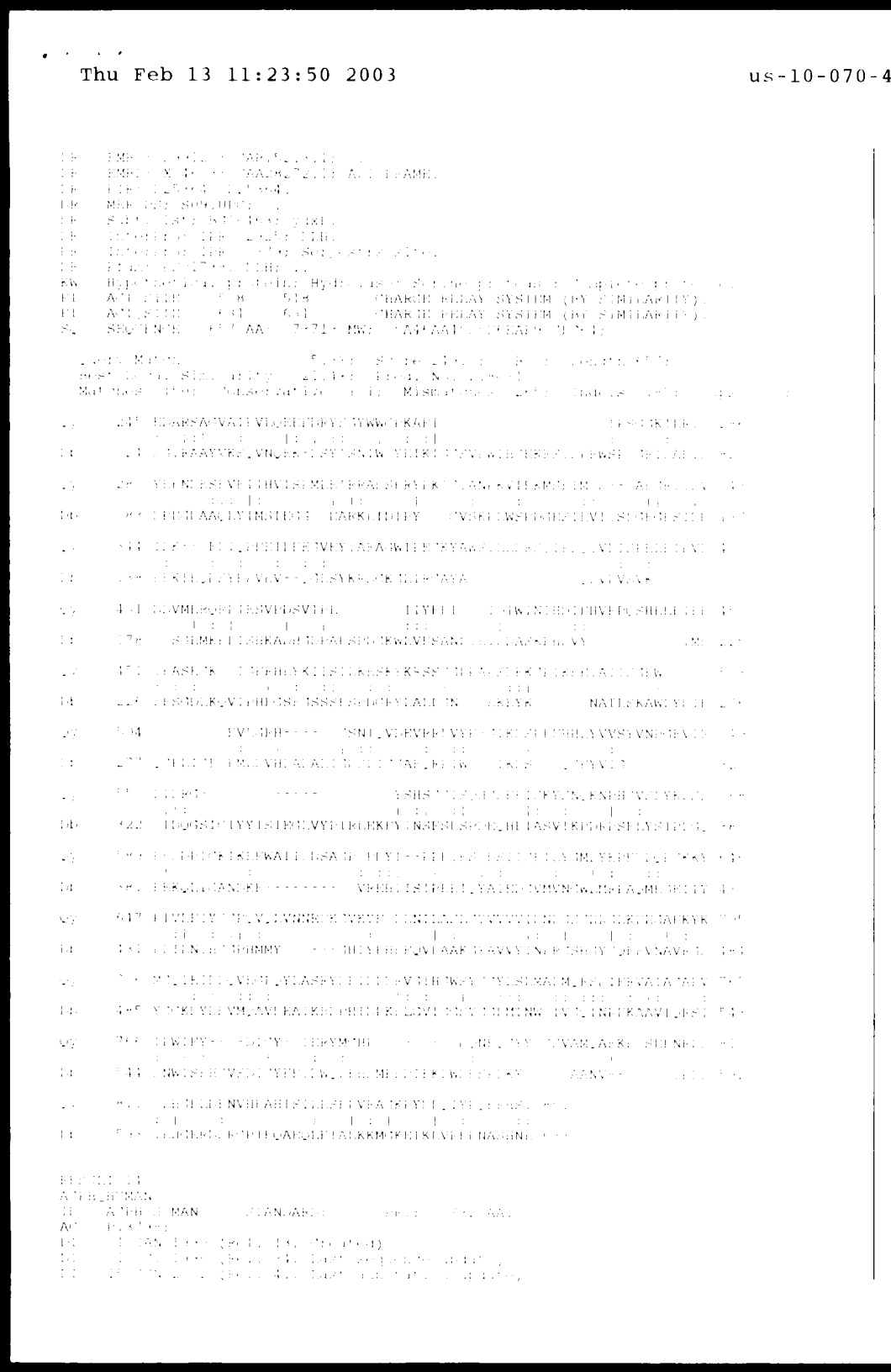


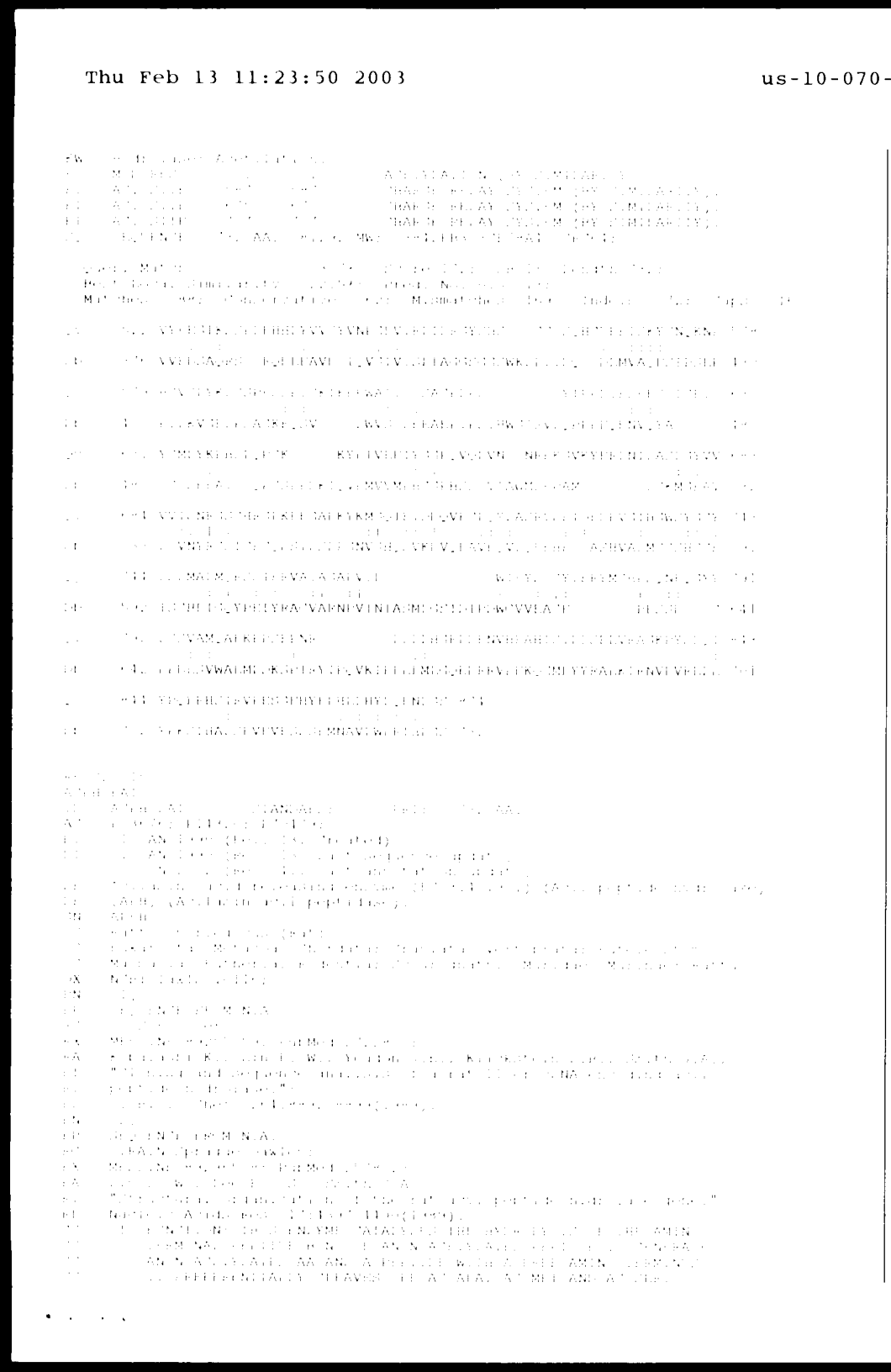


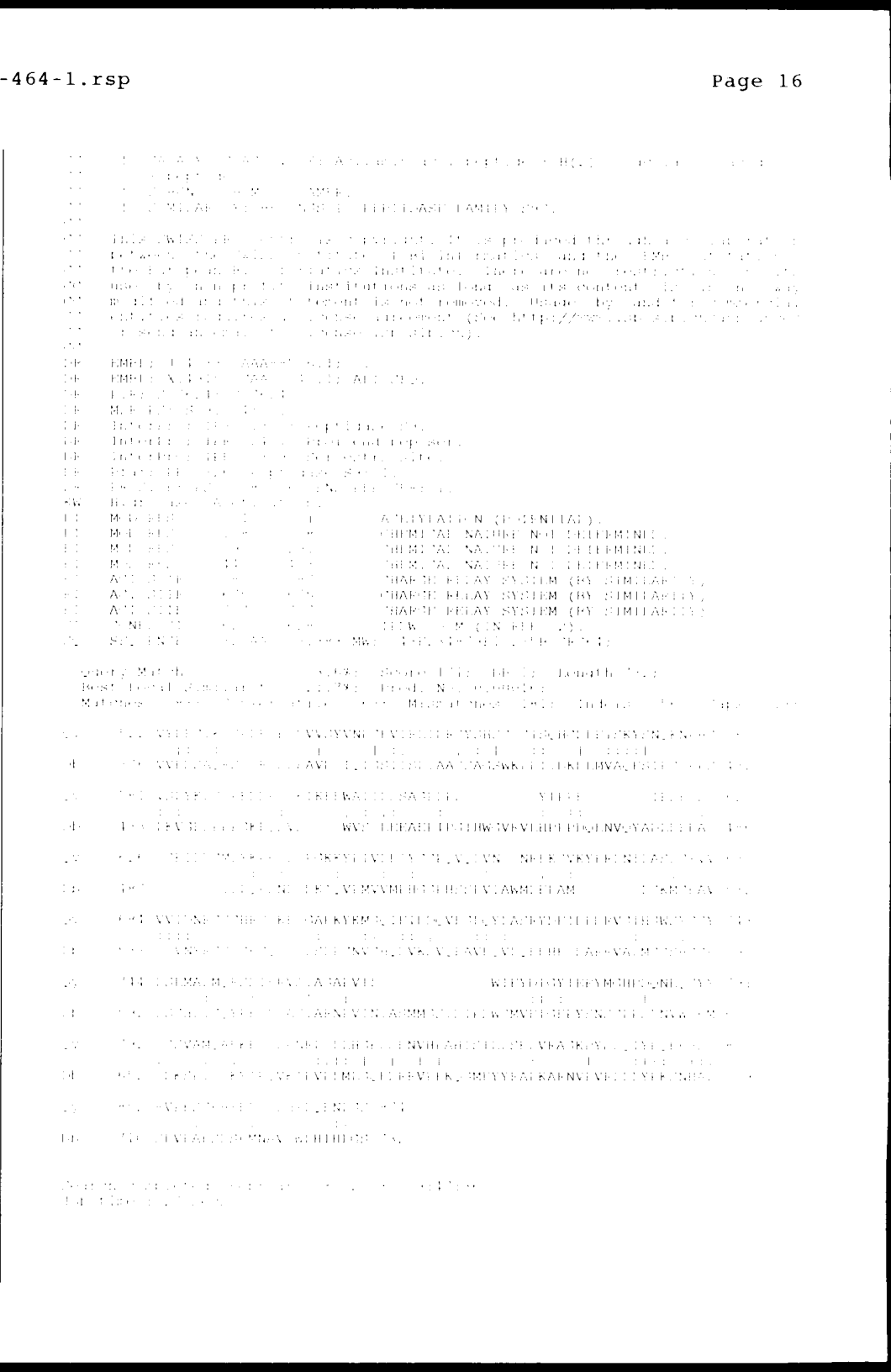




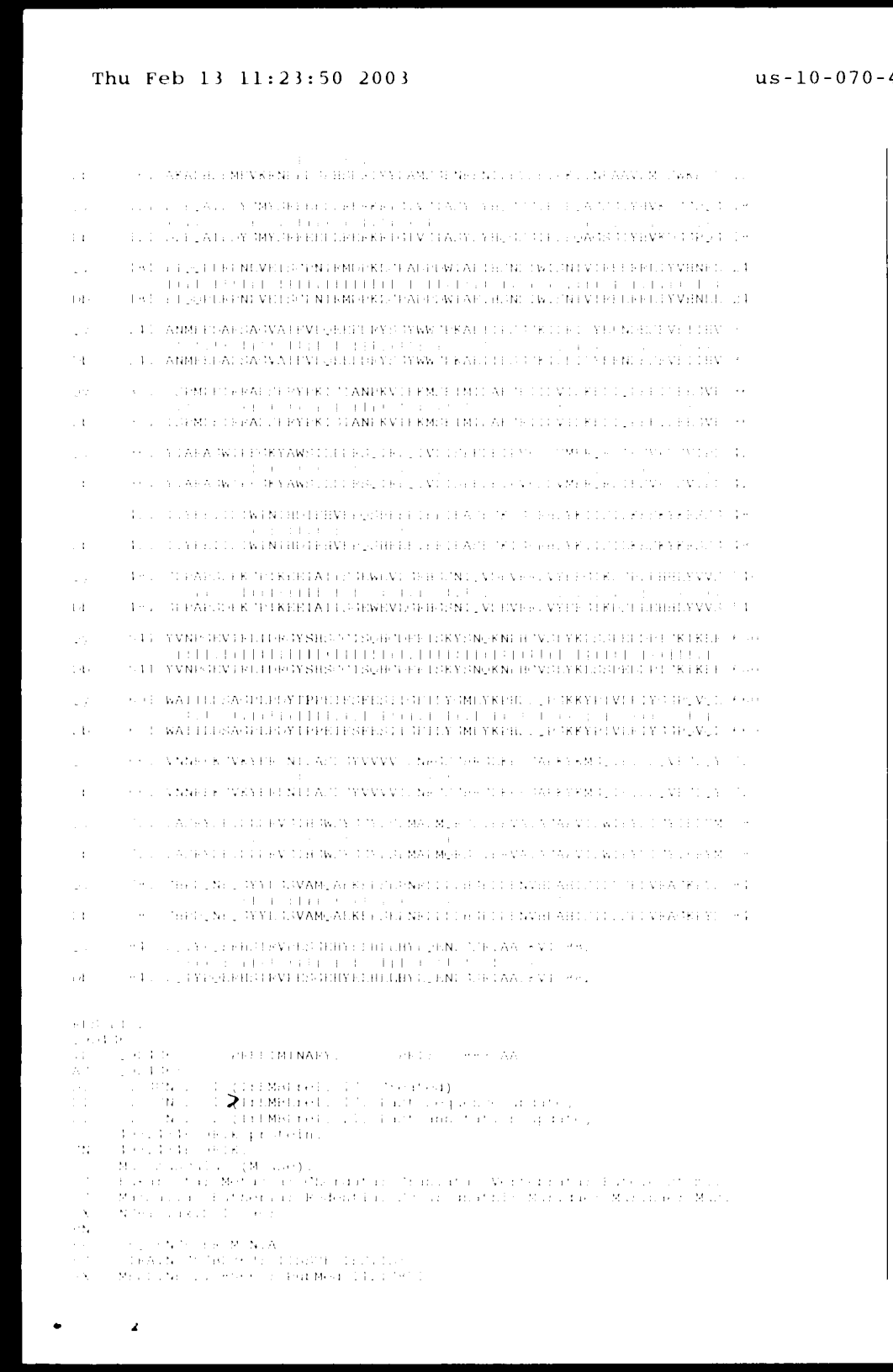


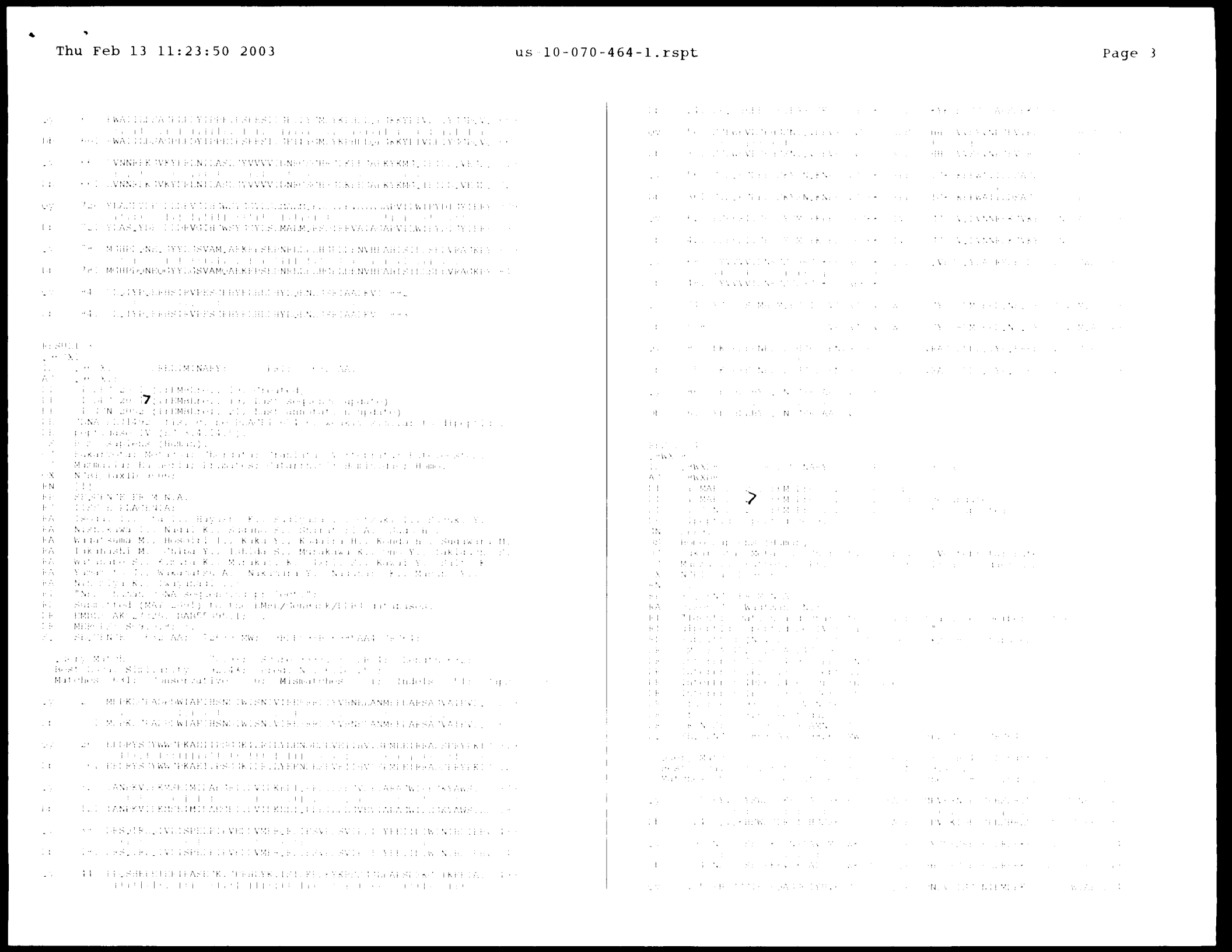


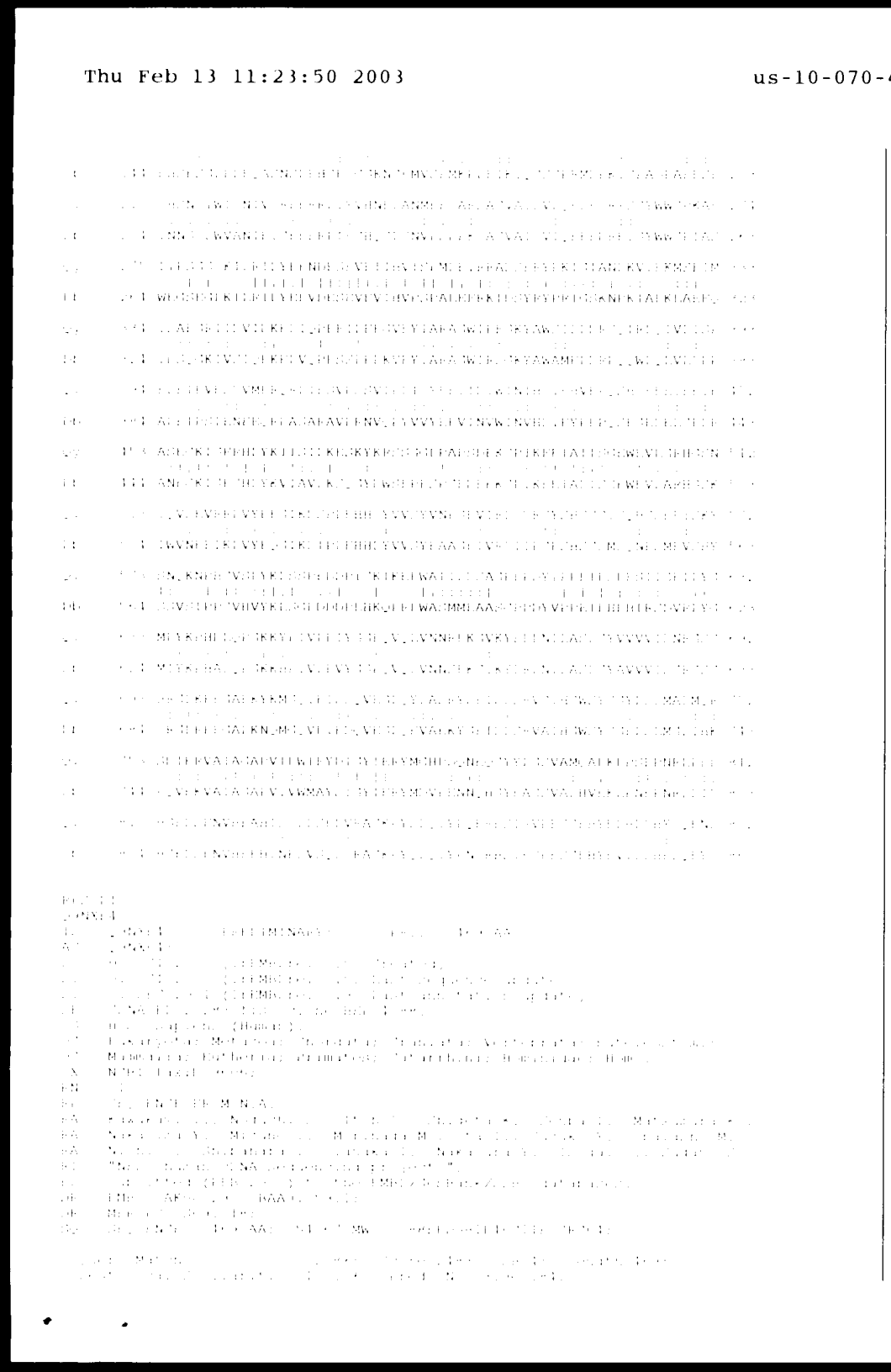


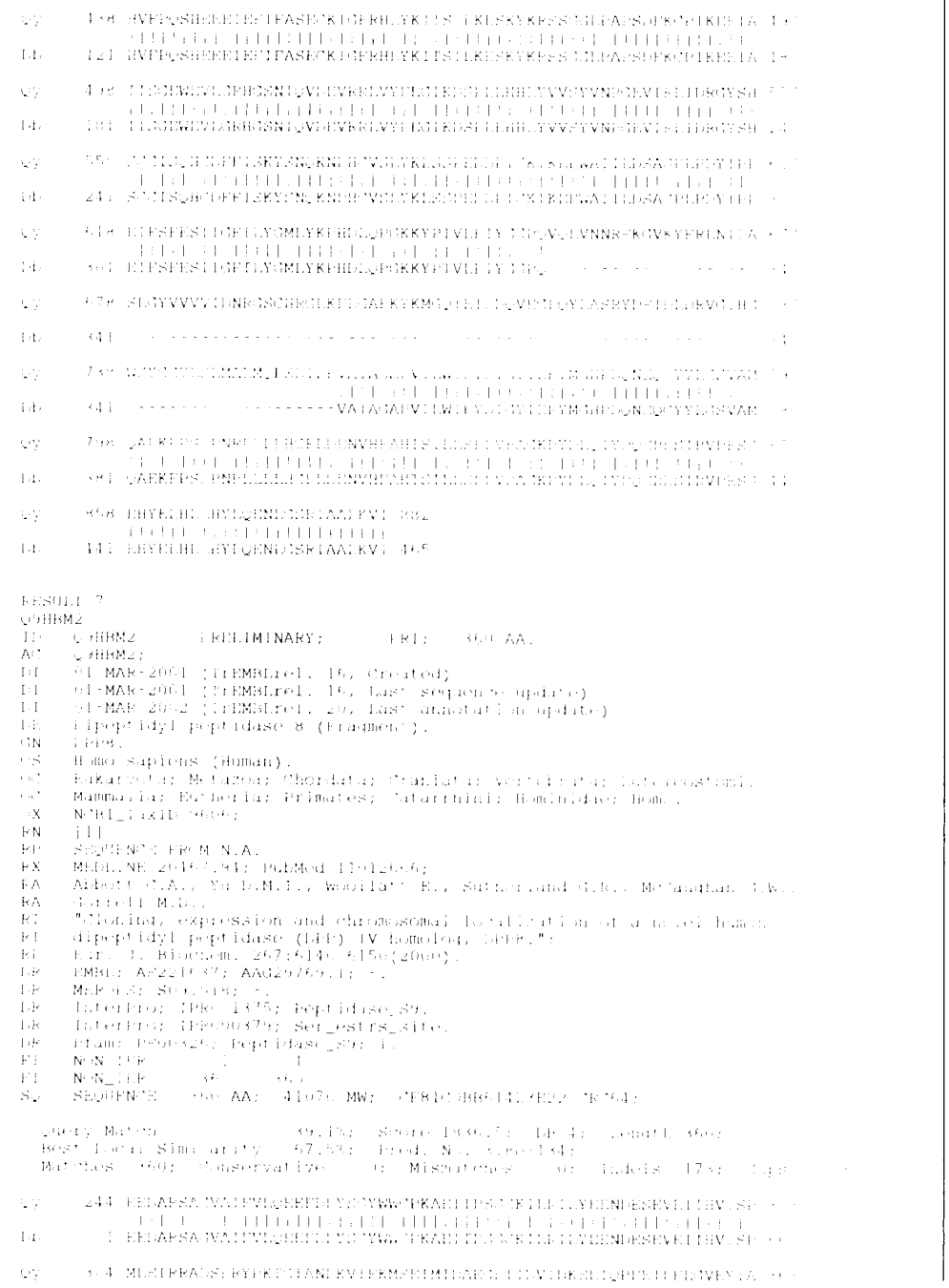






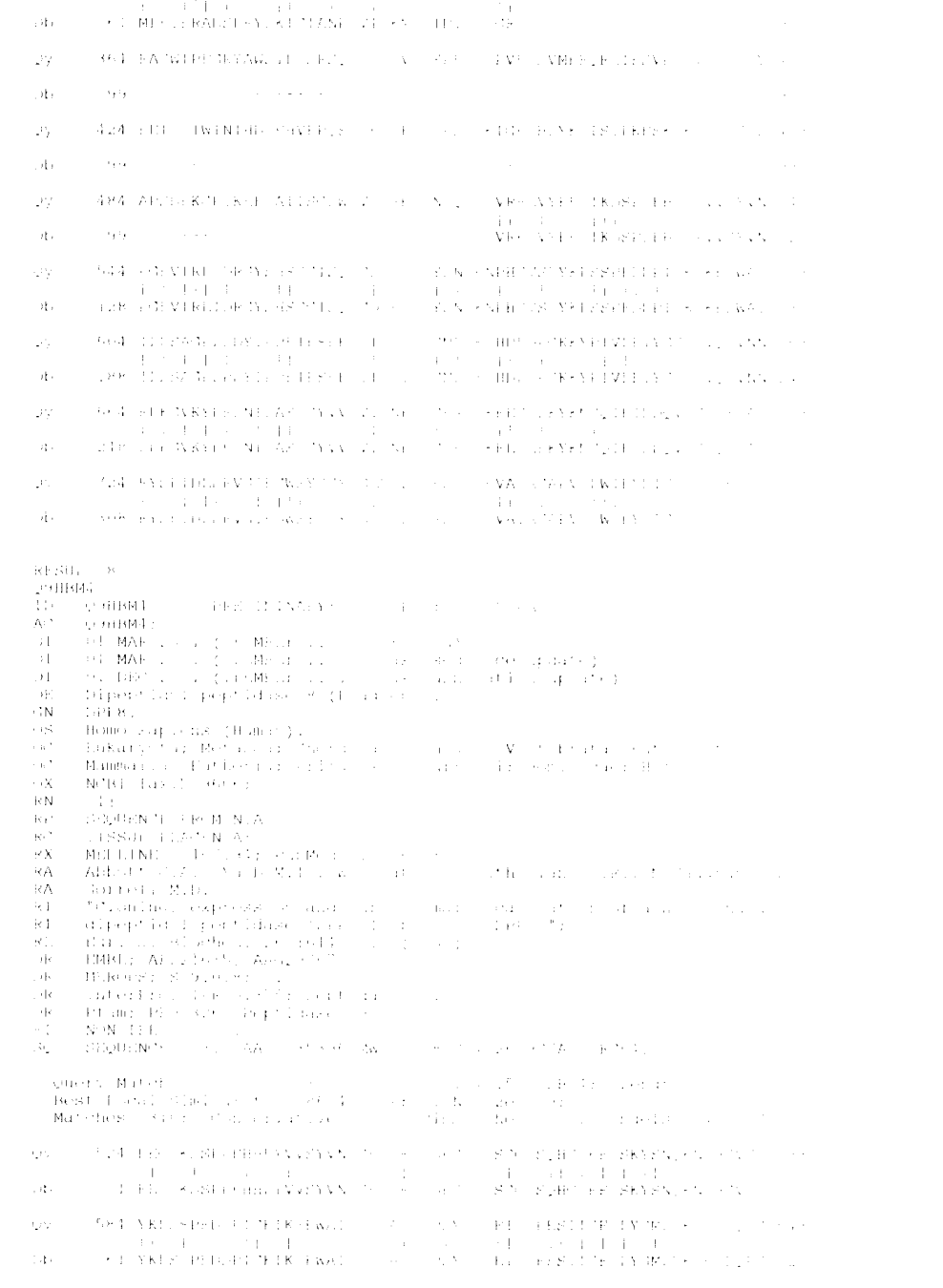


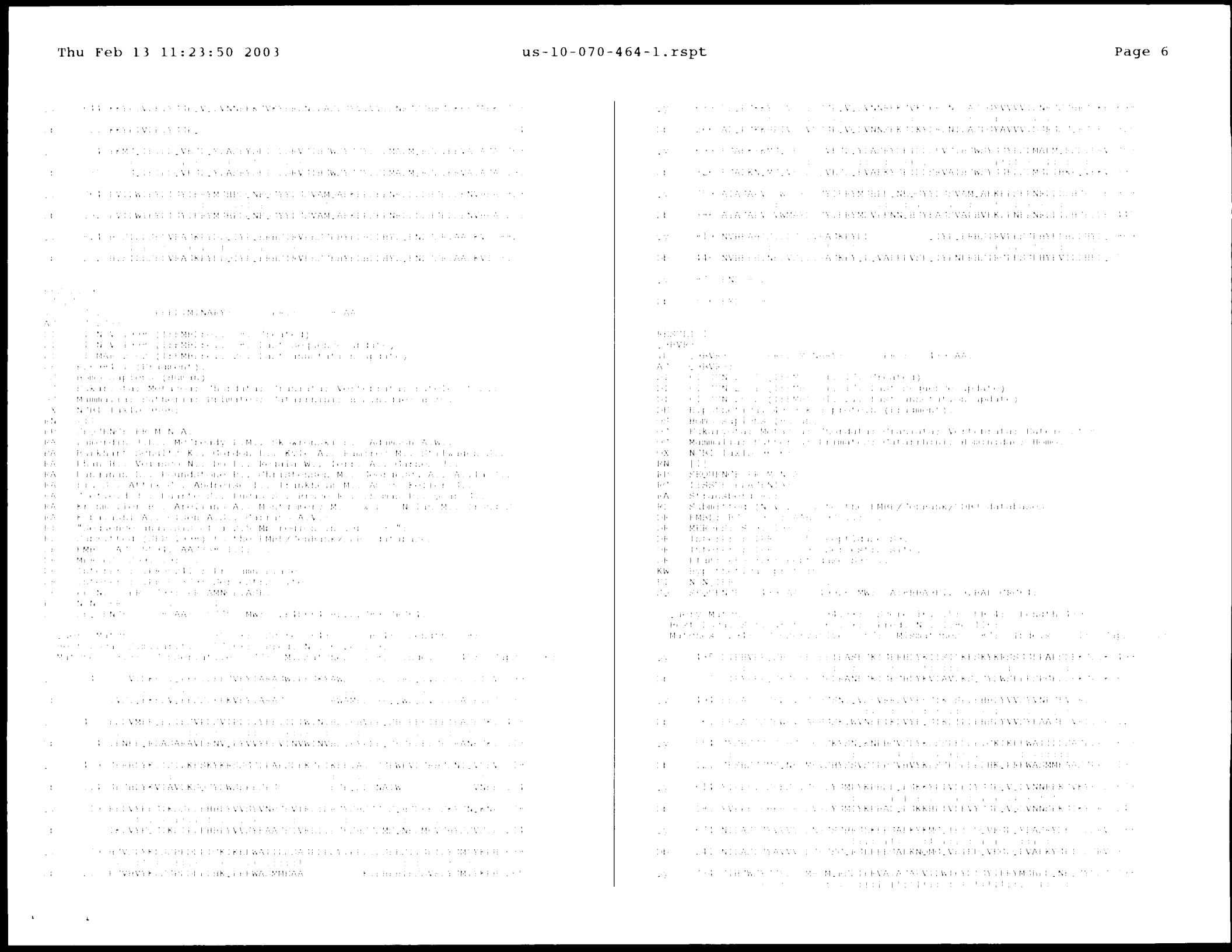


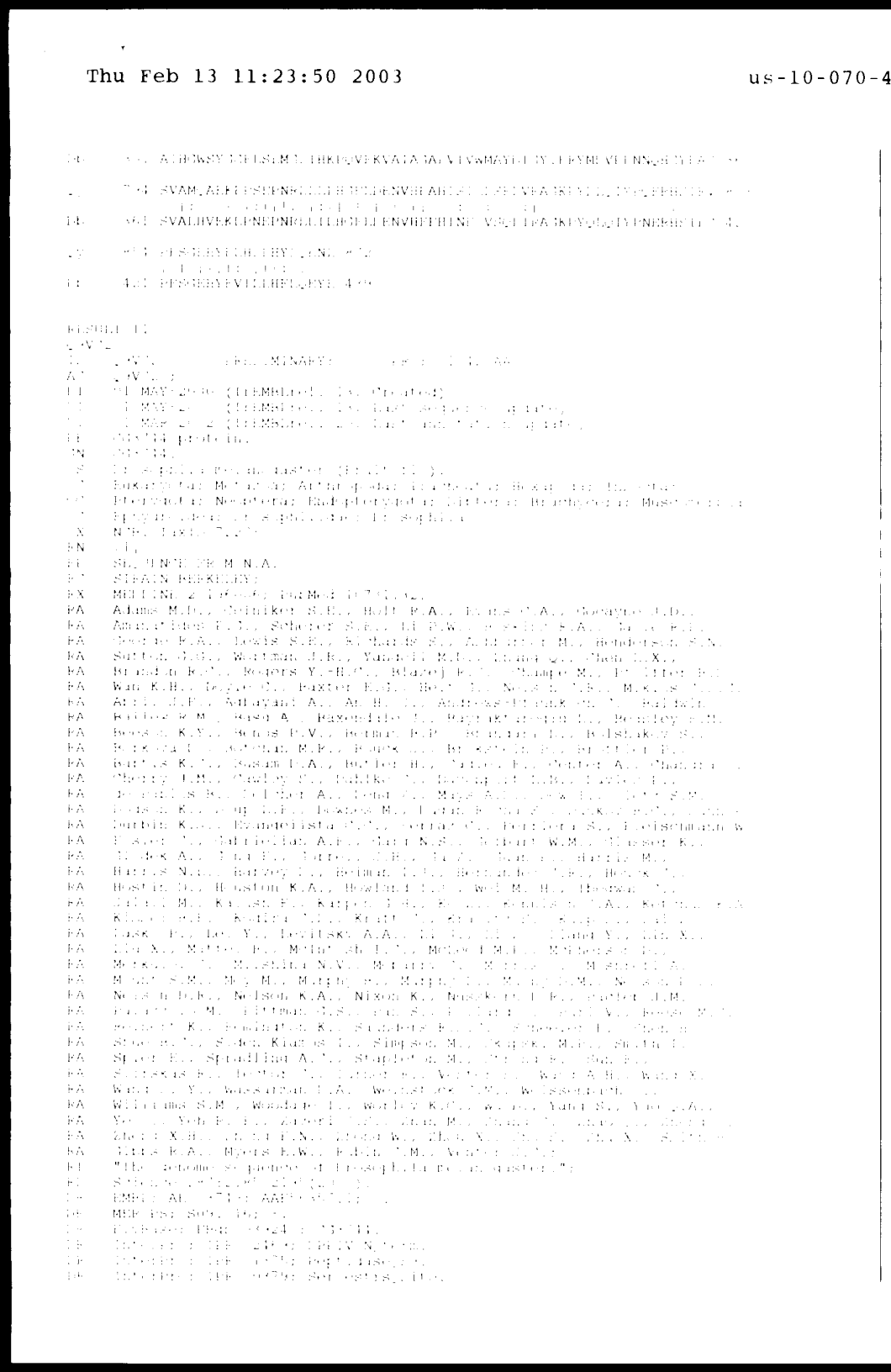


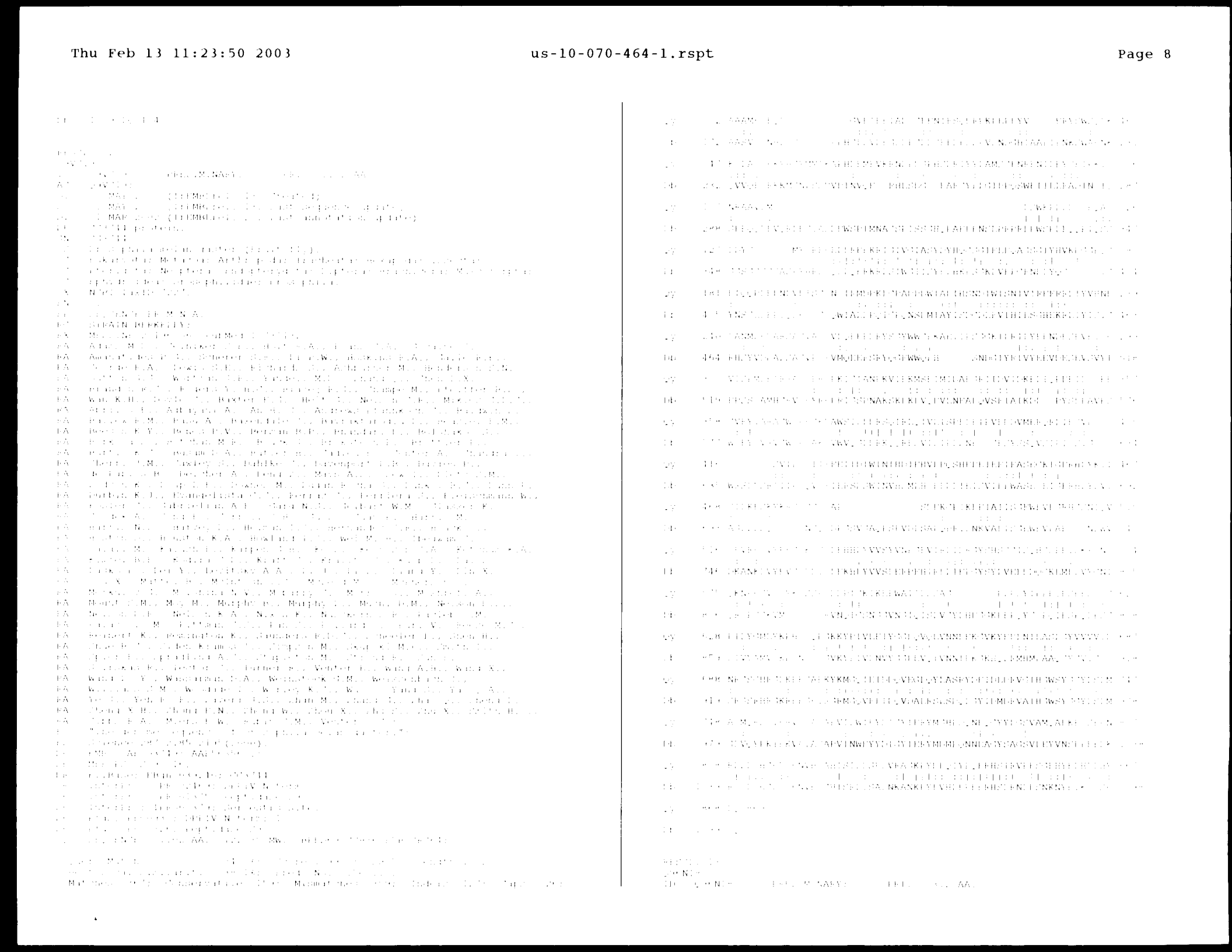
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ID Q9BBM2 PRELIMINARY; PRT; 360 AA.
AC Q9BBM2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Dipeptidyl peptidase 8 (Fragment).
GN DPP8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20147341; PubMed=11076866;
RA Abbott C.A., Yu D.M.T., Woollatt E., Sutherland G.R., McCaughan G.W.,
RA Gorrell M.D.;
RT "Cloning, expression and chromosomal localization of a novel human
RT dipeptidyl peptidase (DPP) IV homolog, DPP8.";
RL Eur. J. Biochem. 267:6140-6150(2000).
DR EMBL; AF221497; AAG29769.1; -.
DR MEROPS; S09.018; -.
DR InterPro; IPR001375; Peptidase_S9.
DR InterPro; IPR000379; Ser_estrs_site.
DR Pfam; PF00326; Peptidase_S9; 1.
FT NON_TER 1 1
FT NON_TER 360 360
SQ SEQUENCE 360 AA; 41078 MW; 7FB1C3BB6E1C4E2C CRC64;

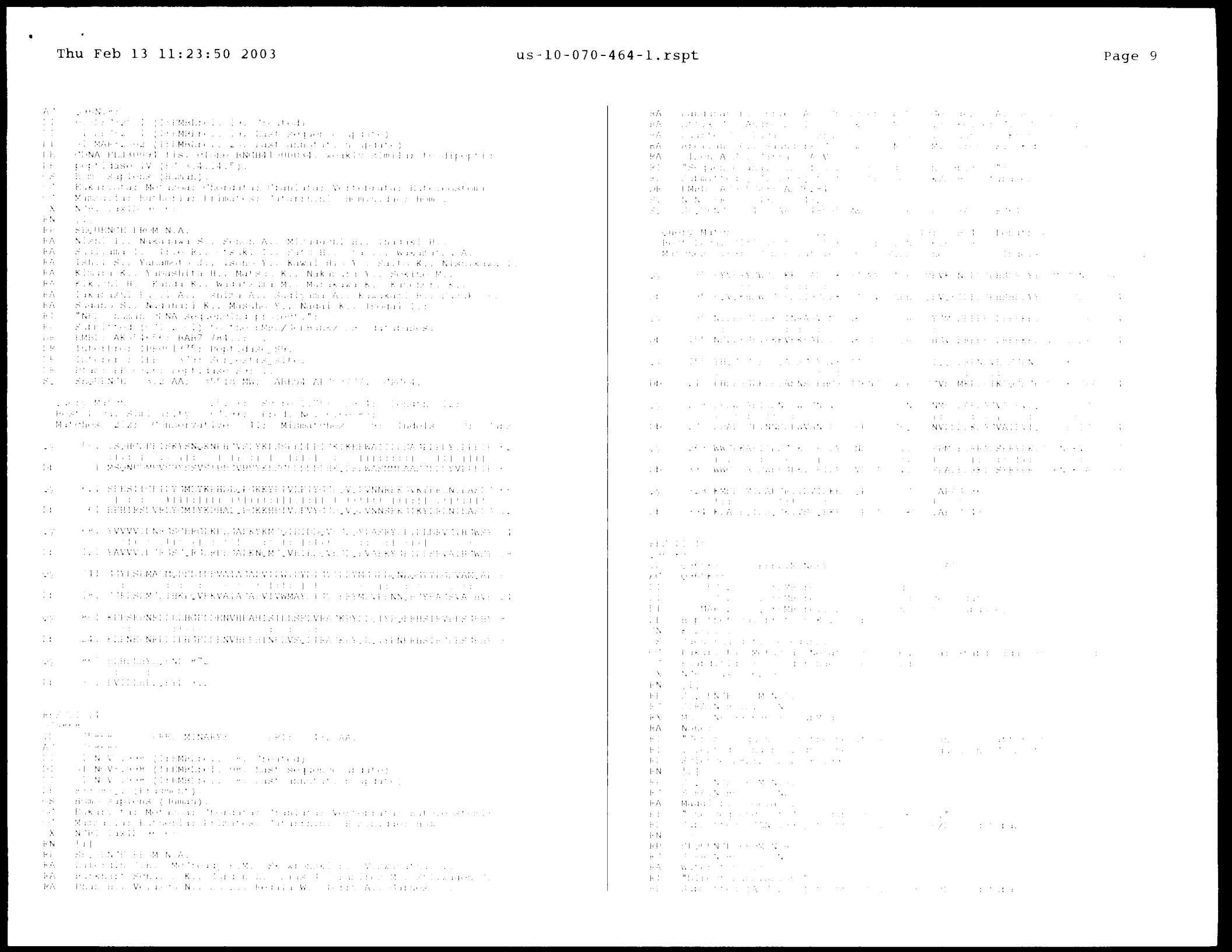
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Best Local Similarity 67.5%; Pred. No. 2.2e-154;
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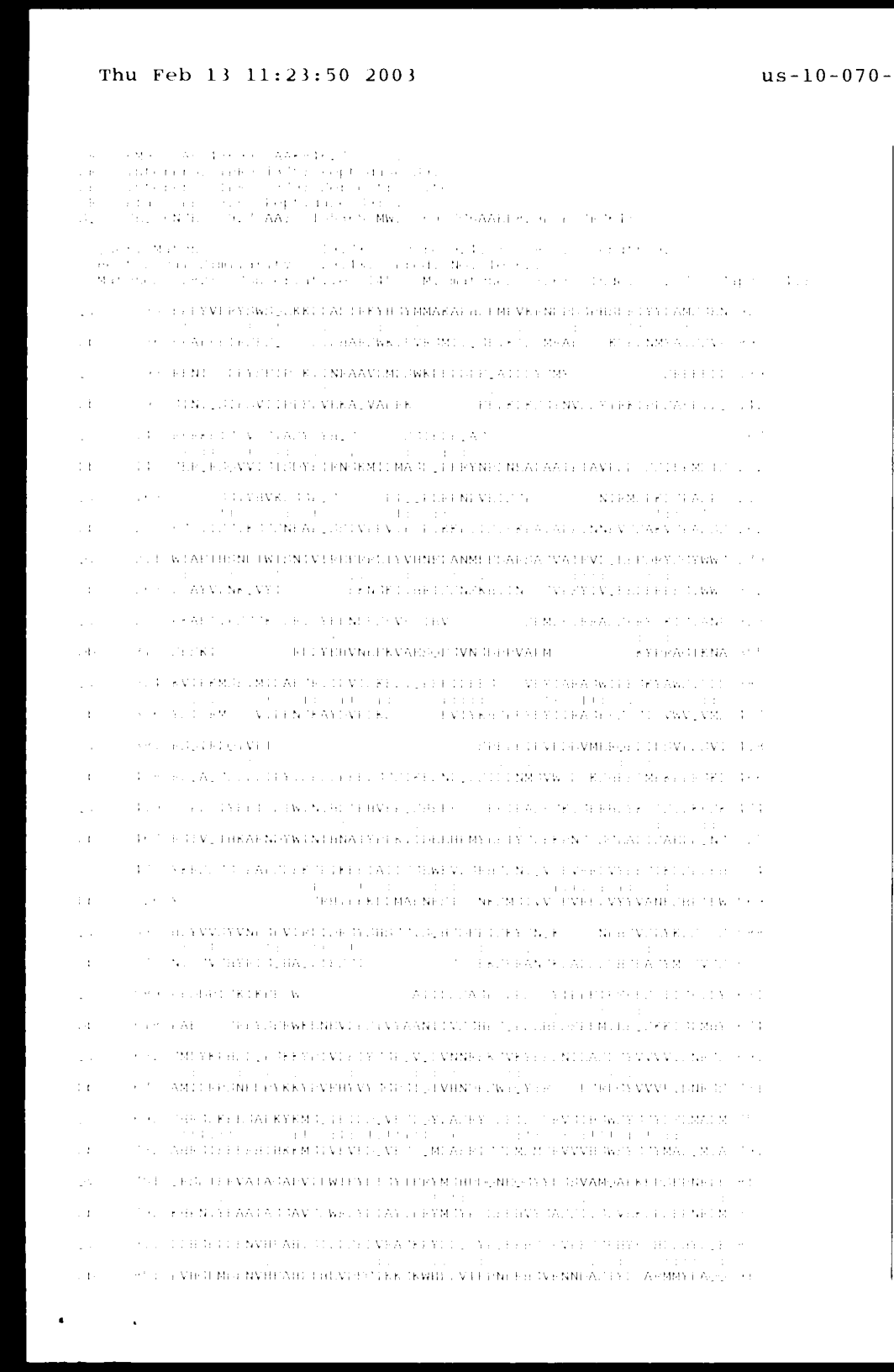


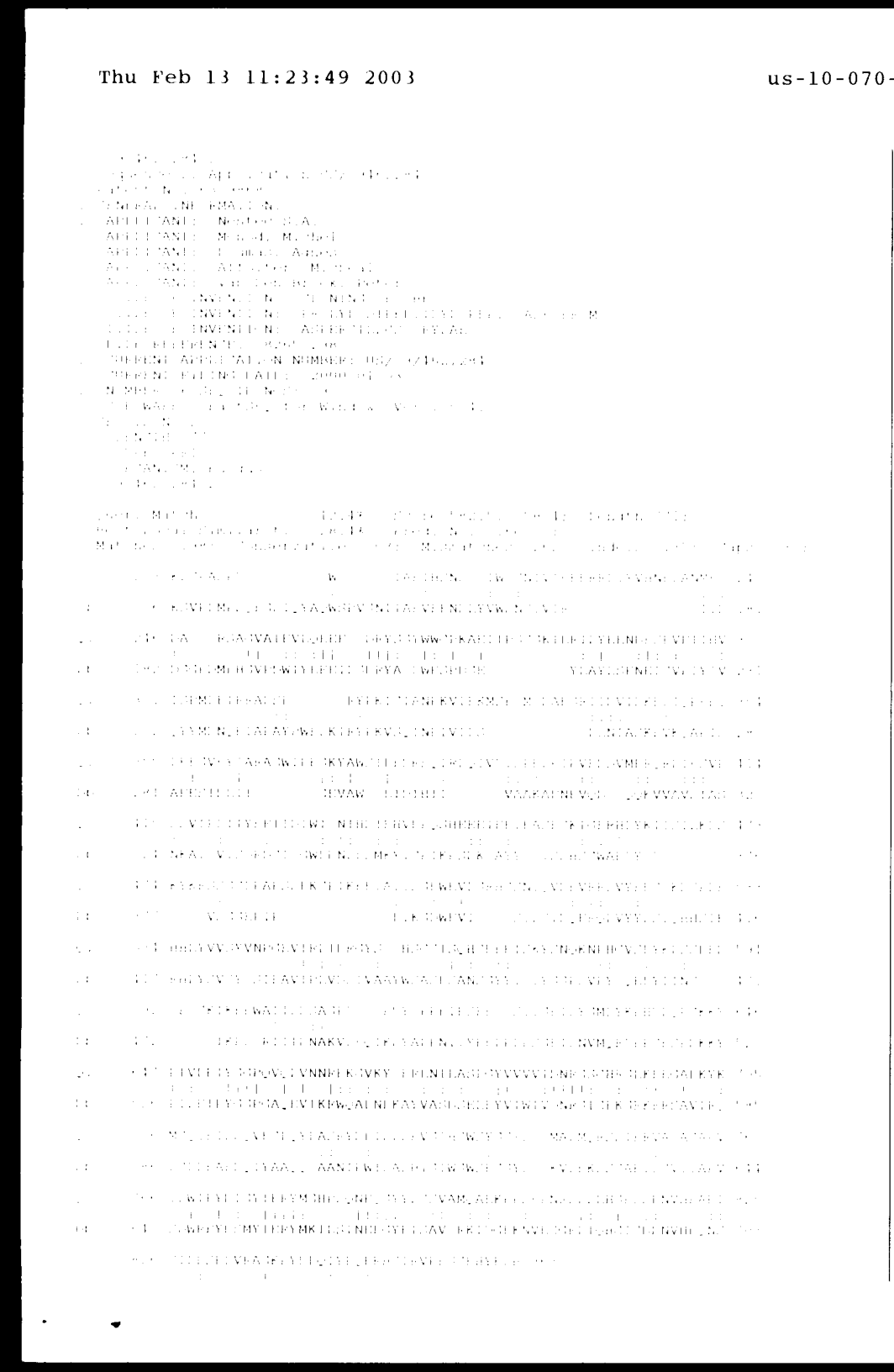


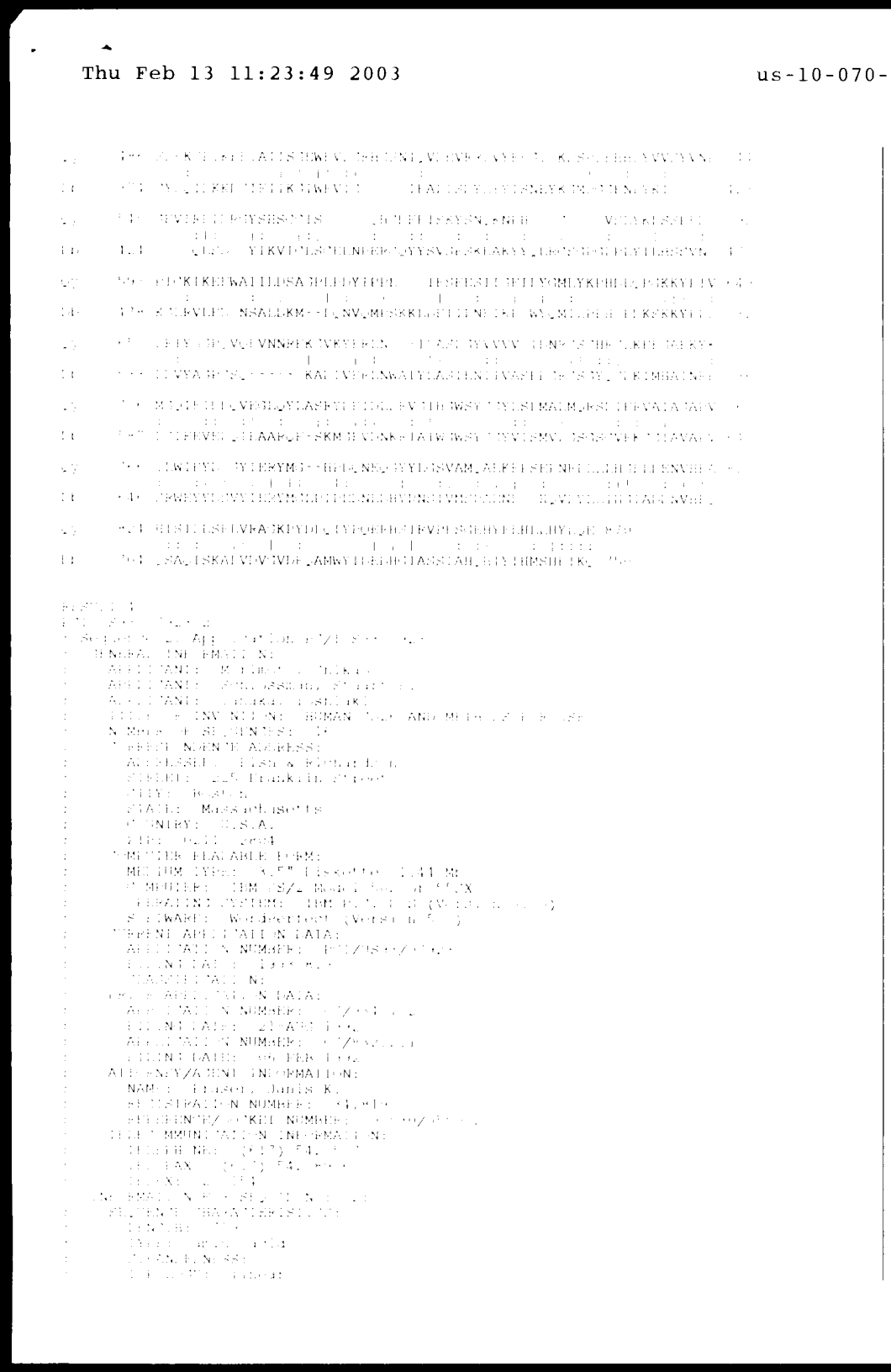


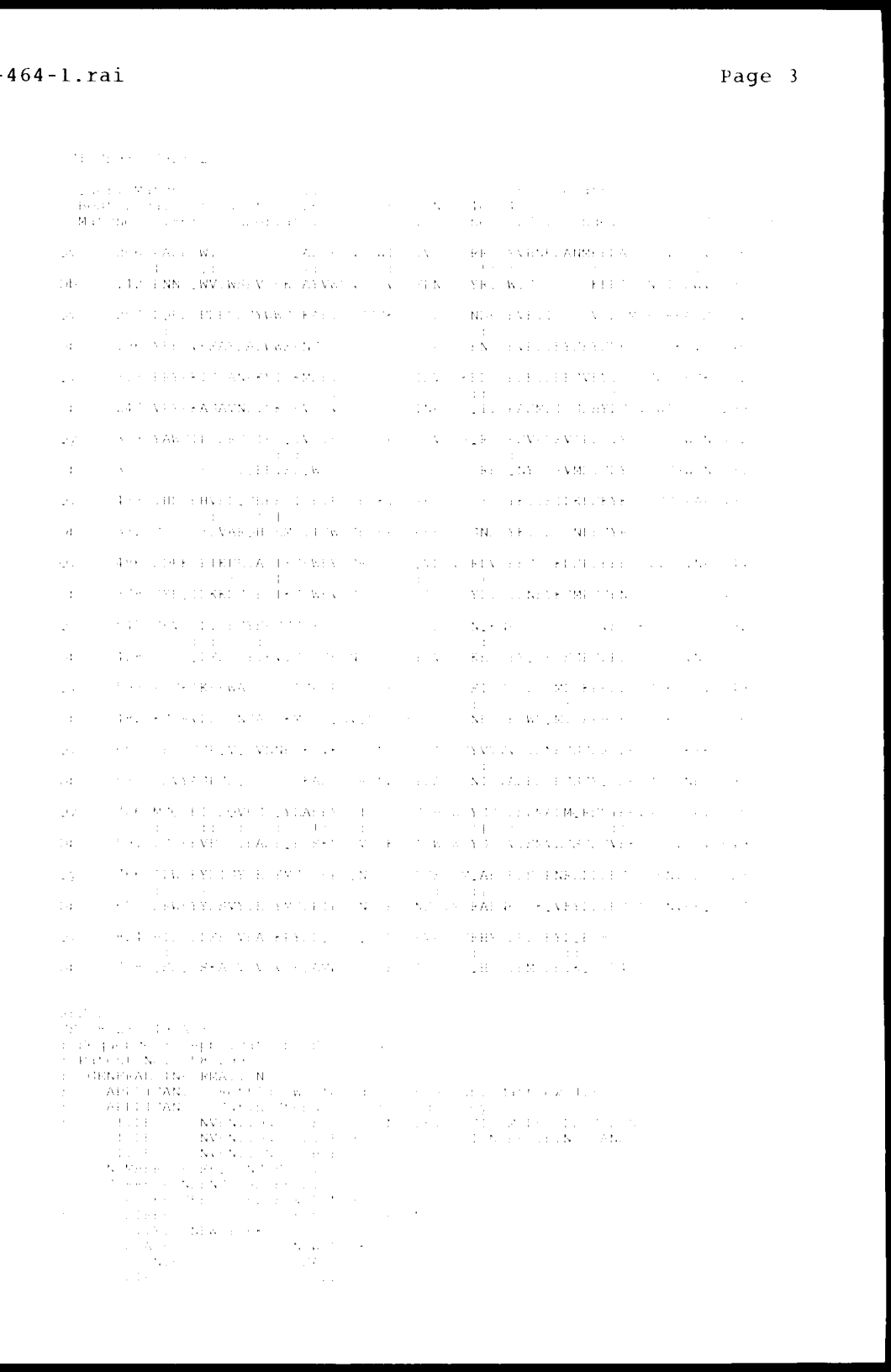


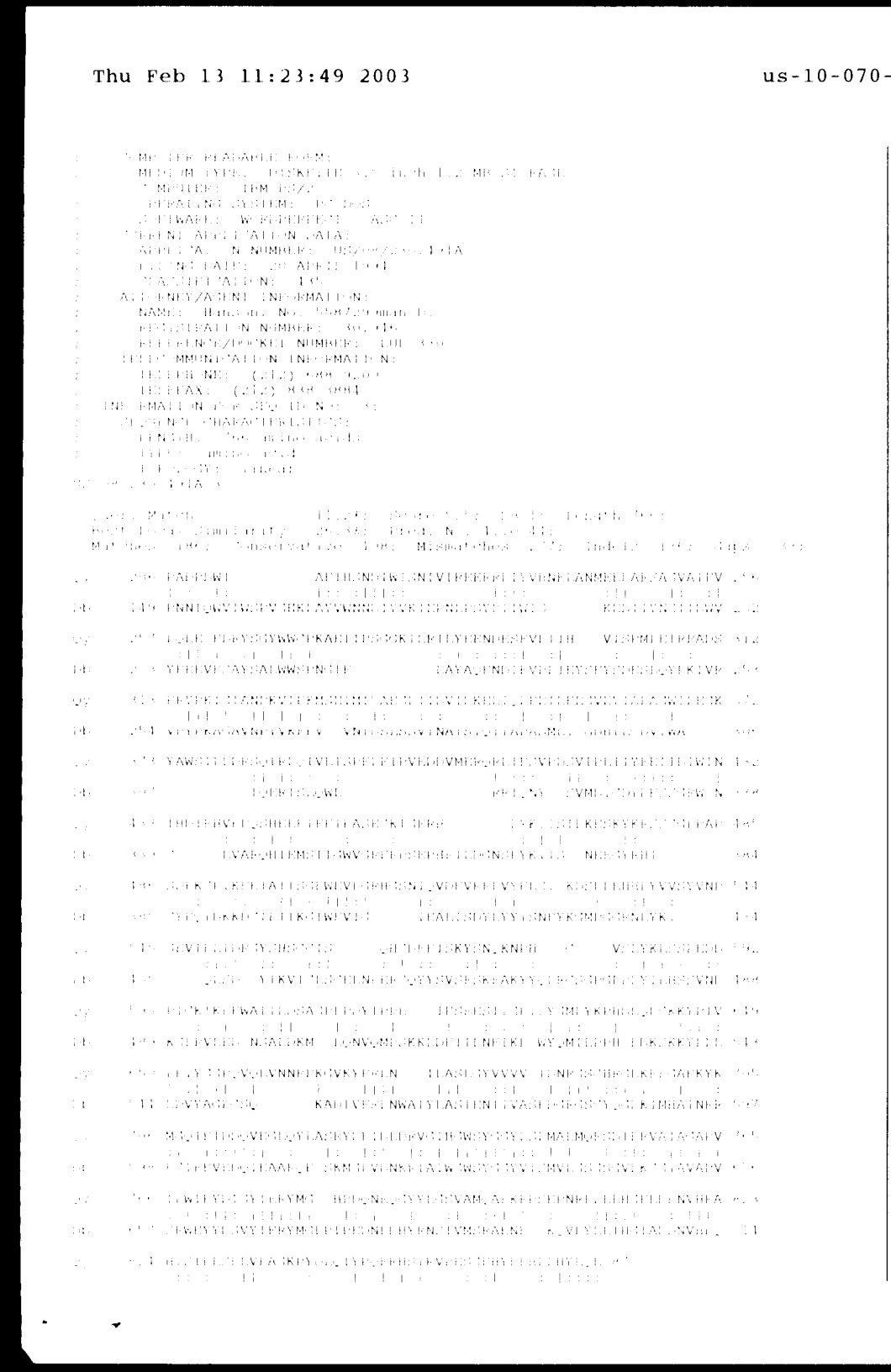


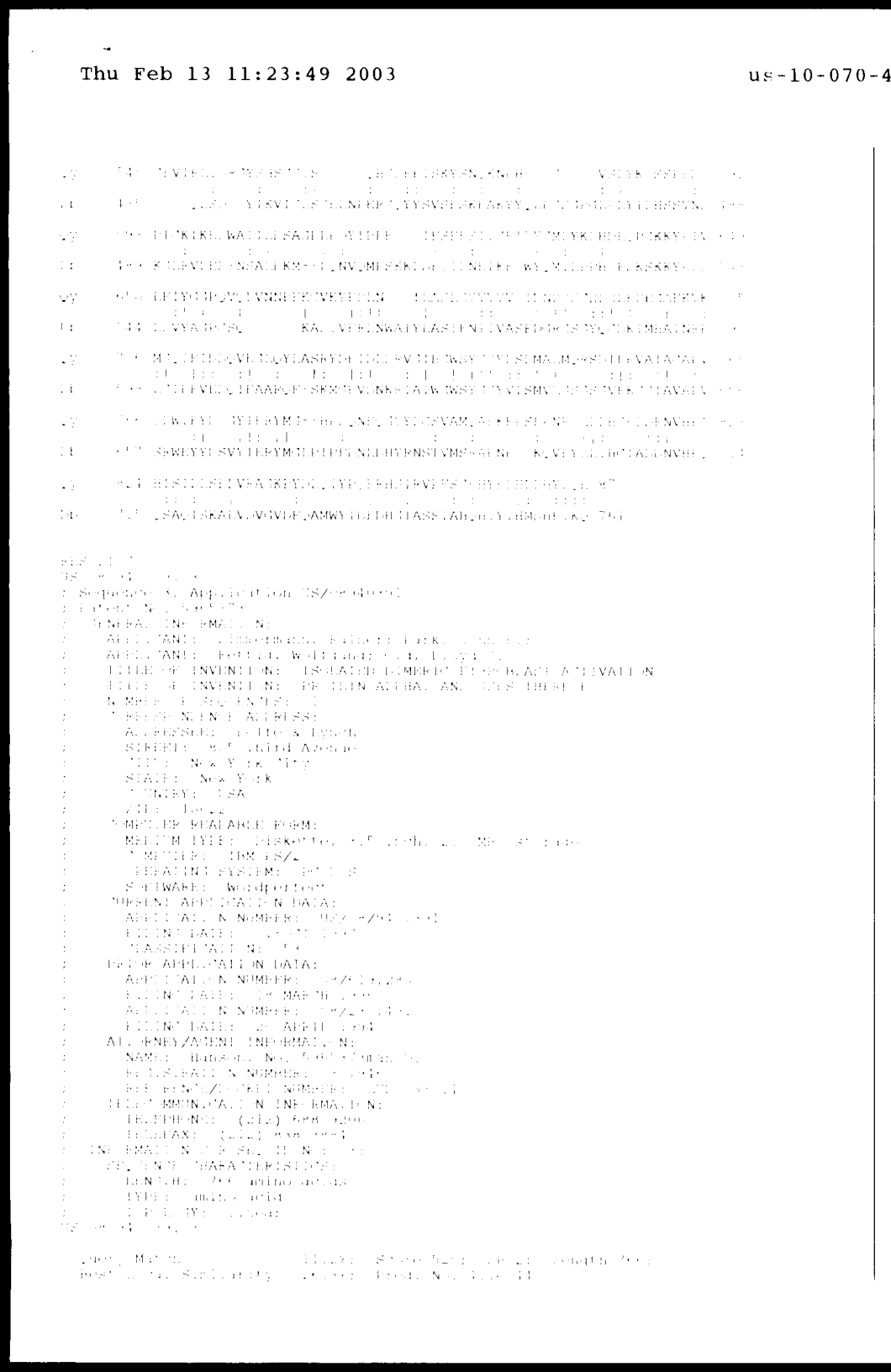


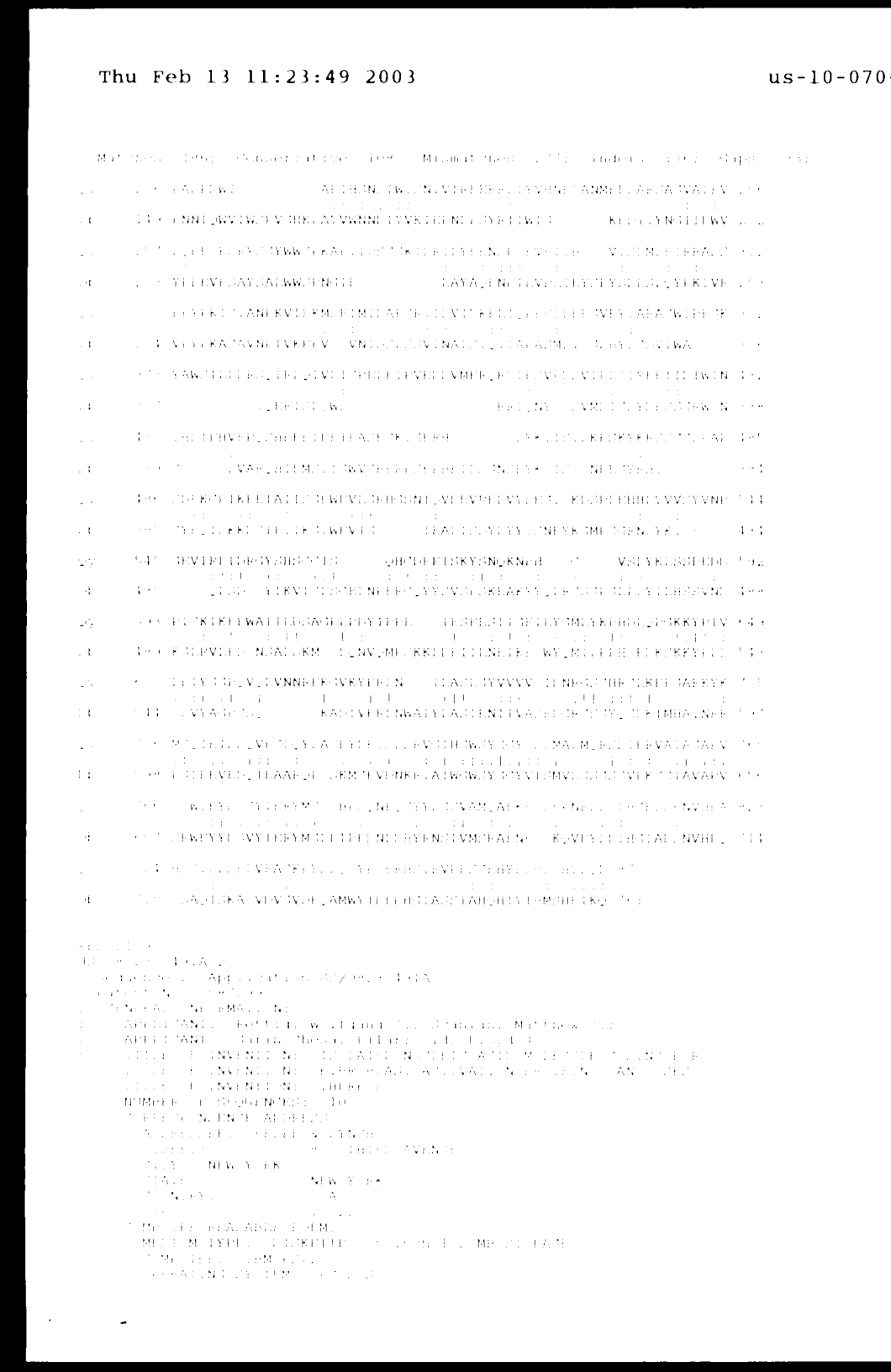


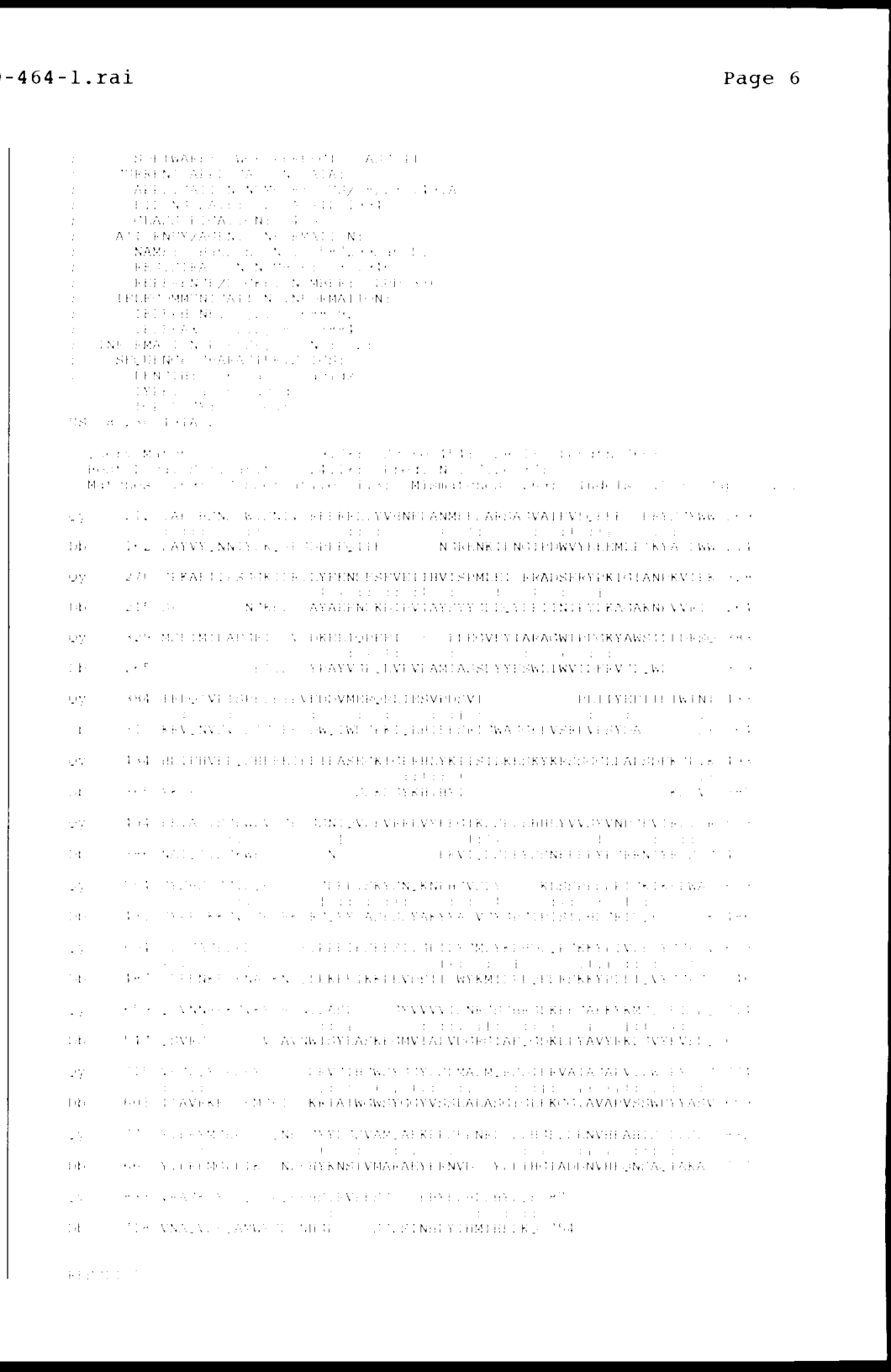


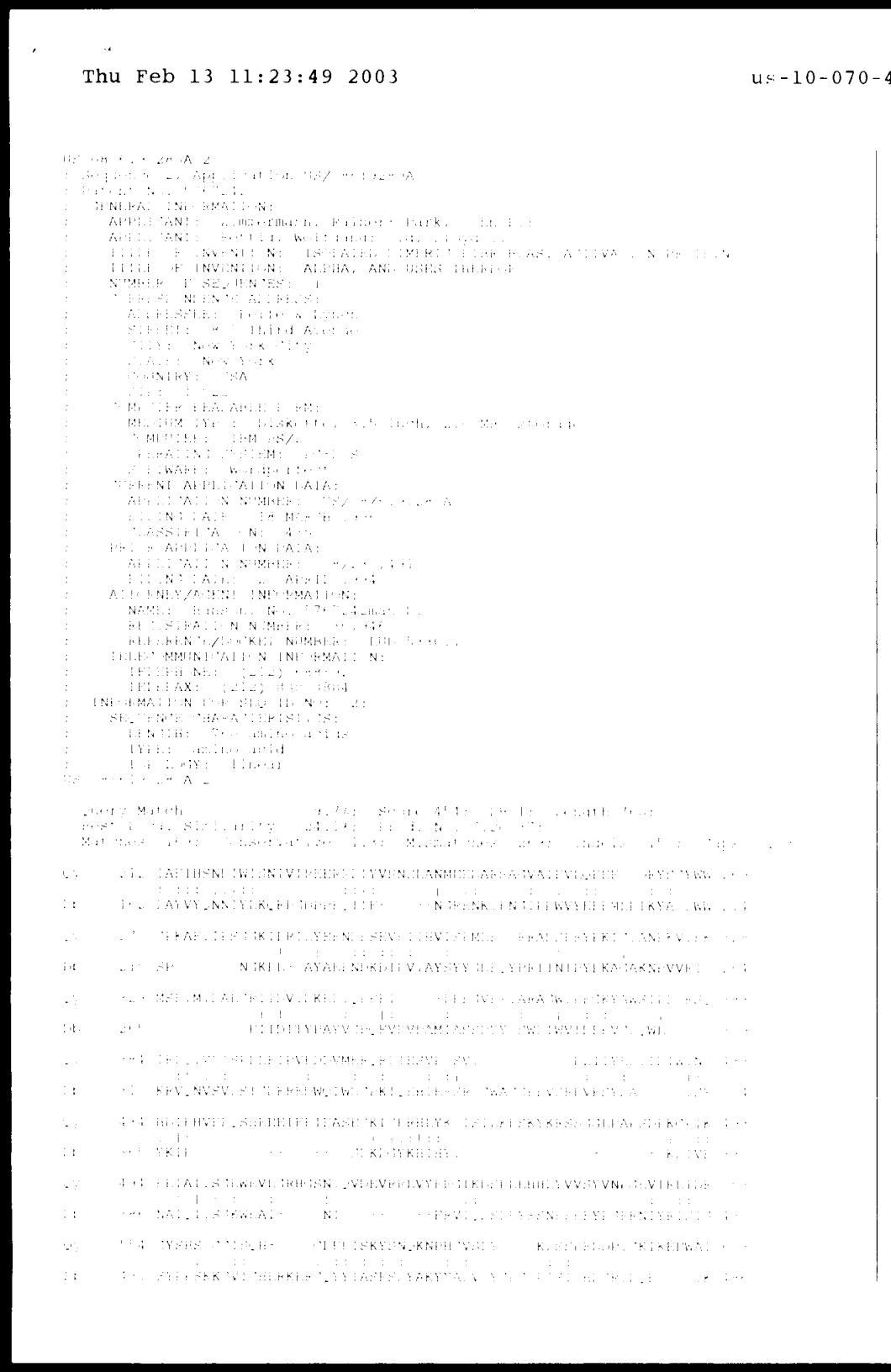


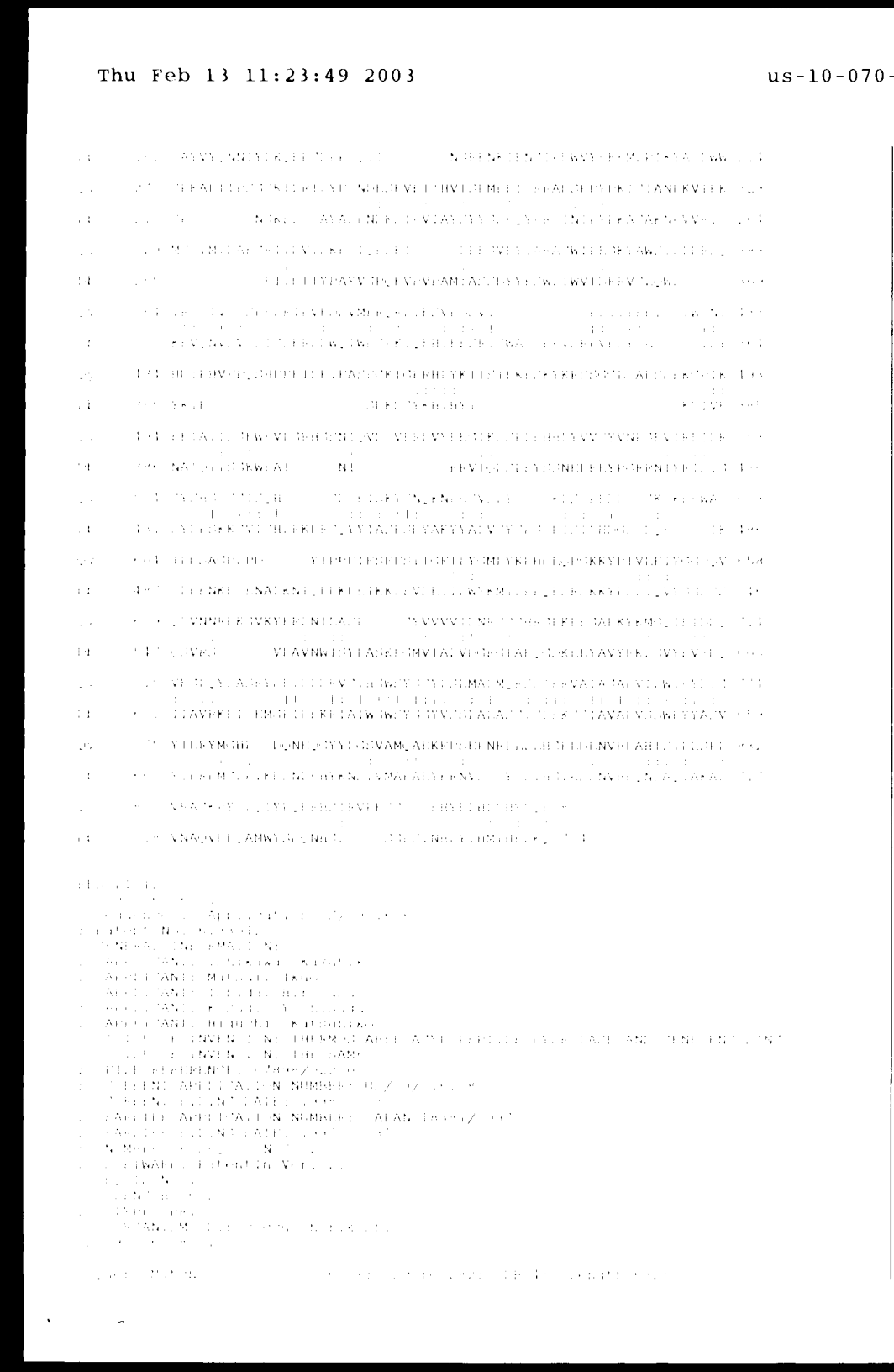


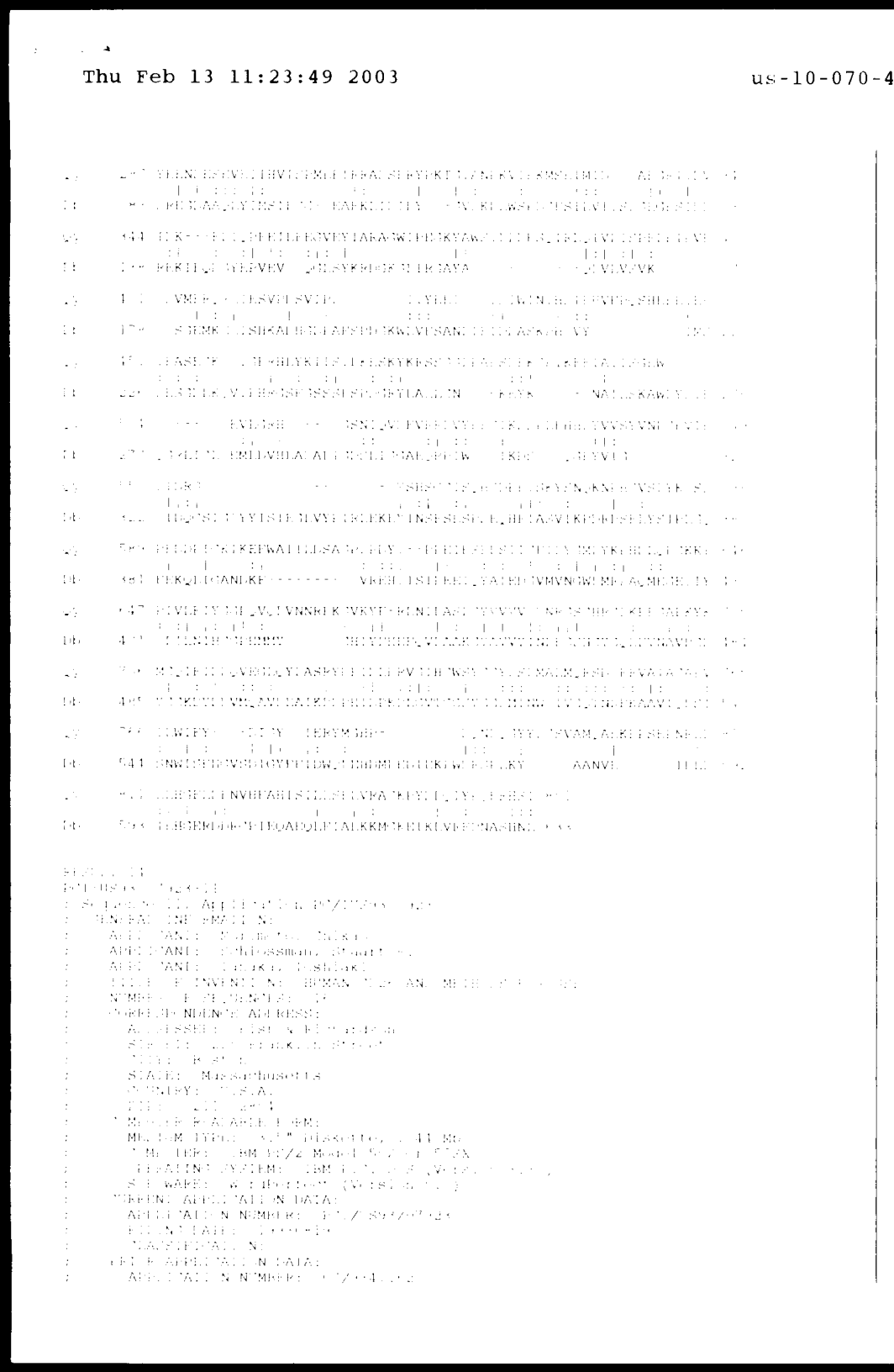


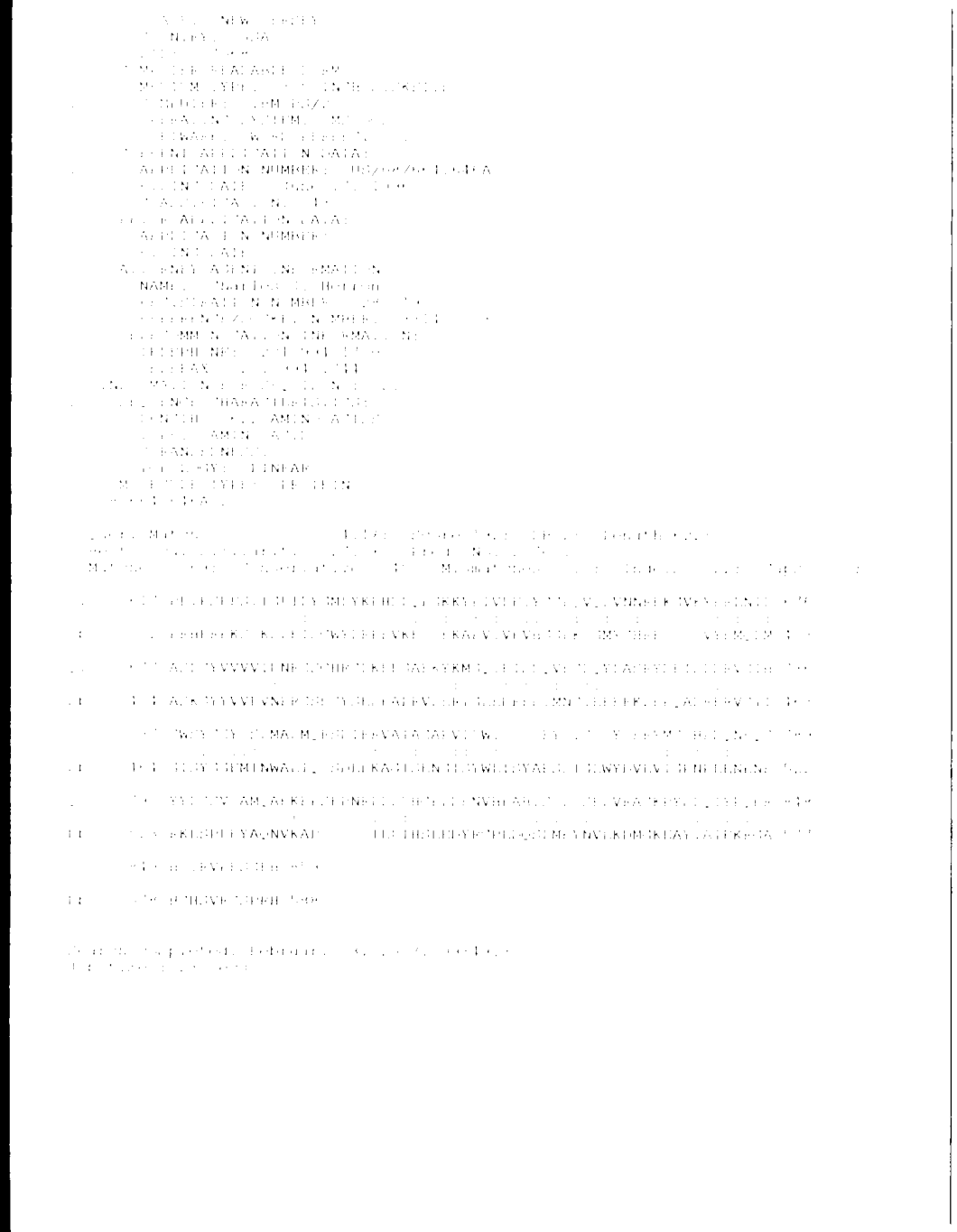












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GM protein - protein search, using sw model

Run on: February 3, 2003, 13:47:33 ; Search time 14 Seconds
(without alignments)
12.143 Million cell updates/sec

Title: US-10-070-464-1
Perfect score: 1750
Sequence: 1 MAAAMEIHQGSVEIFEIADG..... .....PLGSVQIINLGSKLAALKV 344

Scoring table: pG_SUM62
Xgap 10.0 , Ygap 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubaa/US_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score listed. The higher the Pred. No. the more likely the match is due to chance. Pred. No. is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	4750	100.0	892	10	US-10-070-464-1
2	4754	71.6	658	10	US-10-070-464-1a
3	4604	74.6	661	10	US-10-070-464-1b
4	4574	74.6	830	10	US-10-070-464-1
5	4258	68.4	613	10	US-10-070-464-1
6	2878	61.1	863	10	US-10-070-464-1
7	2878	61.1	892	10	US-10-070-464-1
8	2878	61.1	892	10	US-10-070-464-1
9	2863.5	60.9	879	10	US-10-070-464-1
10	2863.5	60.9	879	10	US-10-070-464-1
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ALIGNMENTS

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US-10-070-464-1
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; Publication No. US20030027781A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, Shiow
; APPLICANT: Akiskal, Hagop
; APPLICANT: Rice, Kenner
; APPLICANT: Gershon, Elliot
; TITLE OF INVENTION: NOVEL
; FILE REFERENCE: 7
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE:
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS:
; SOFTWARE:
; SEQ ID NO
; LENGTH:
; TYPE:
; ORGANISM:
US-10-070-464-1

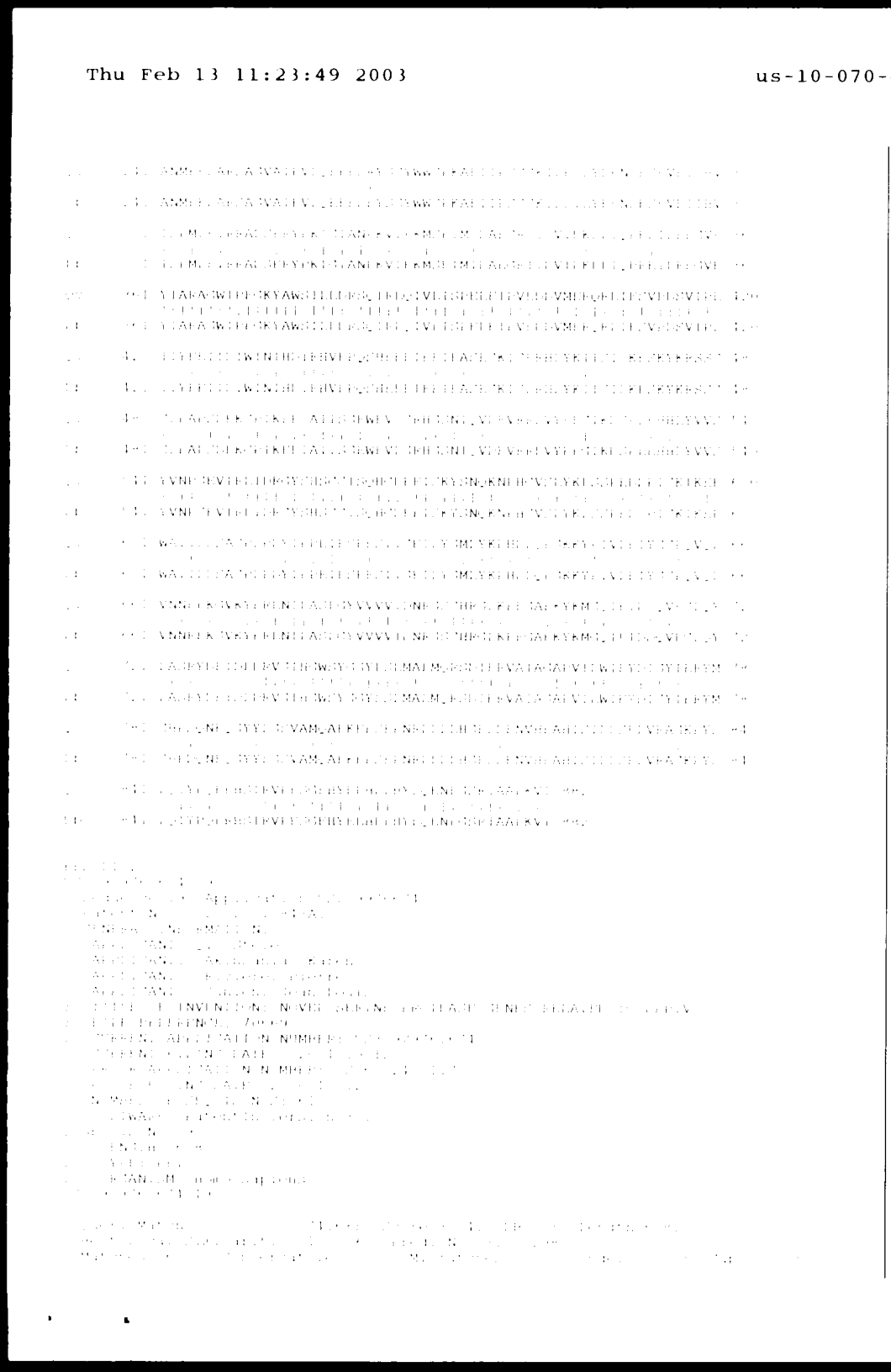
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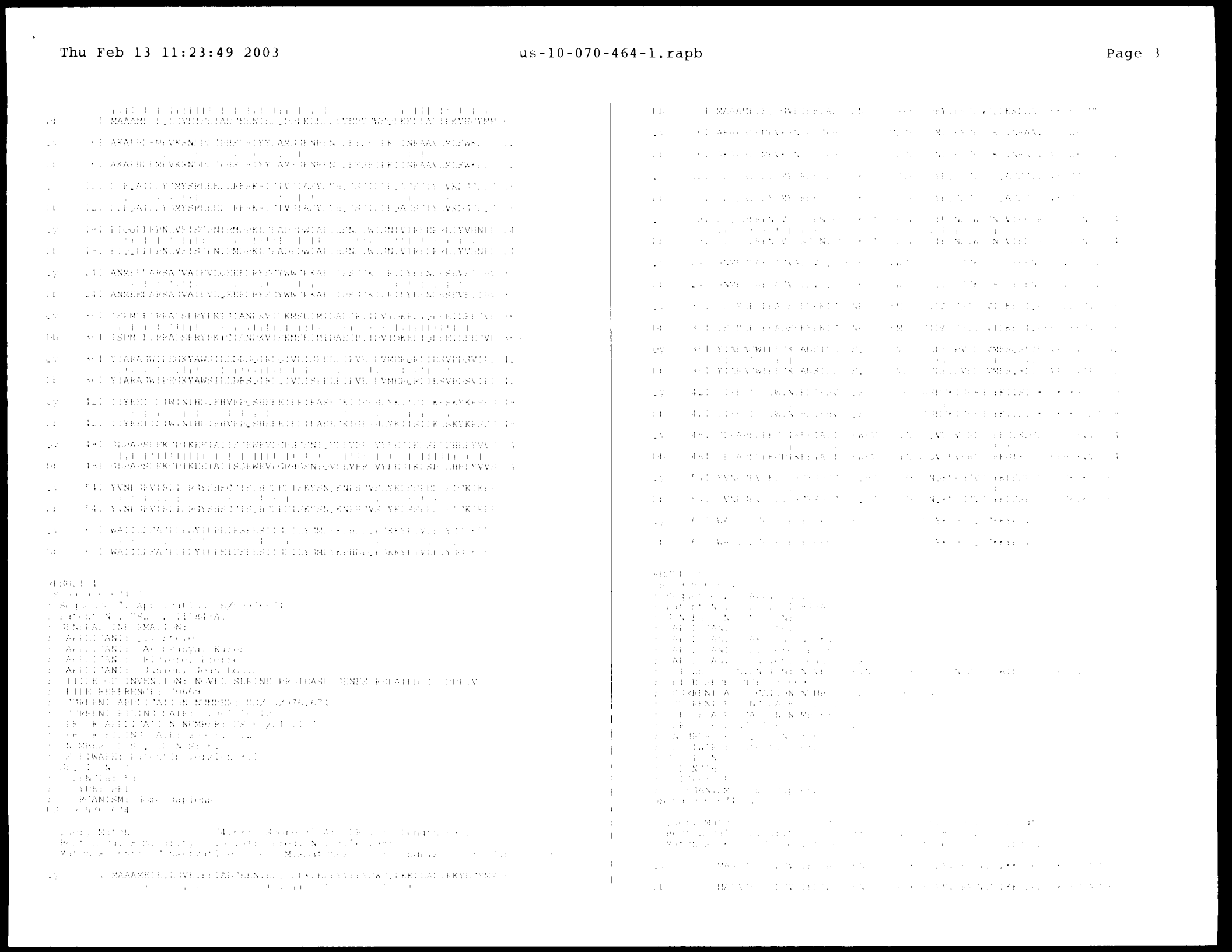
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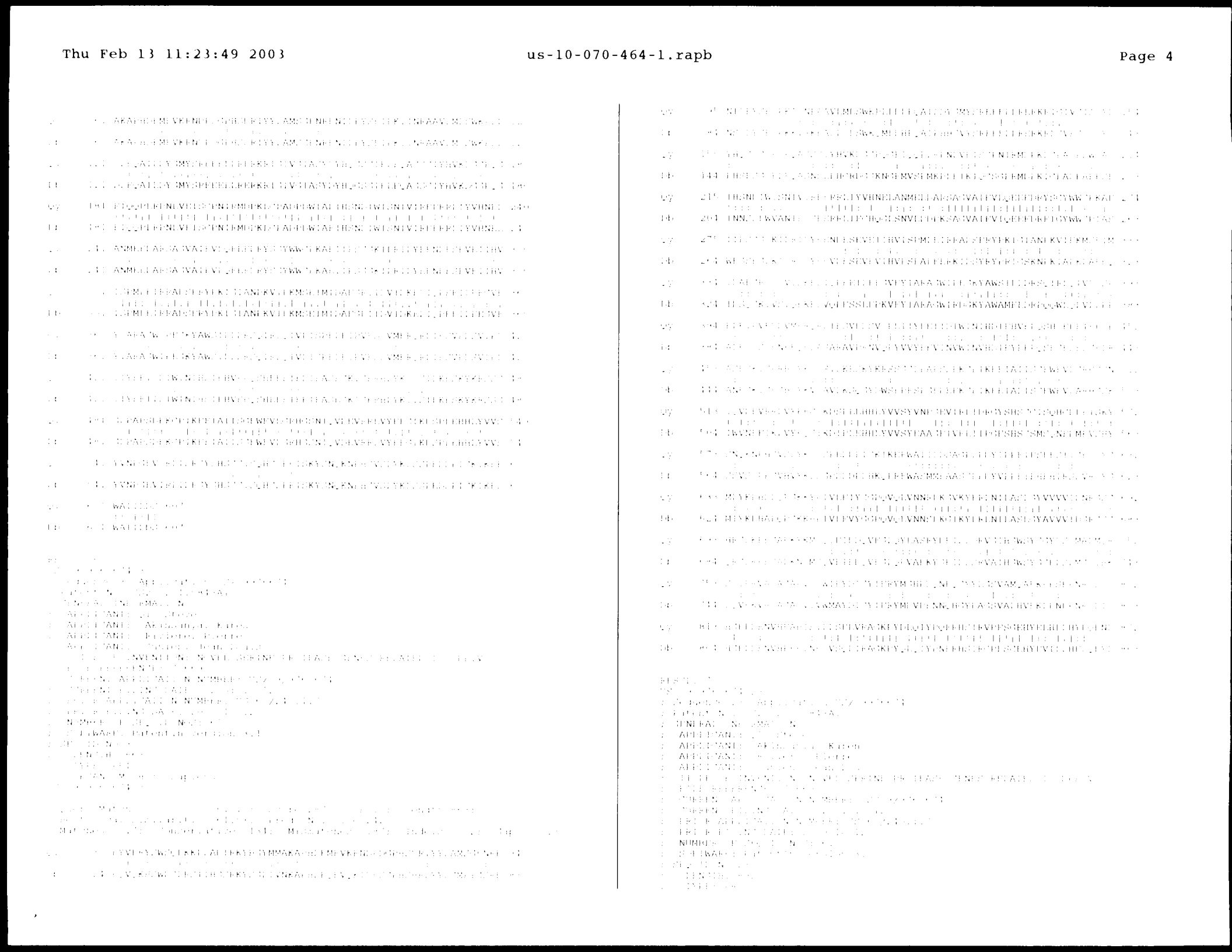
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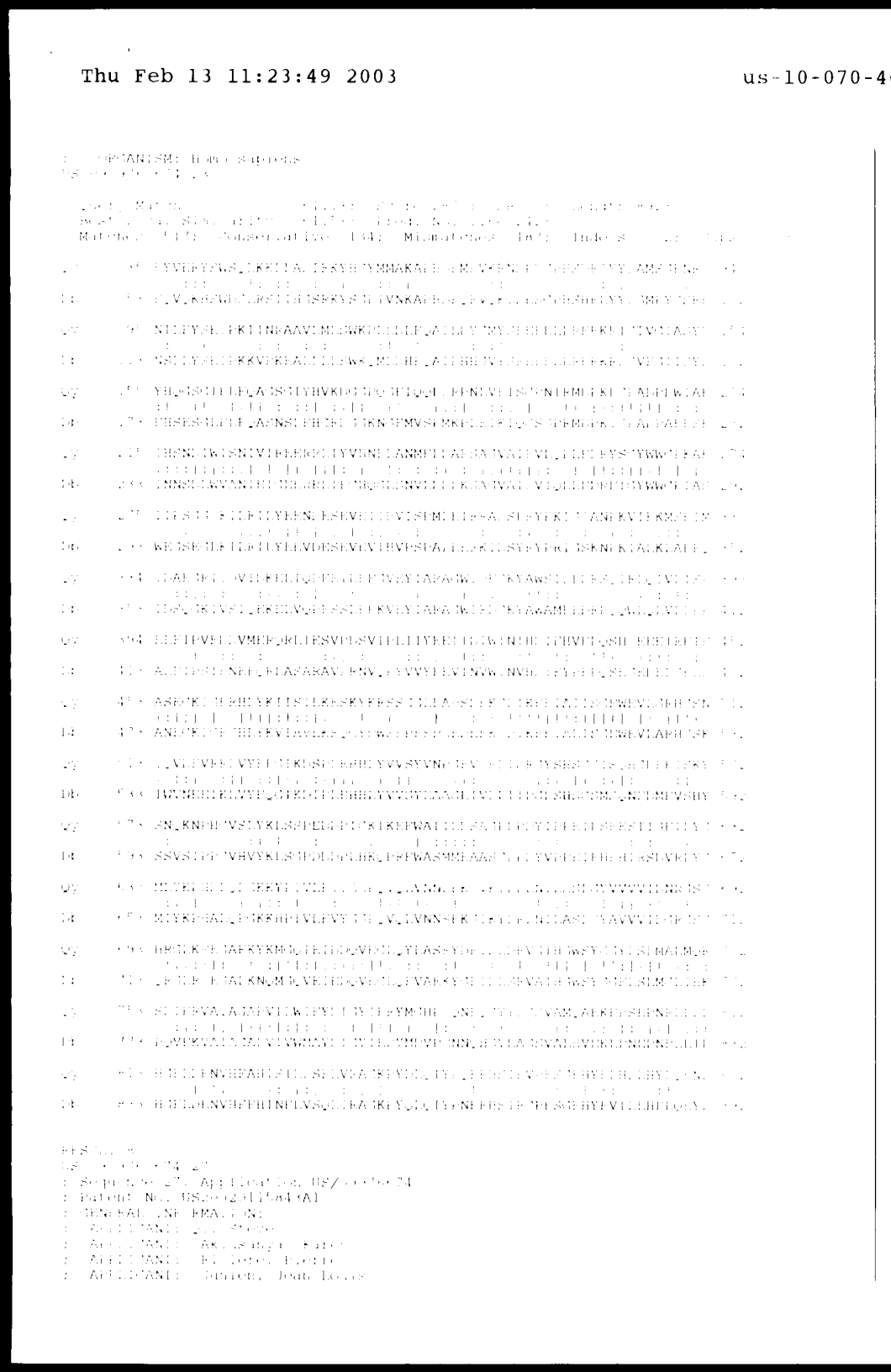
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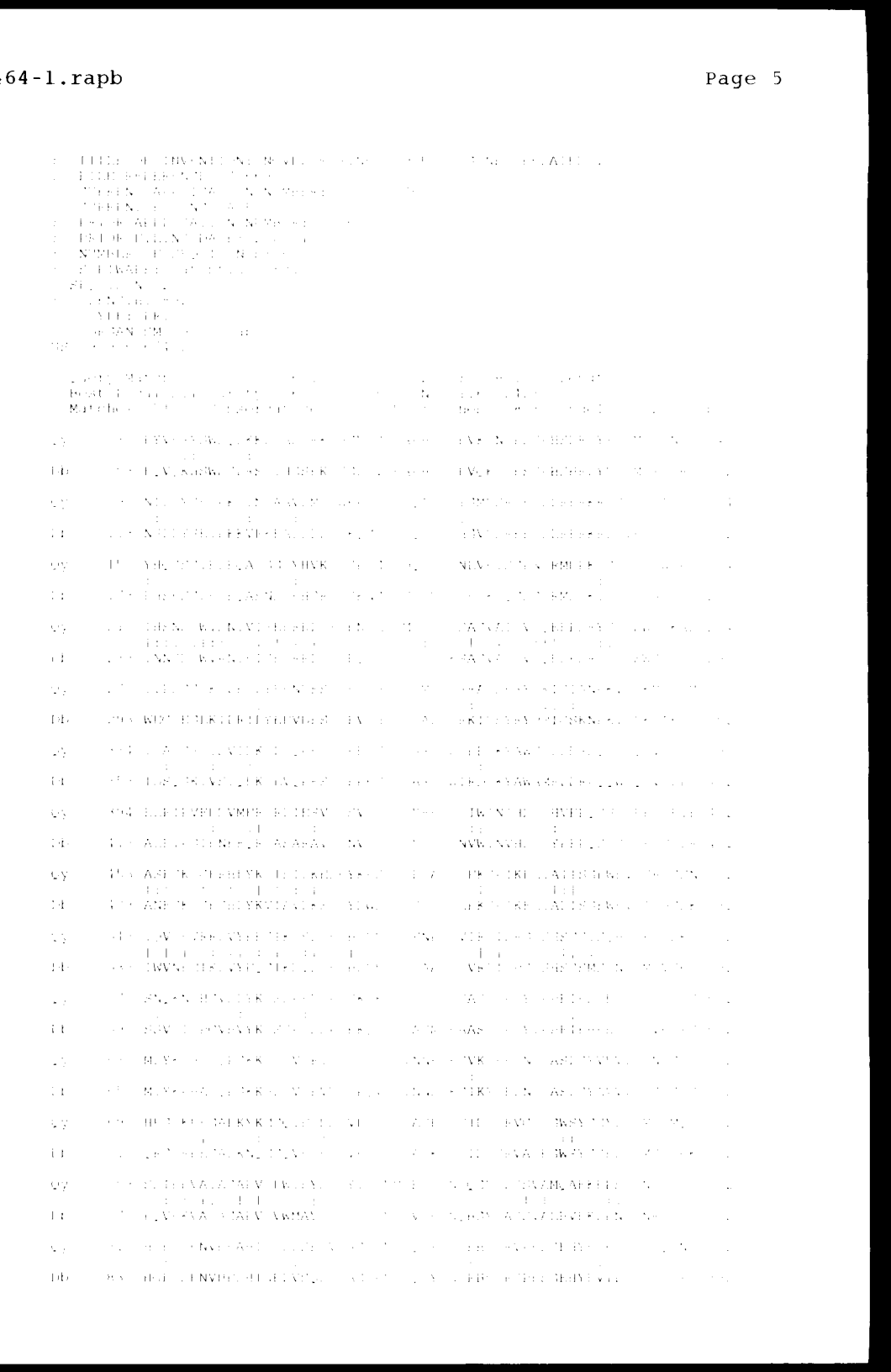
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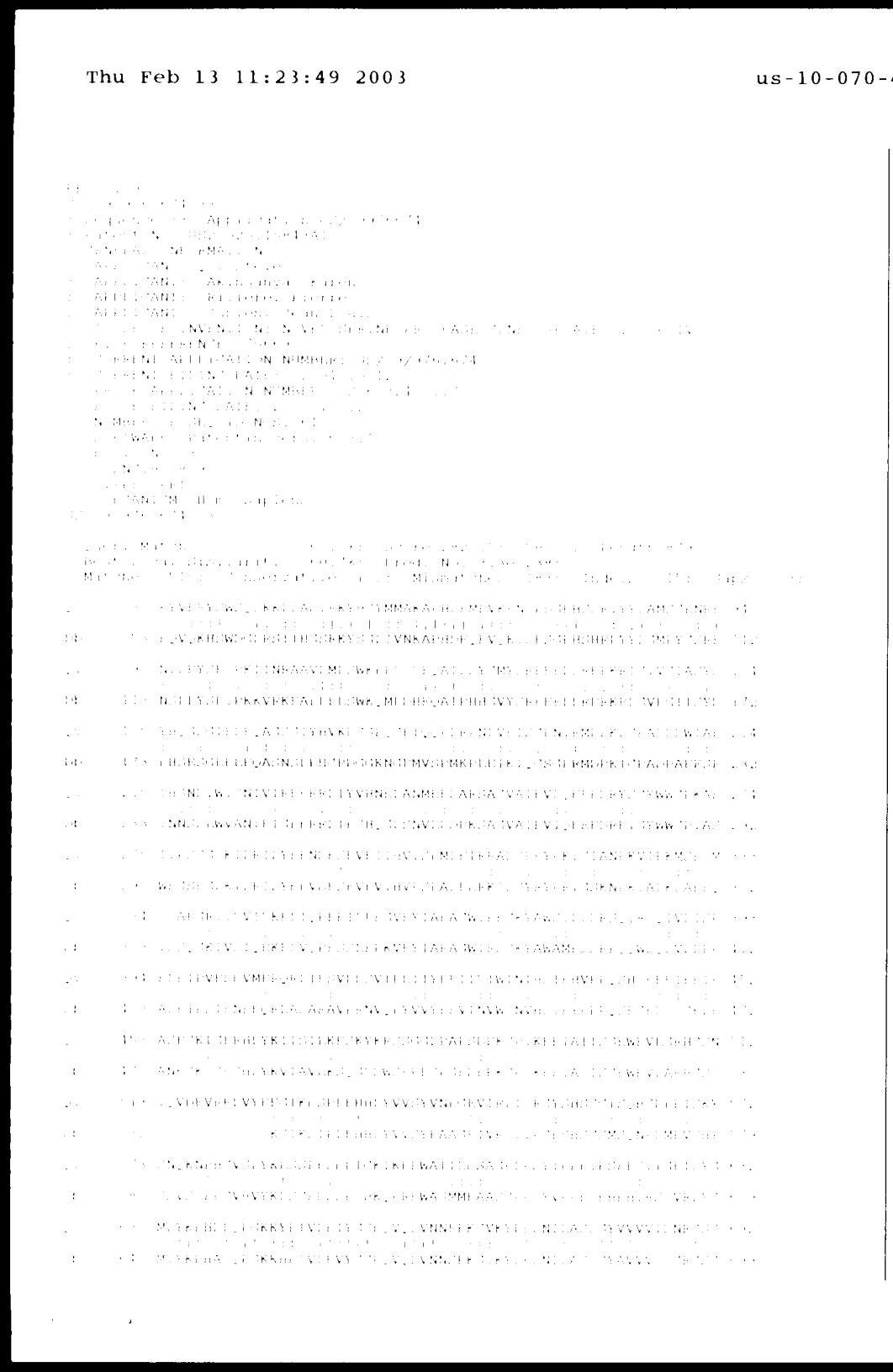


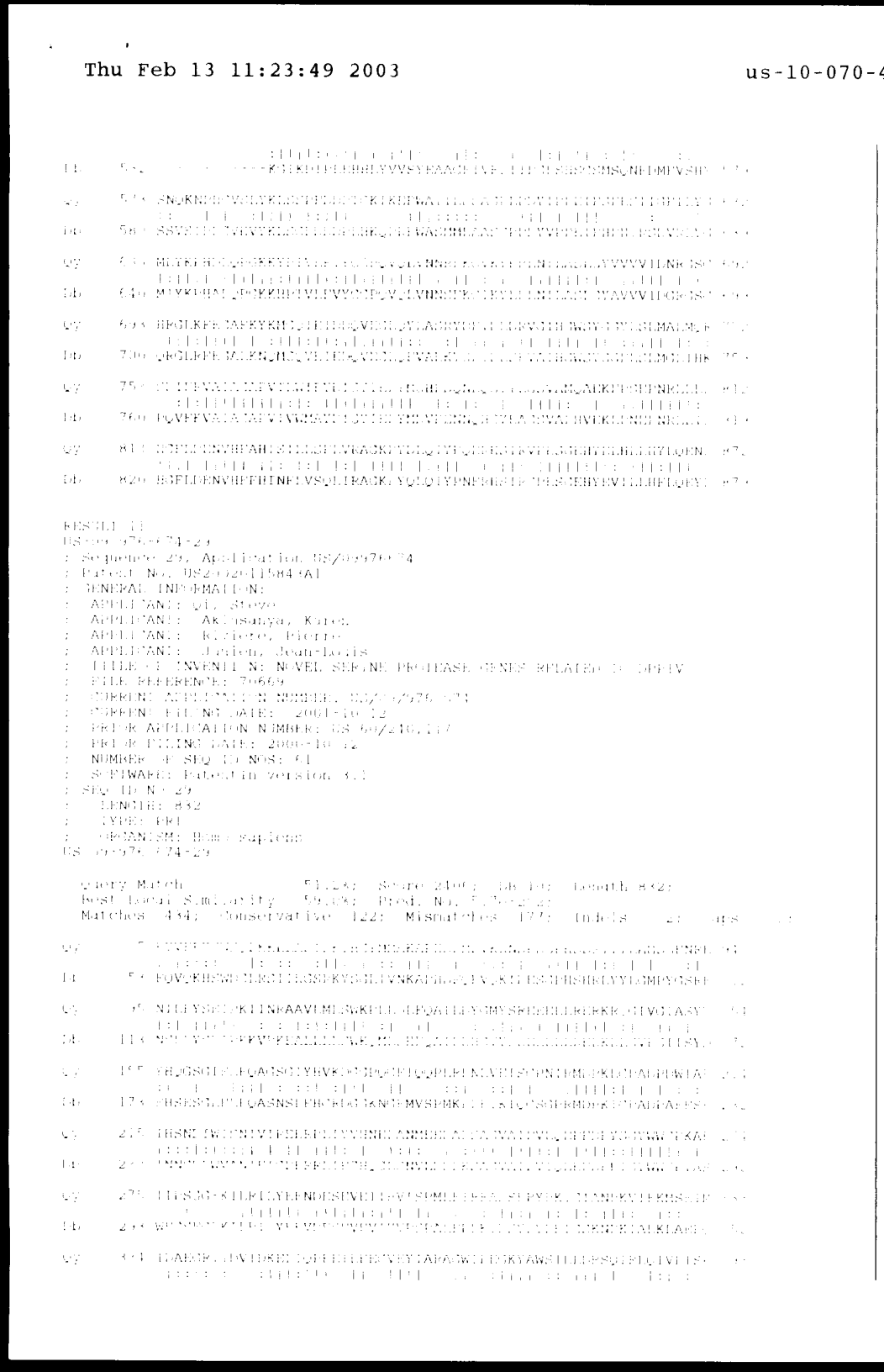






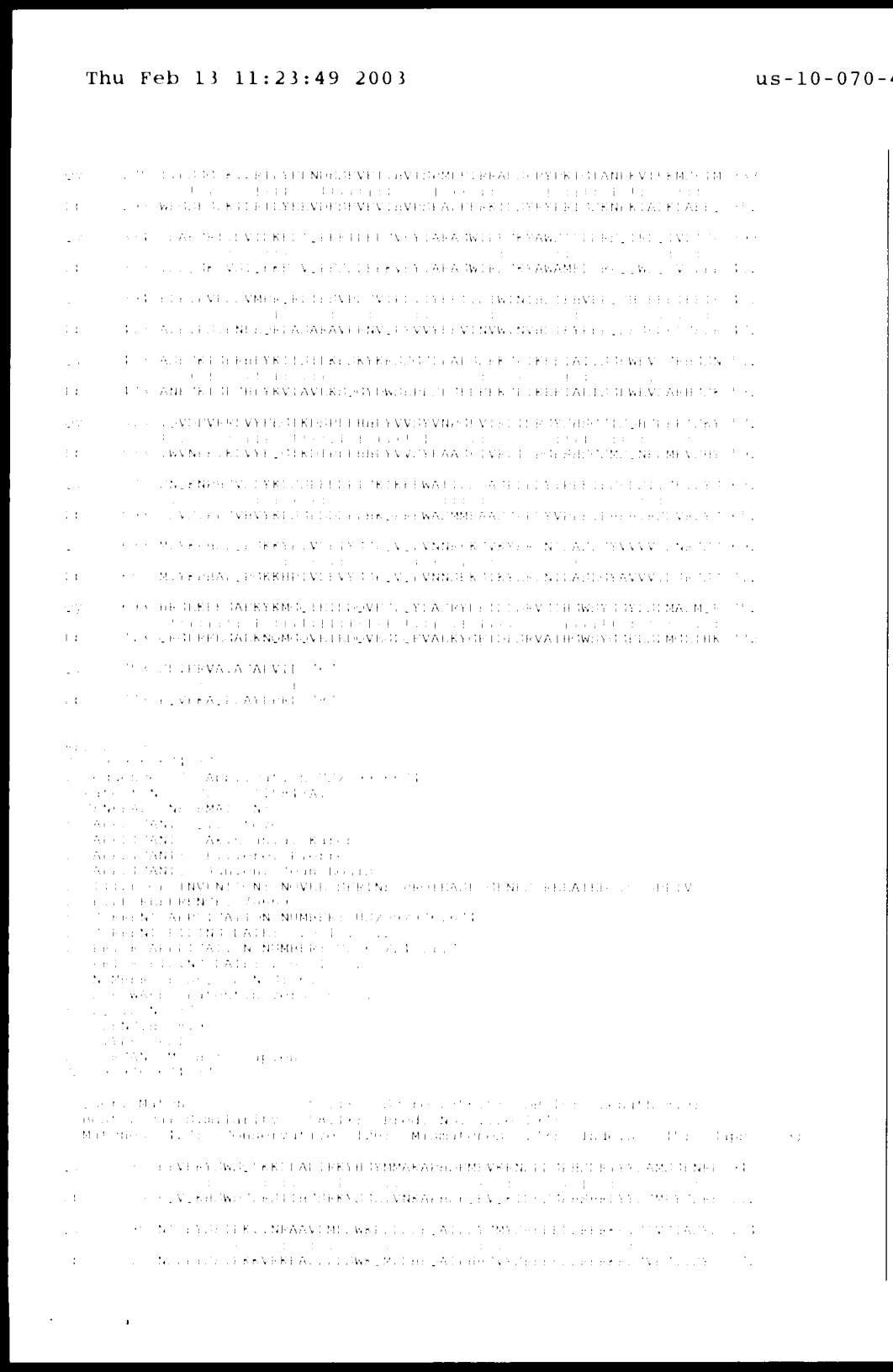


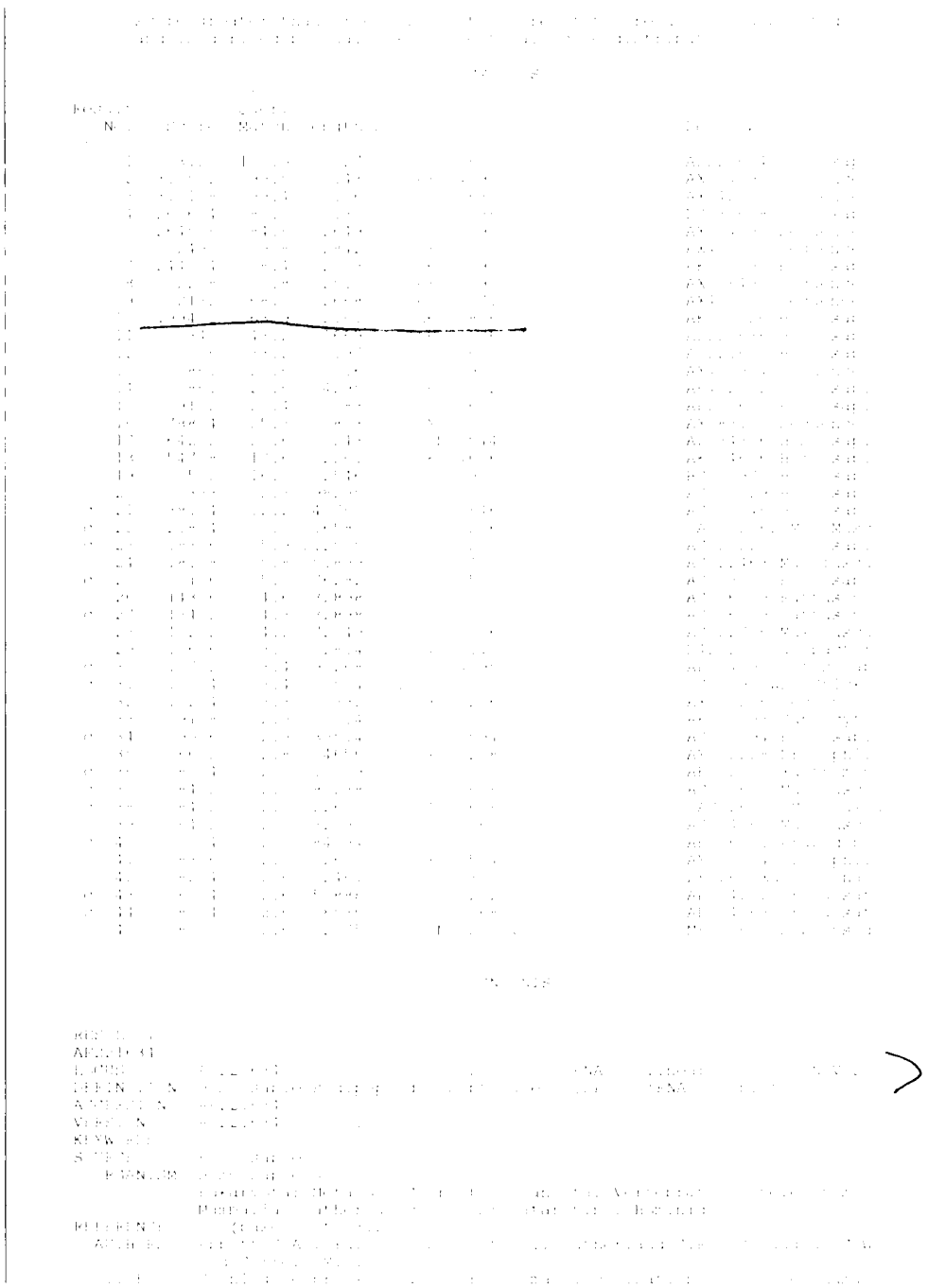


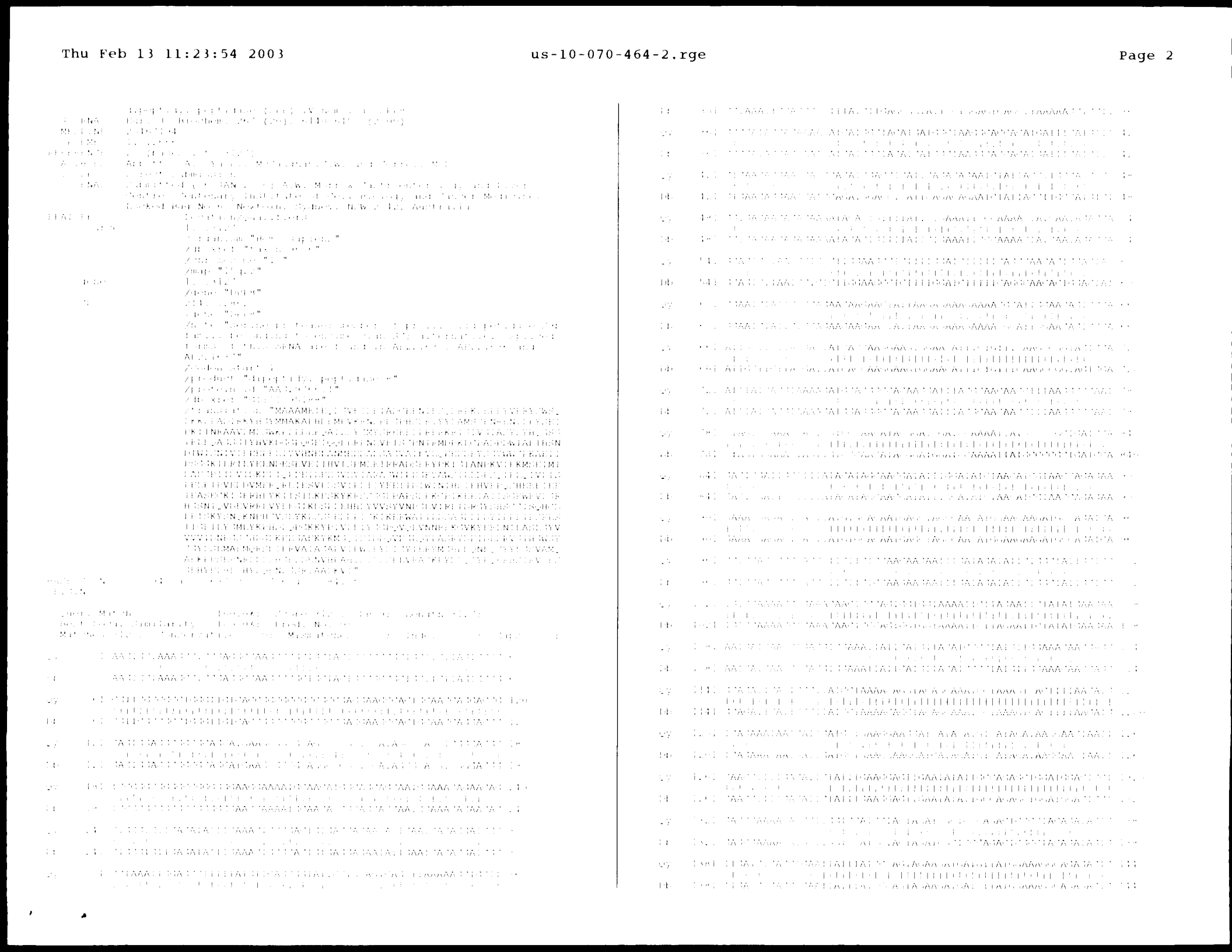


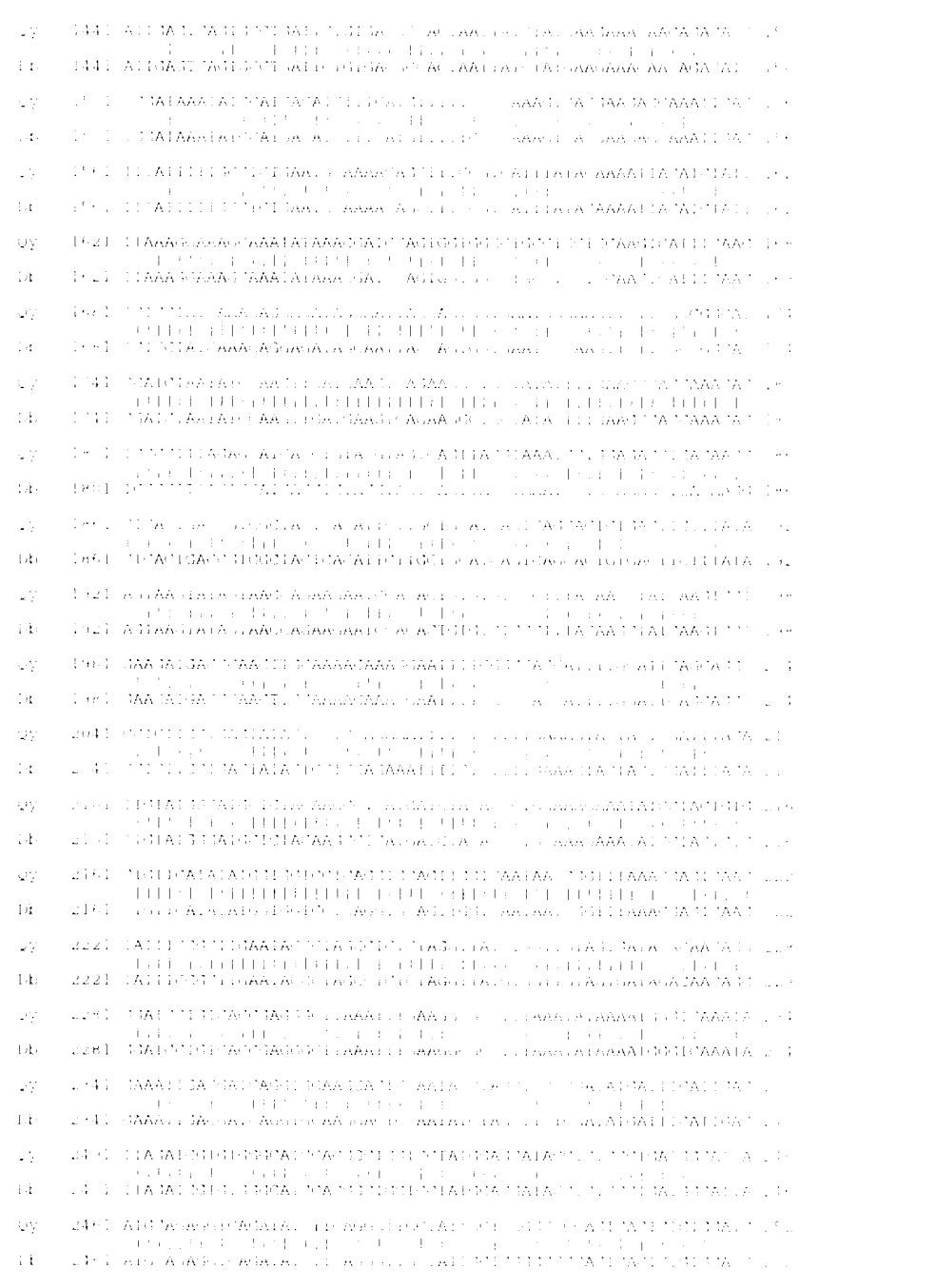
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; Patent No. US20020115844A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Steve
; APPLICANT: Akiyama, Kaoru
; APPLICANT: Richter, Pierre
; APPLICANT: Jarlen, Jean-Louis
; TITLE OF INVENTION: NOVEL SERINE PROTEASE GENES RELATED TO CANCER
; FILE REFERENCE: 7069
; CURRENT APPLICATION NUMBER: US/09/970,774
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,117
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
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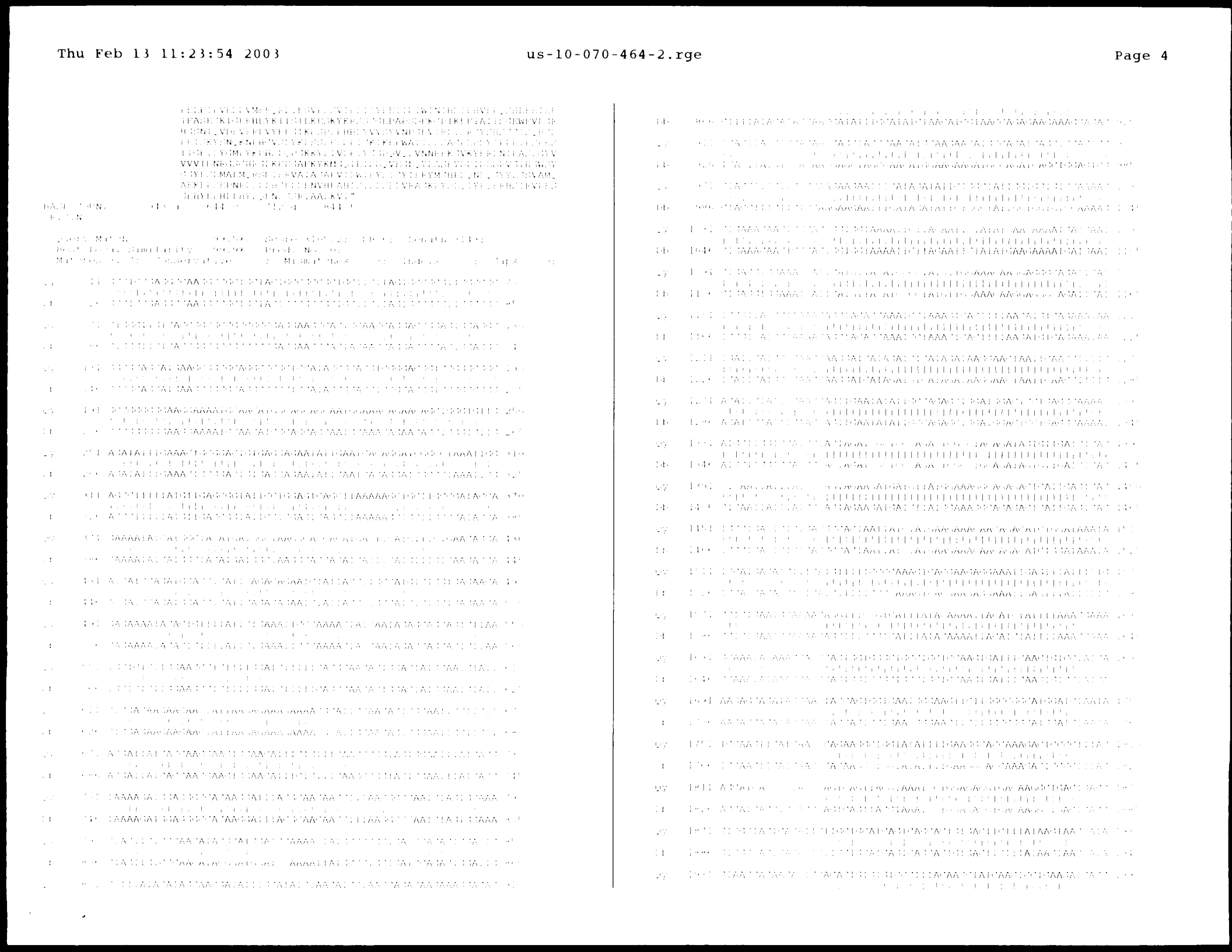
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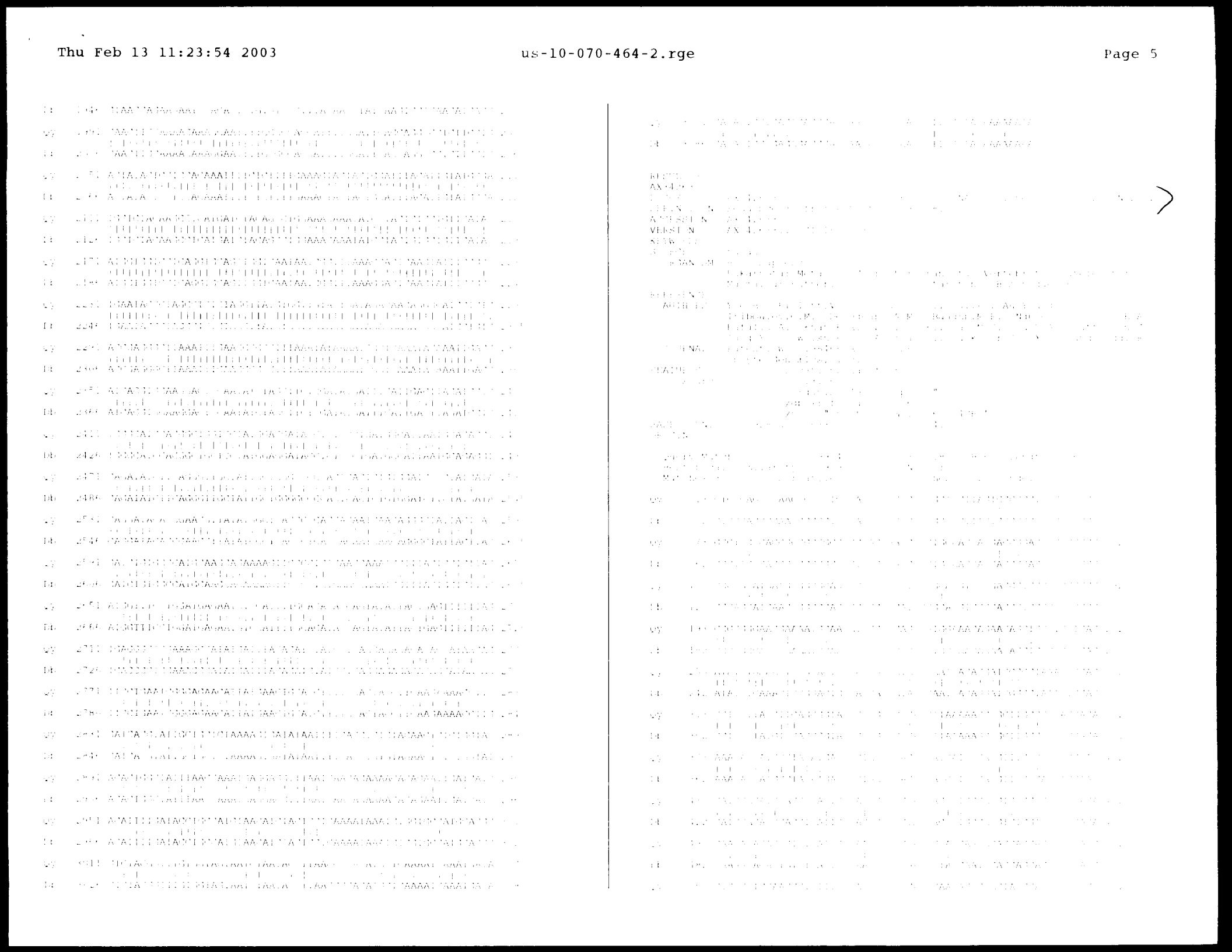


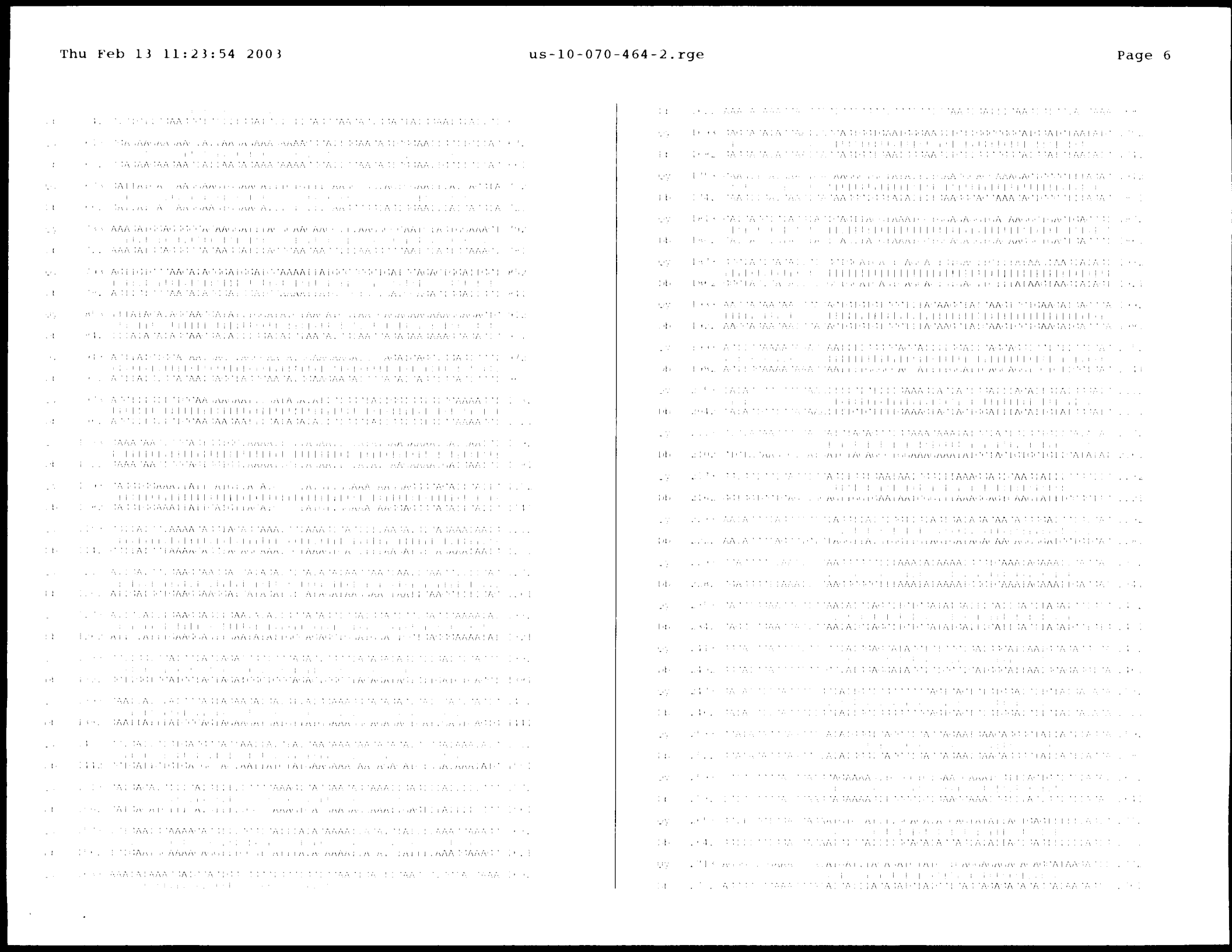


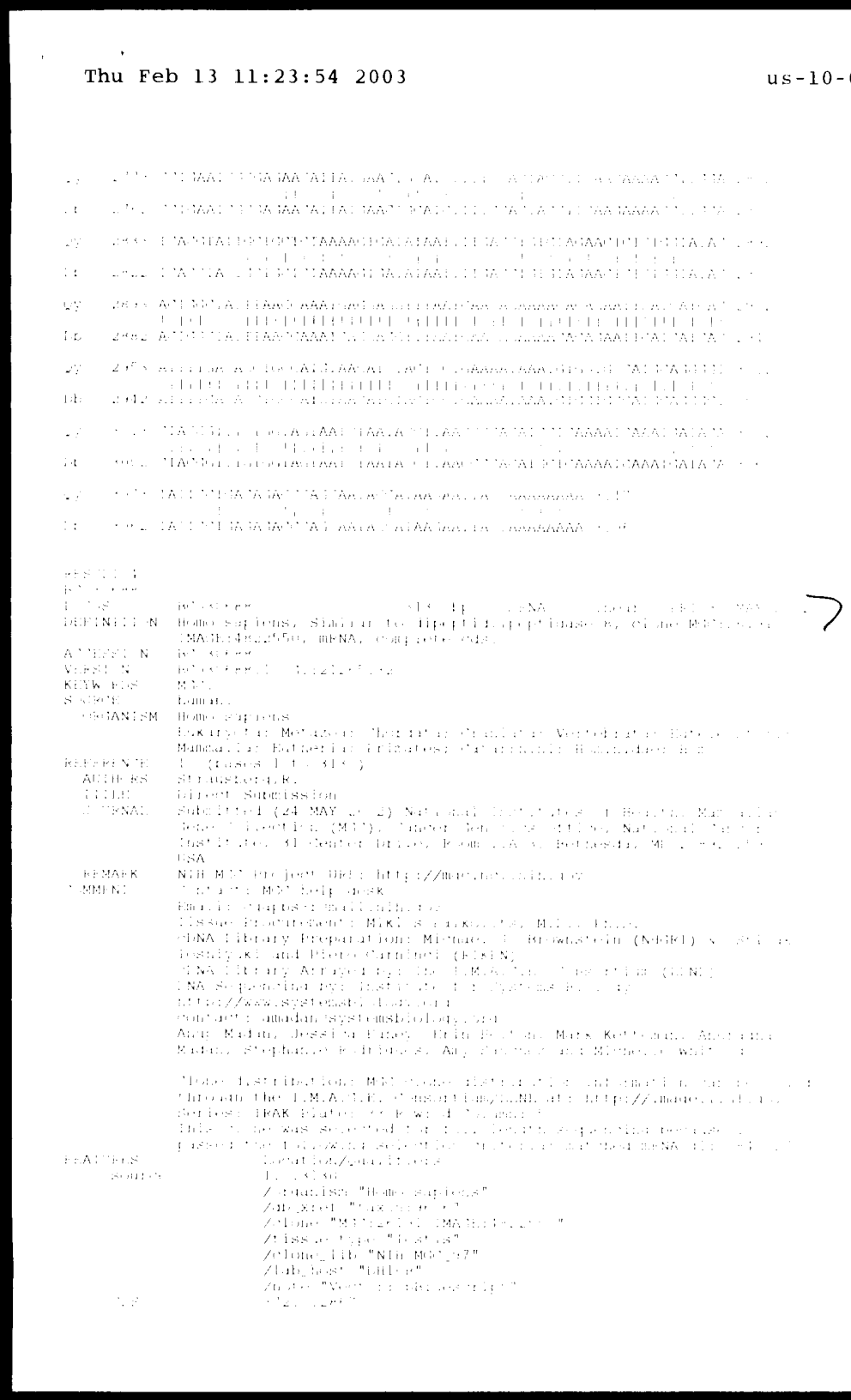






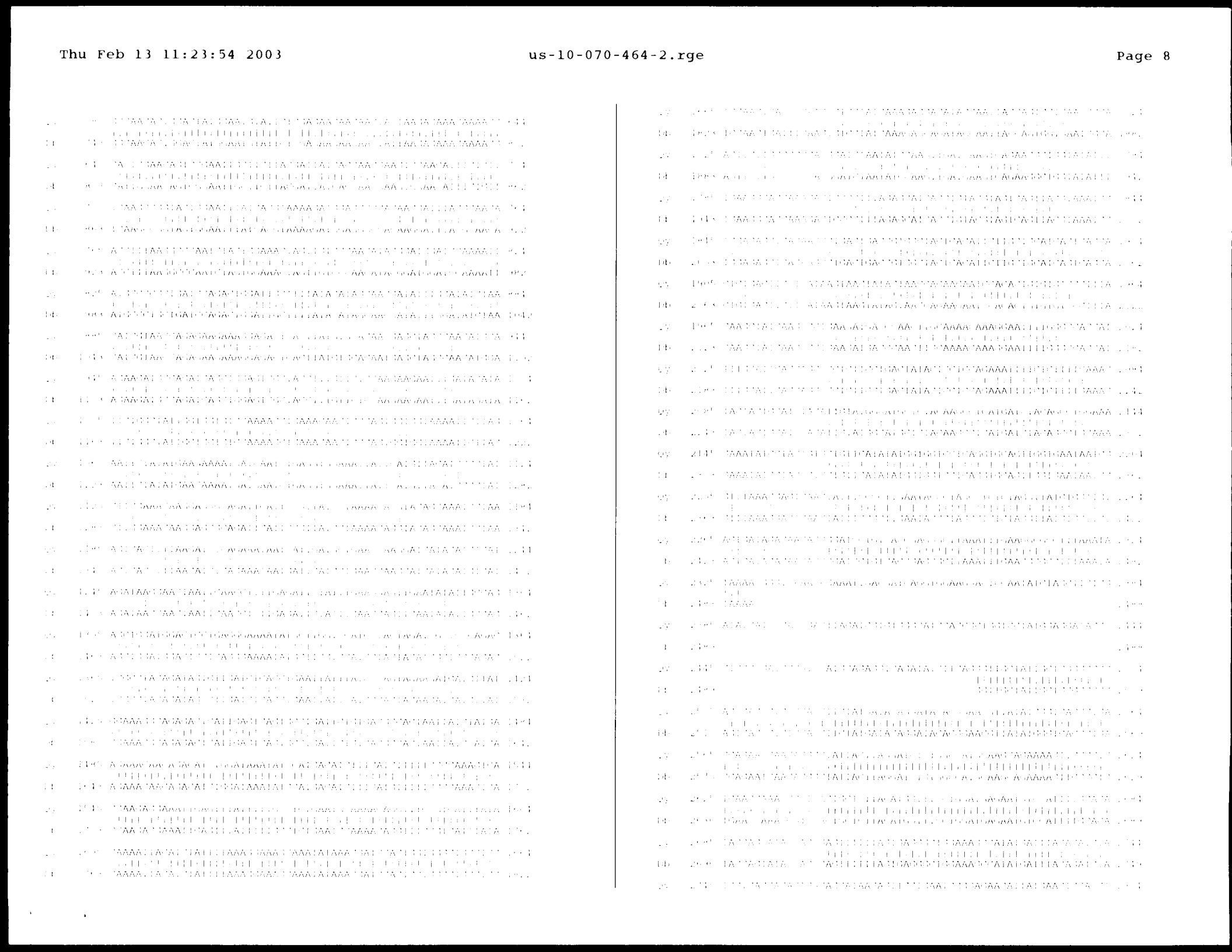


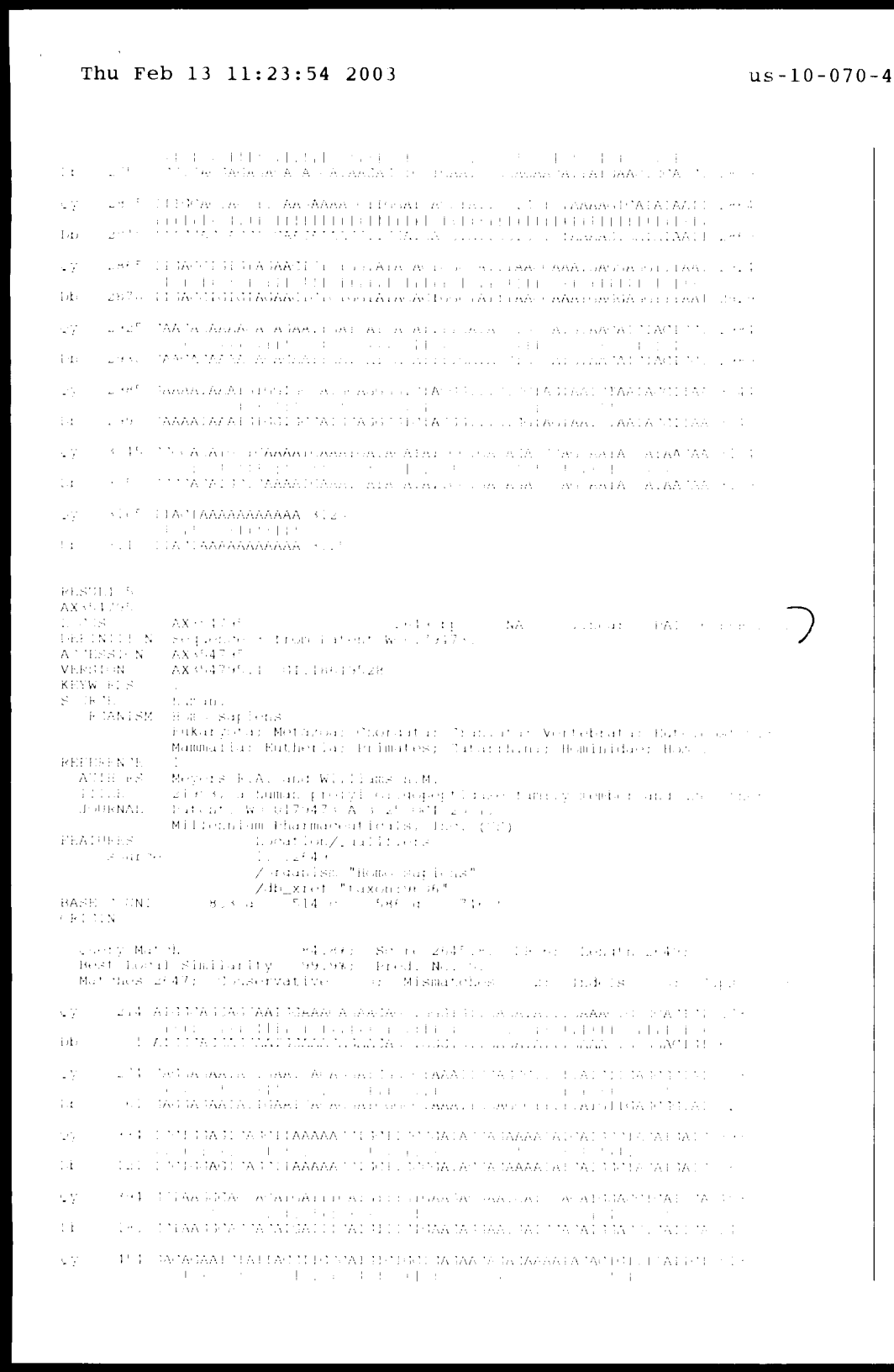




DEFINITION Homo sapiens, Staphylococcus epidermidis, complete genome.
ACCESSION
VERSION
KEYWORDS MCV.
SOURCE Human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE 1 (bases 1 to 45)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (24 MAY 2002) National Institutes of Health, Mail to
Rm. 1103, 31 Center Drive, Room 2A-4, Bethesda, MD 20892-2132
USA
REMARK NIH MCV Project URL: http://mcv.nih.gov
COMMENT Contact: MCV help desk
Email: mcvhelp@mail.nih.gov
Tissue Procurement: Mike Stanley, M.D., Ph.D.,
cDNA Library Preparation: Michael F. Bonaldo (NIGMS) and Jeffrey
Goldsworthy and Pierre Carninci (RIKEN)
cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
URL: http://www.hgsc.bcm.tmc.edu
Contact: amadan@systemsbiology.org
Acc: Madan, Jessica Rose; Erlich, Rachel Lee; Matsen, Kelly Anne; Ahearn,
Mary; Stephanos, Kristine; Ay, Ahmet; and Mitchell, Wolf
Clone distribution: MCV clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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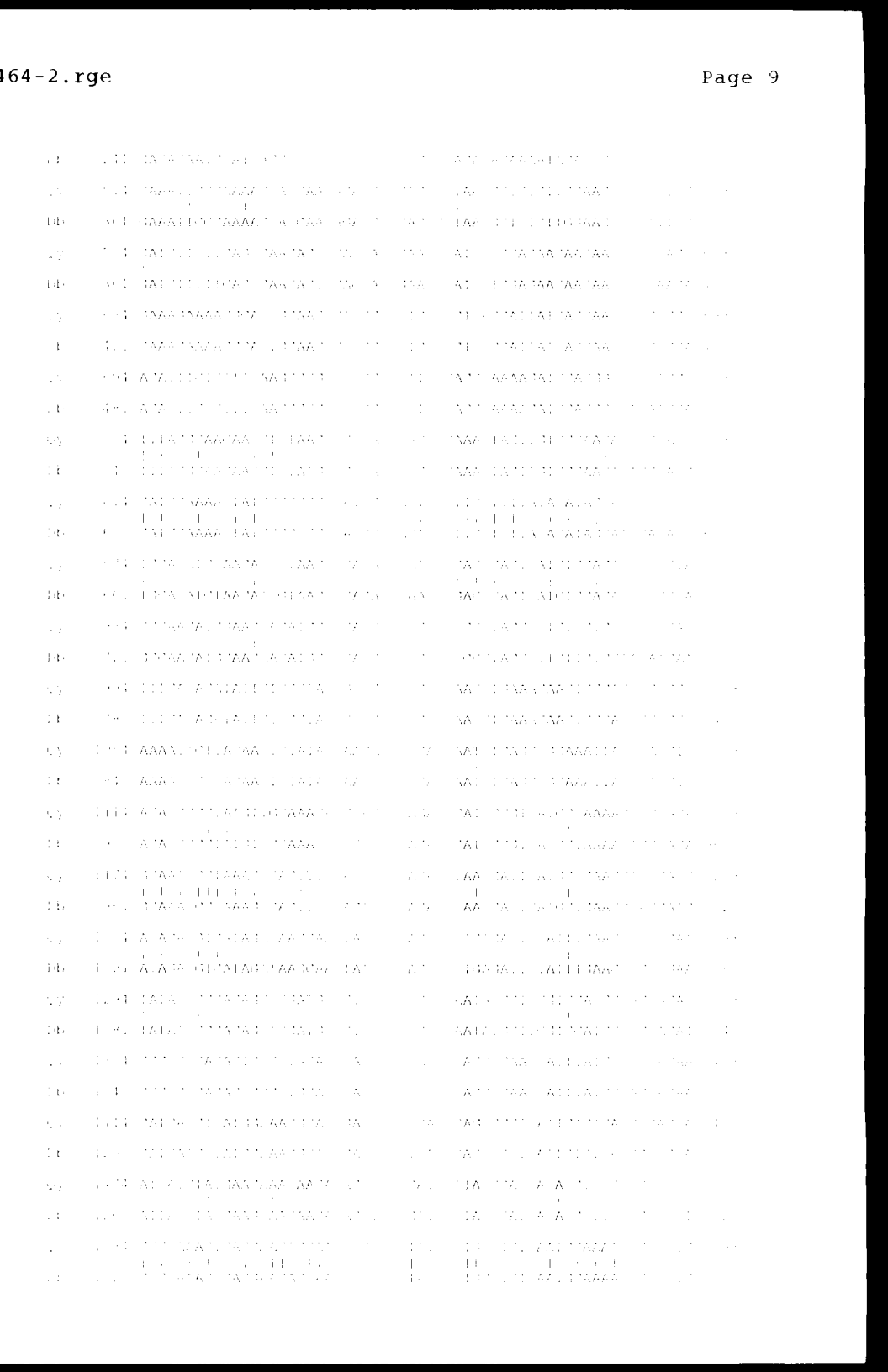
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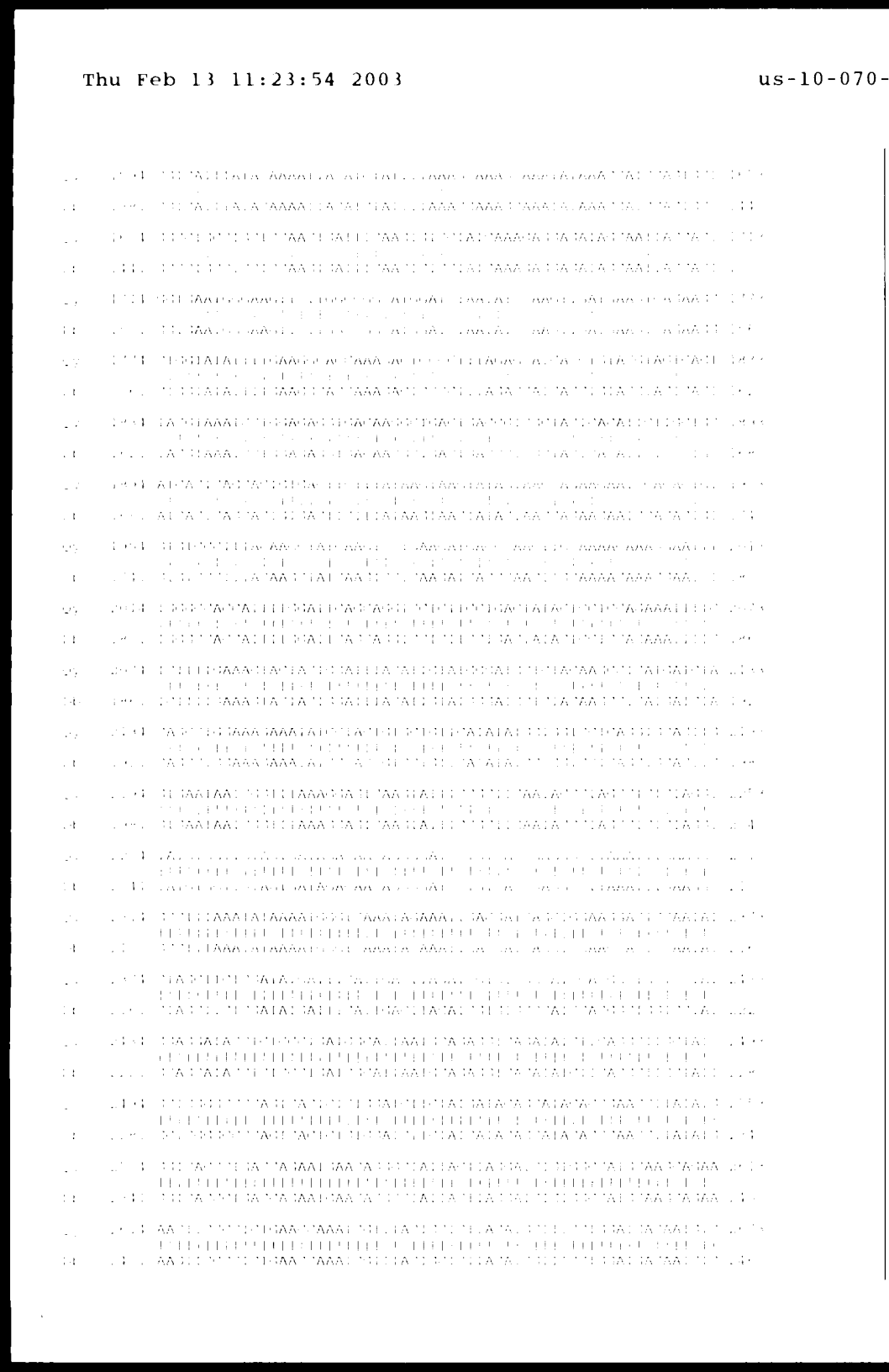


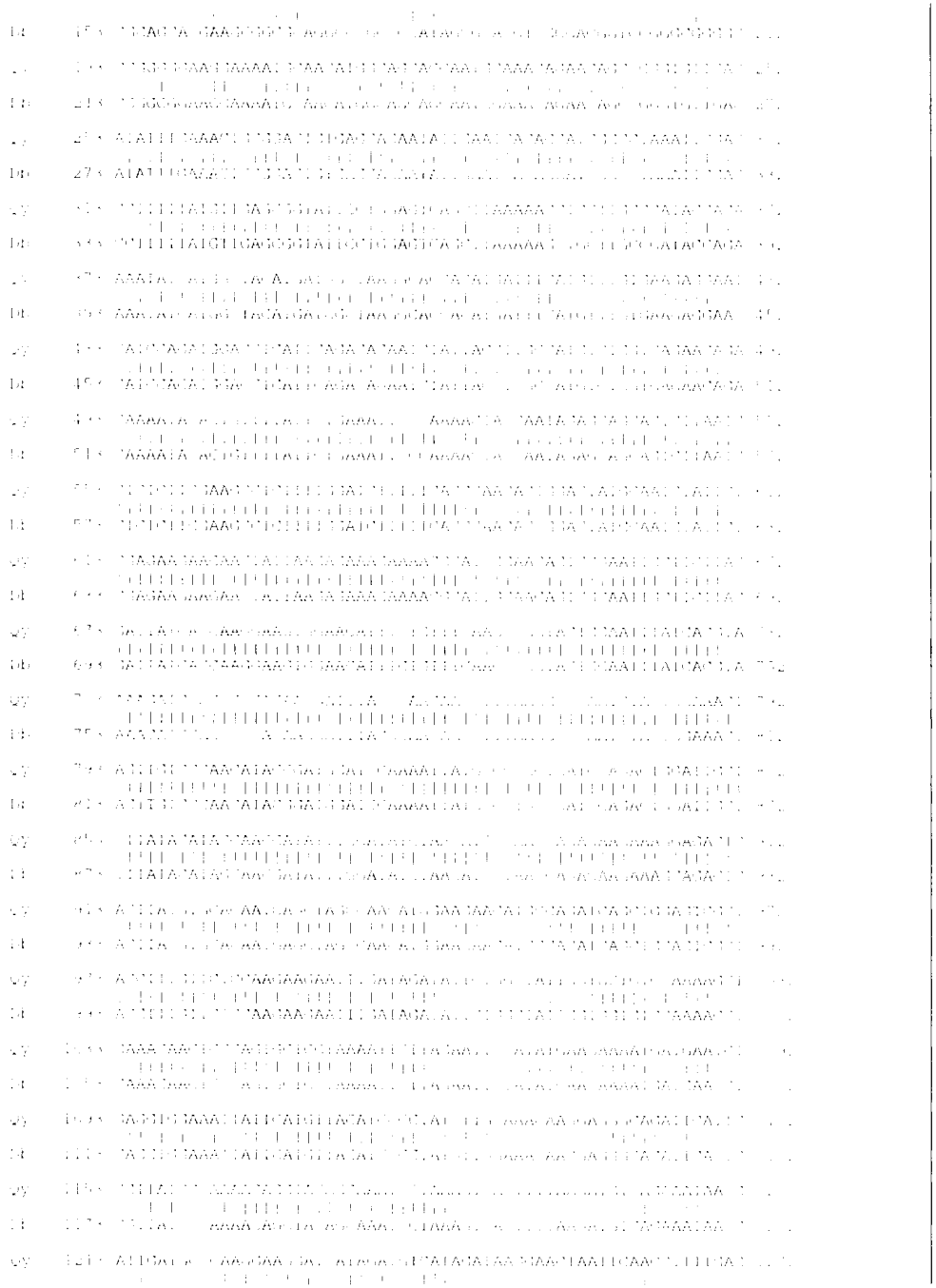


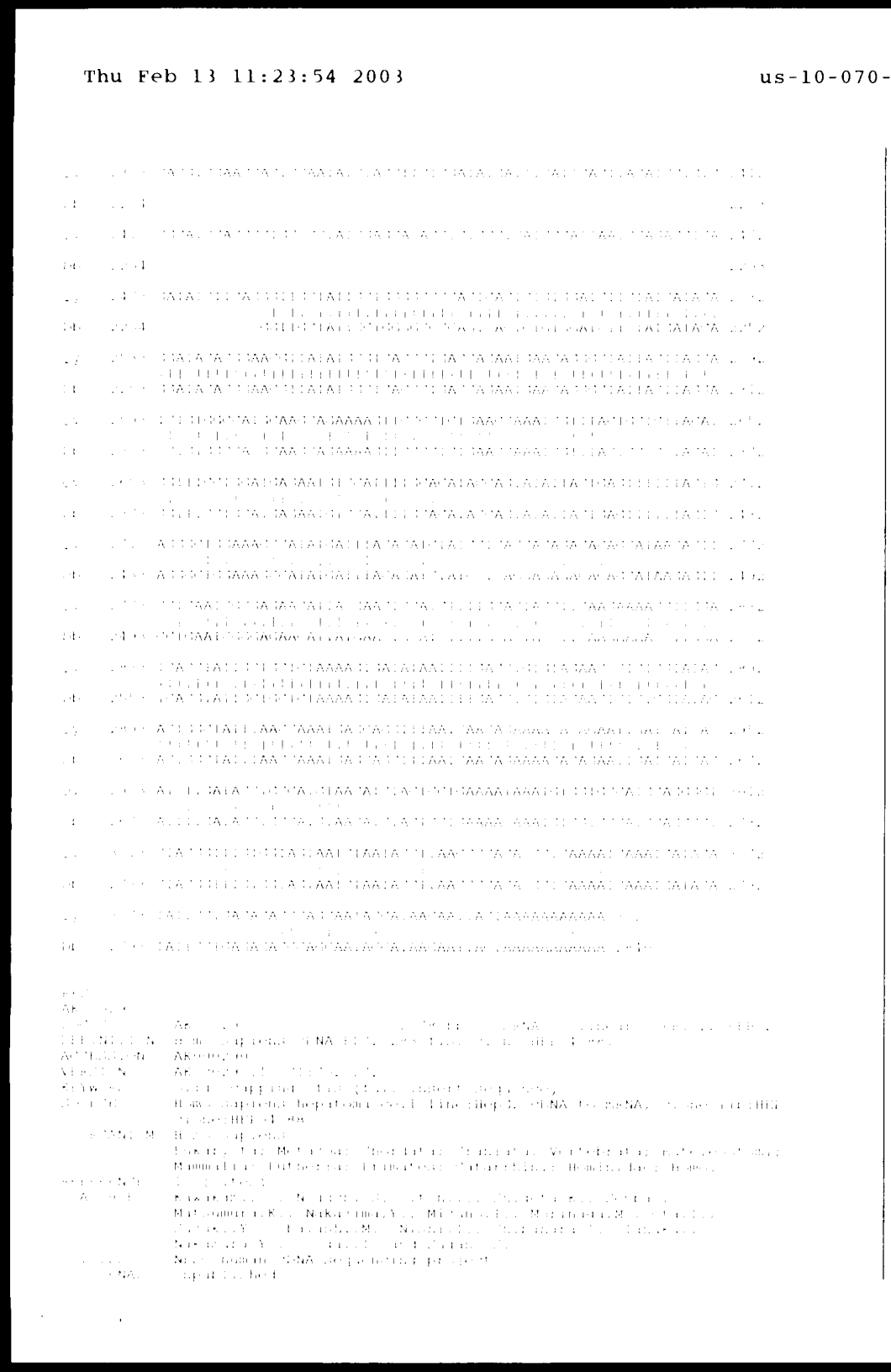
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ACCESSION AX464704
VERSION AX464704.1 GI:18454528
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Meyers R.A. and Williams B.M.
TITLE 2'-5' oligoadenylate probes labeled with energy transfer dyes
JOURNAL Patent: WO 0170473-A 1 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
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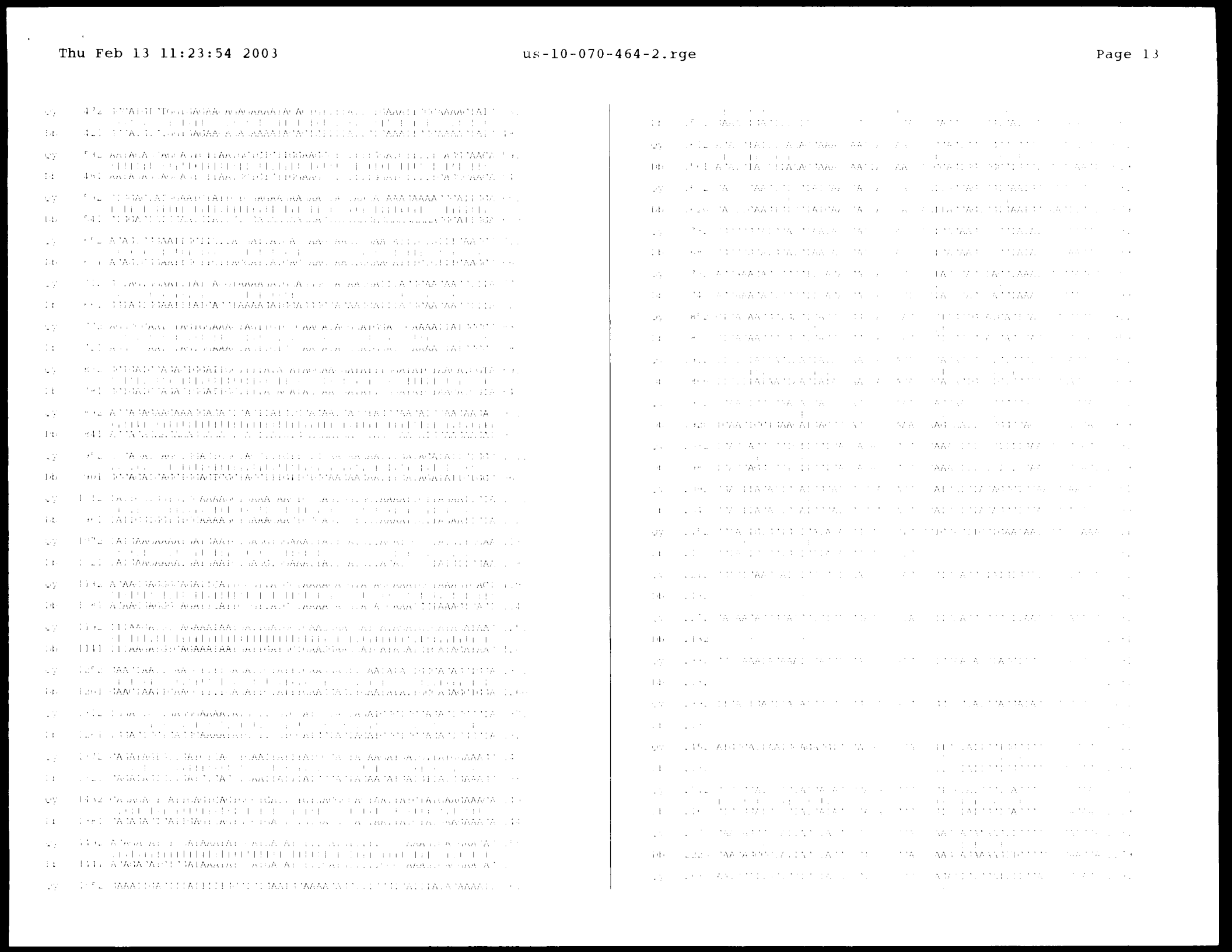
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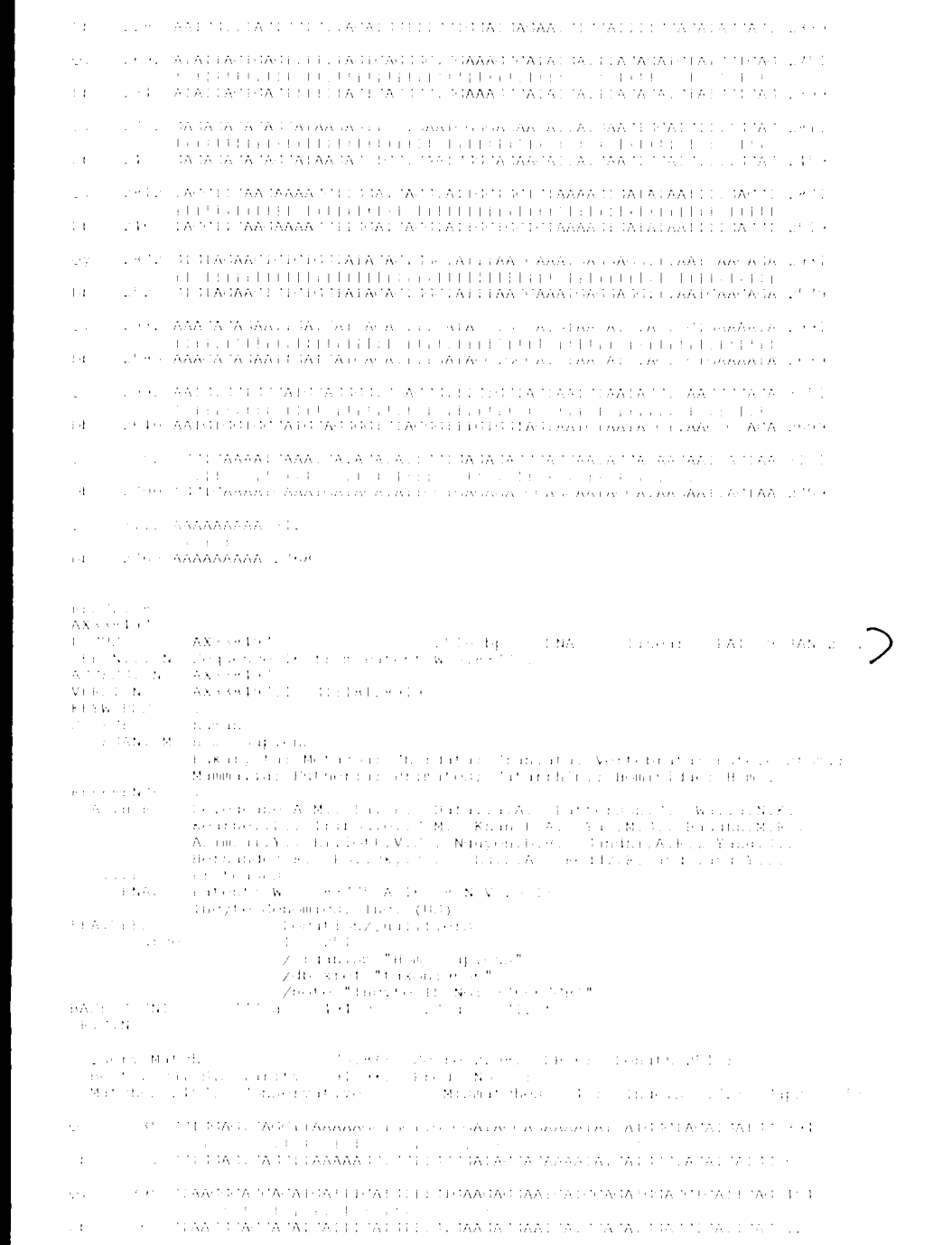


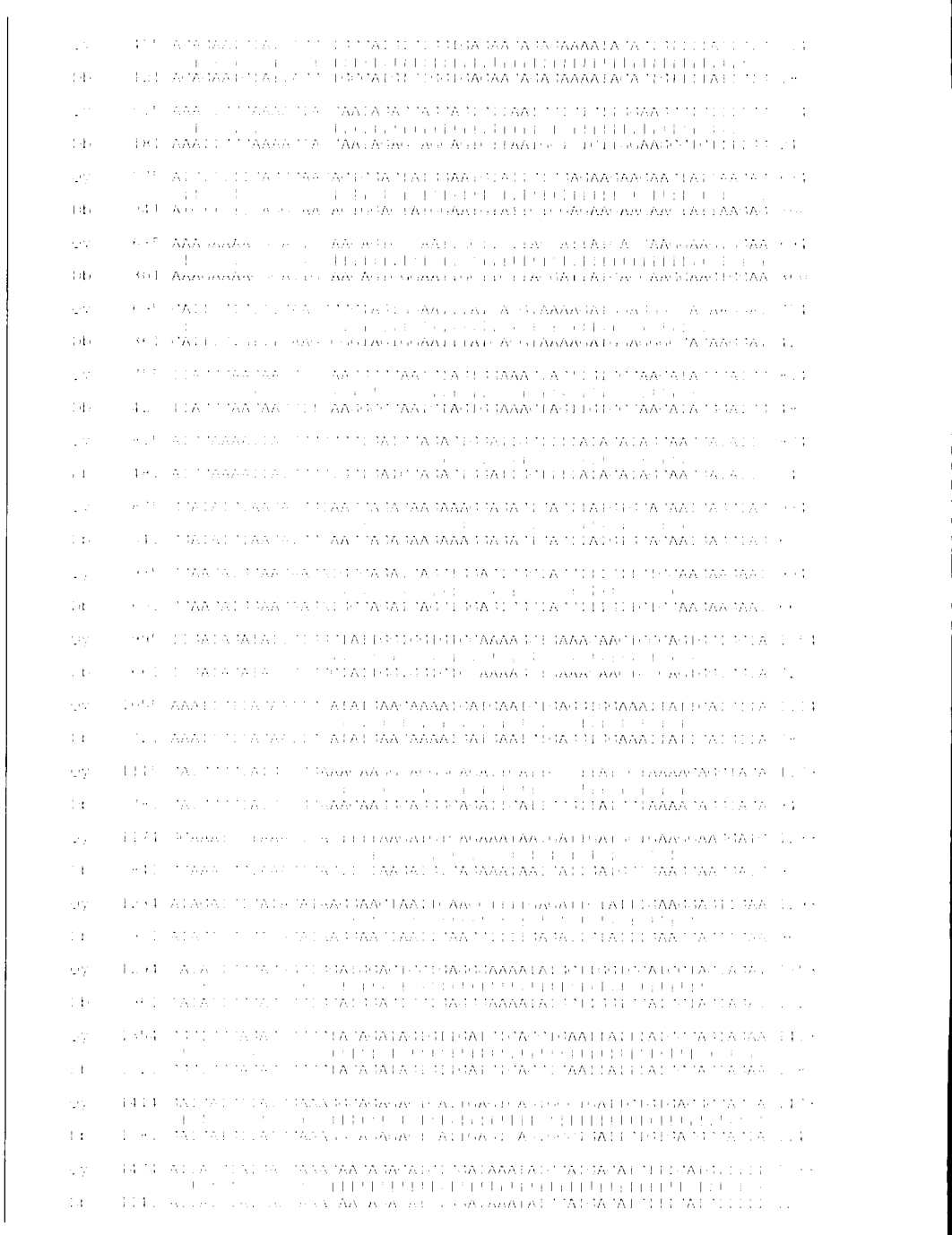


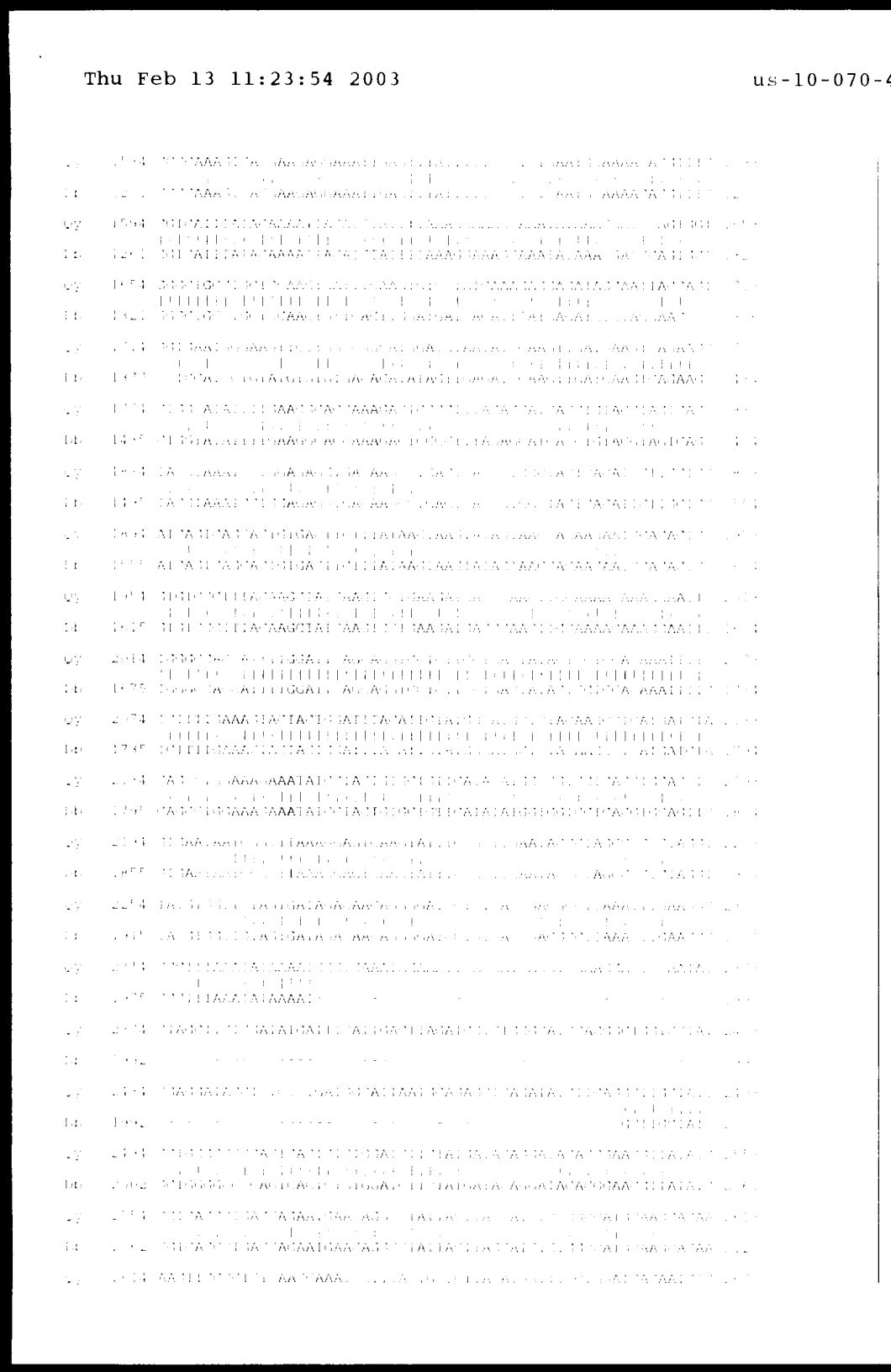


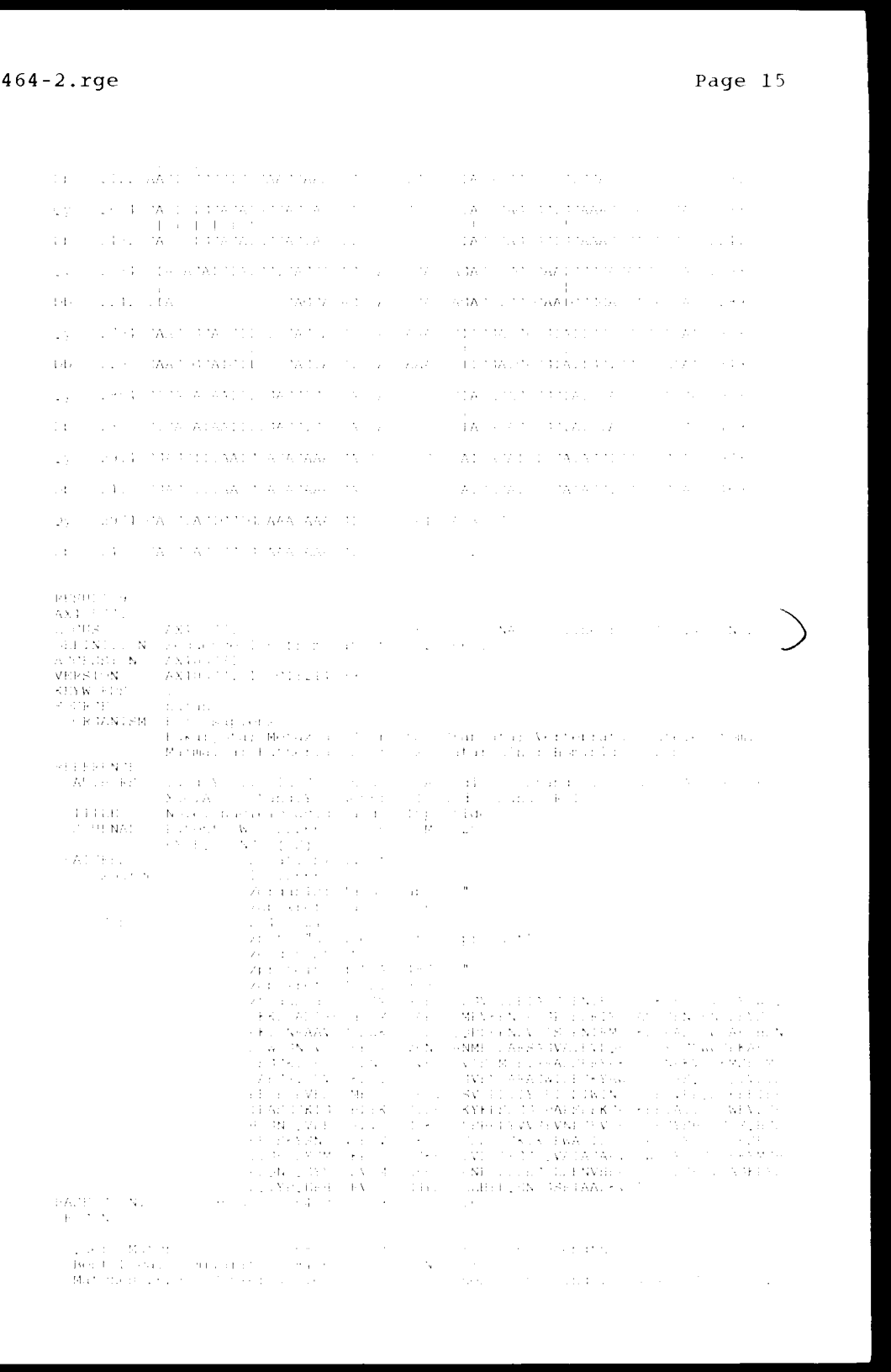


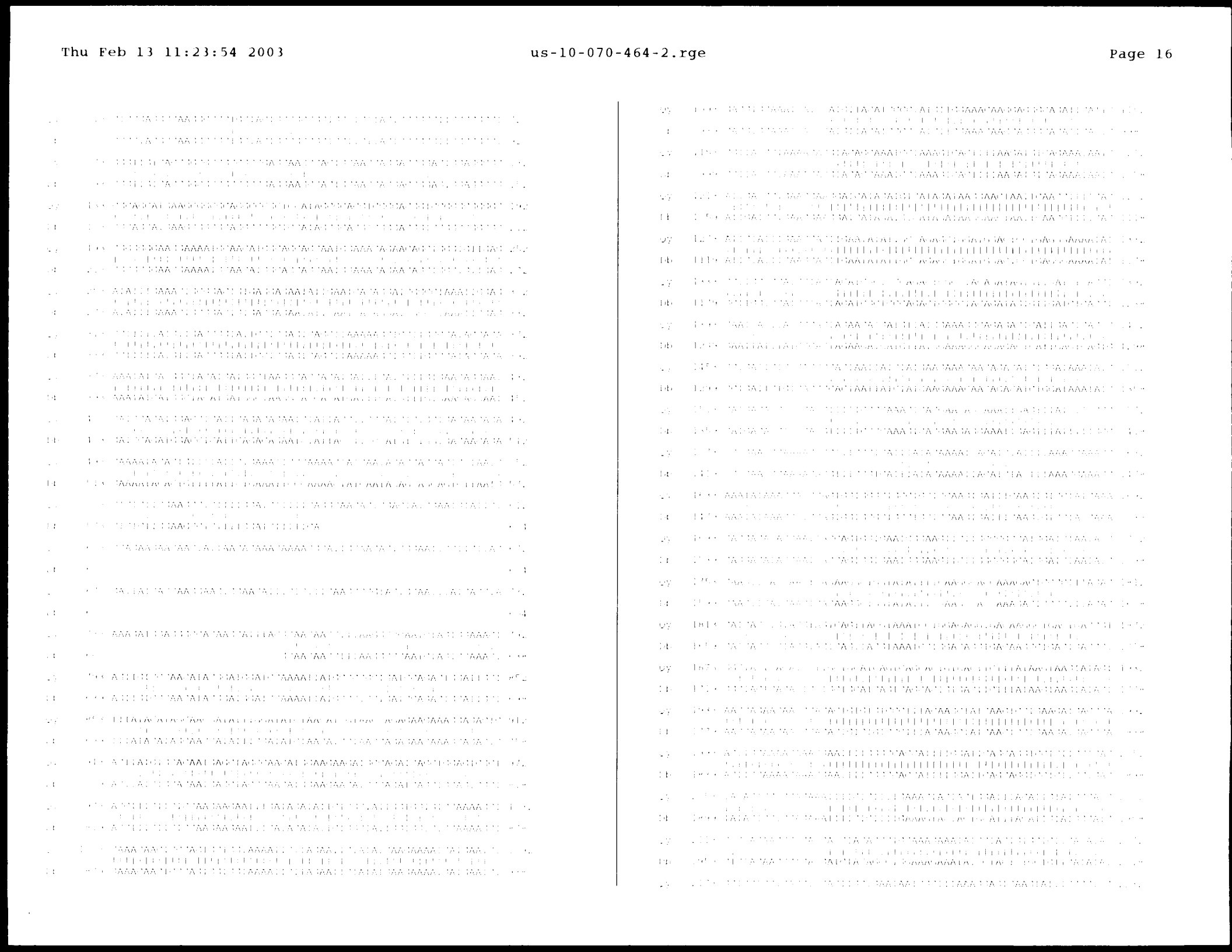


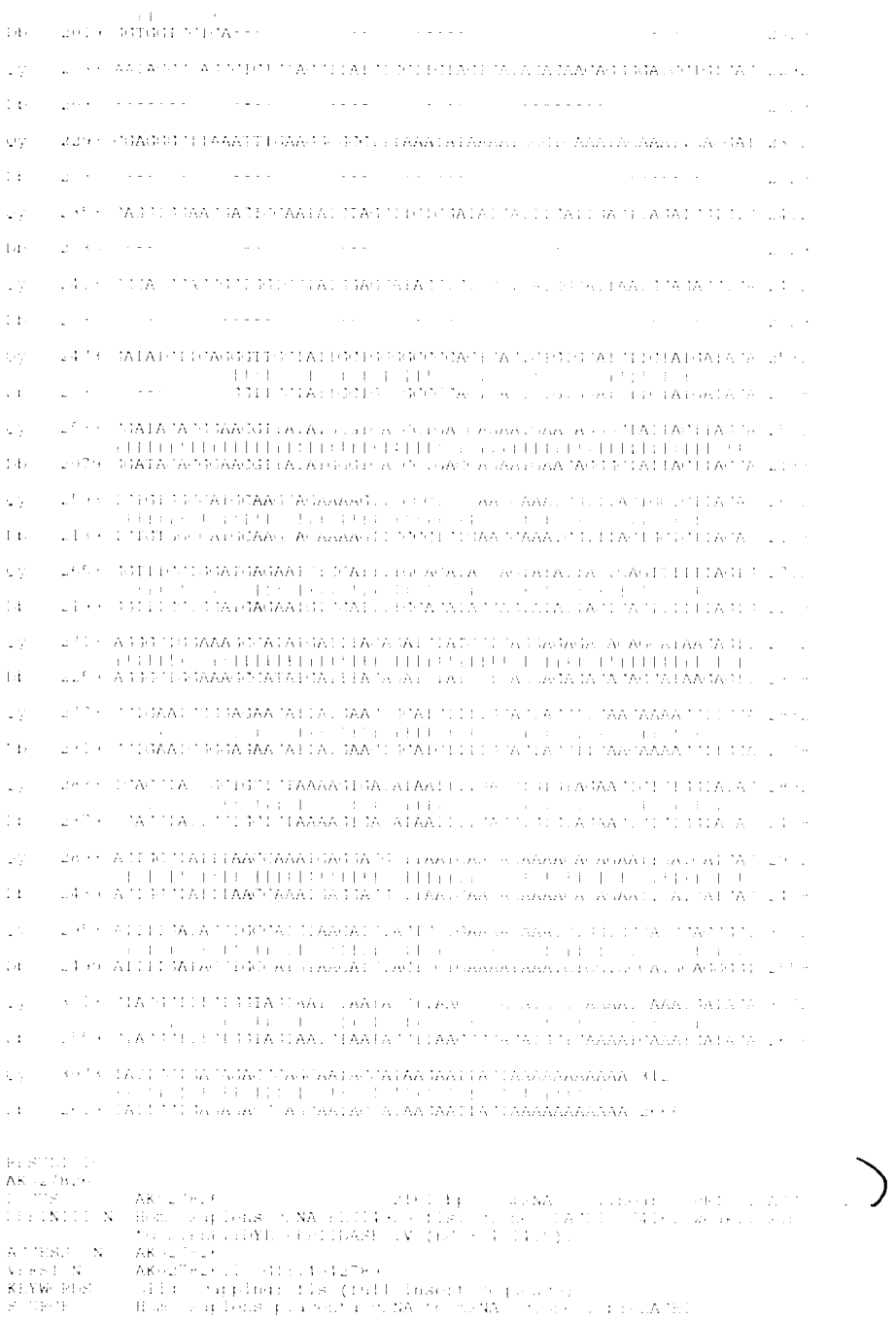


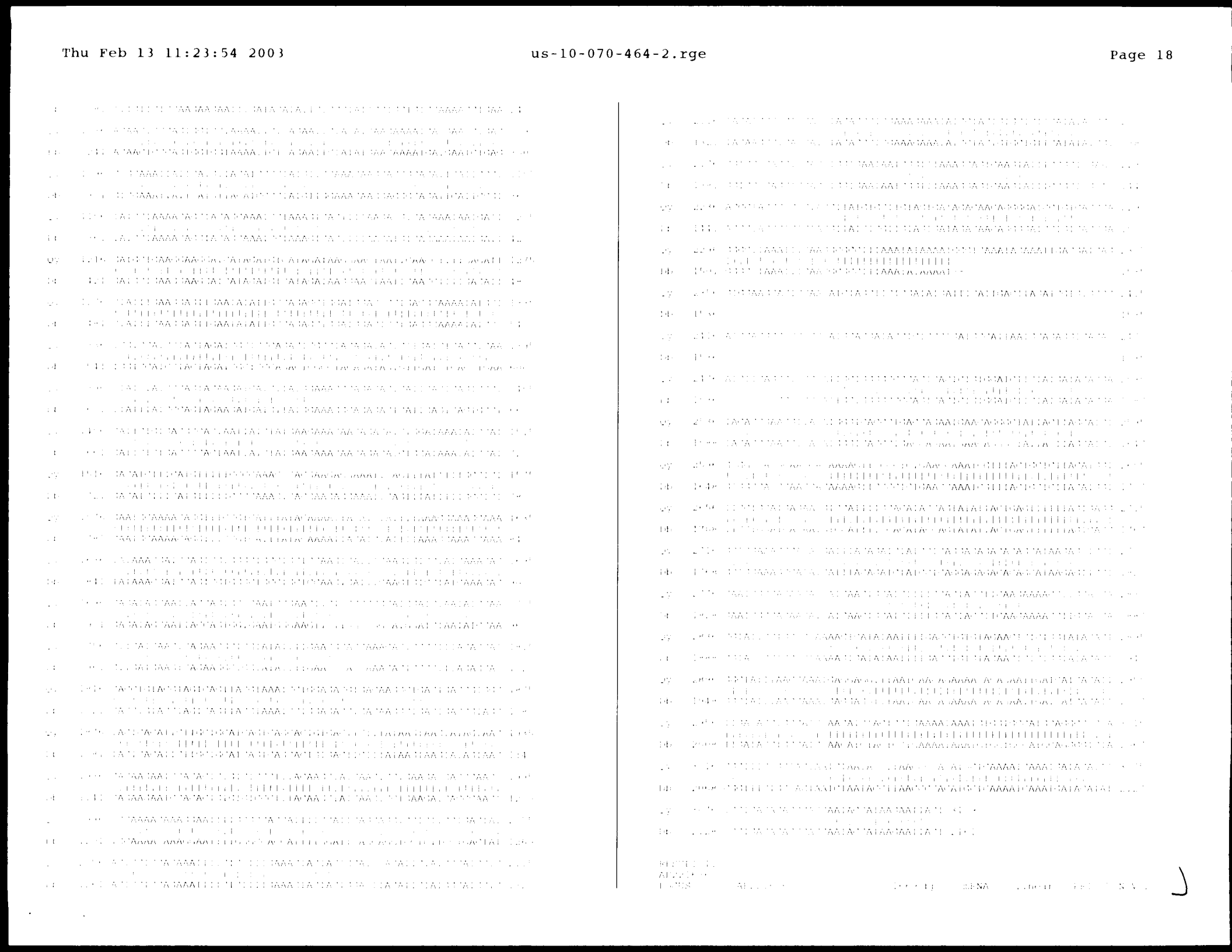


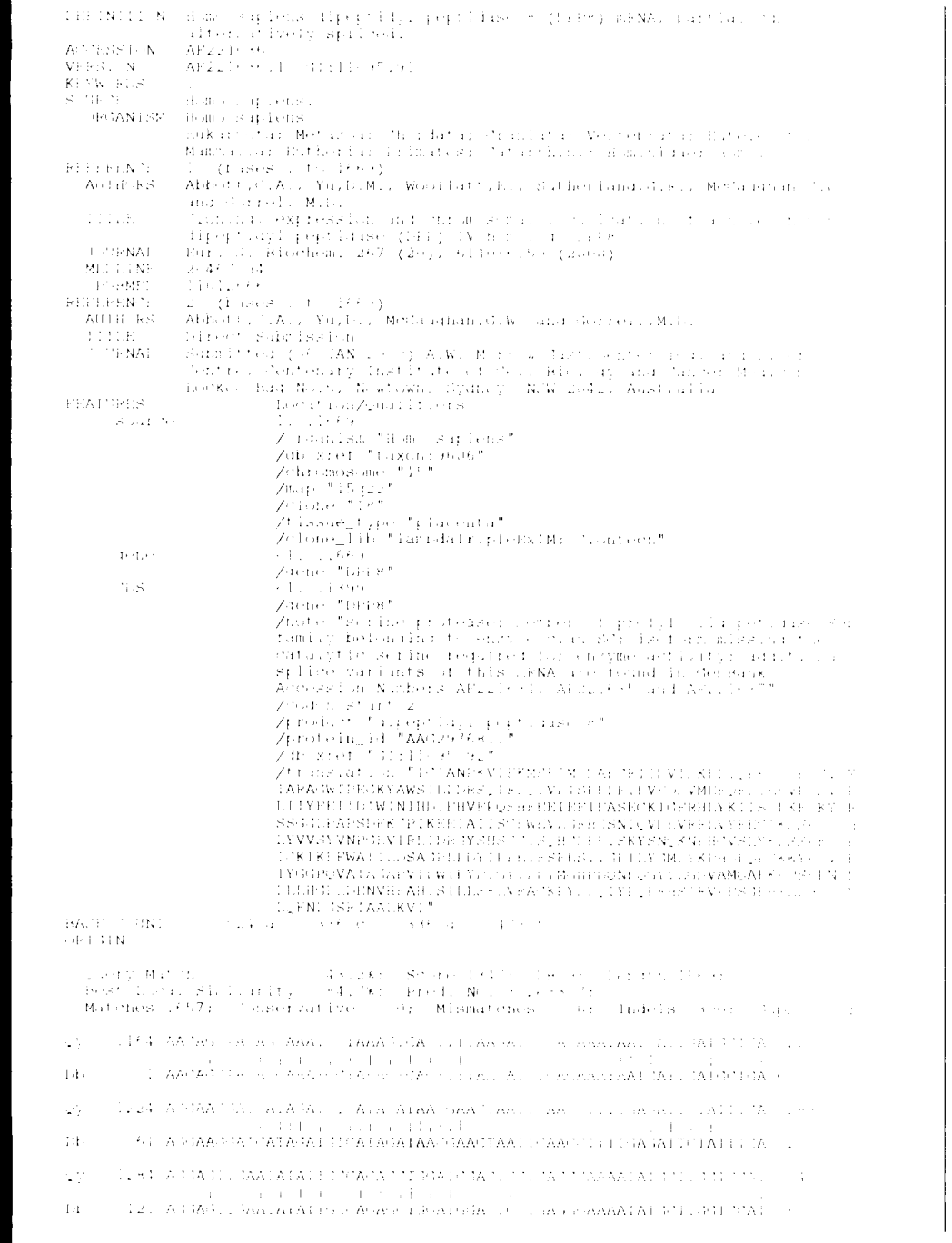


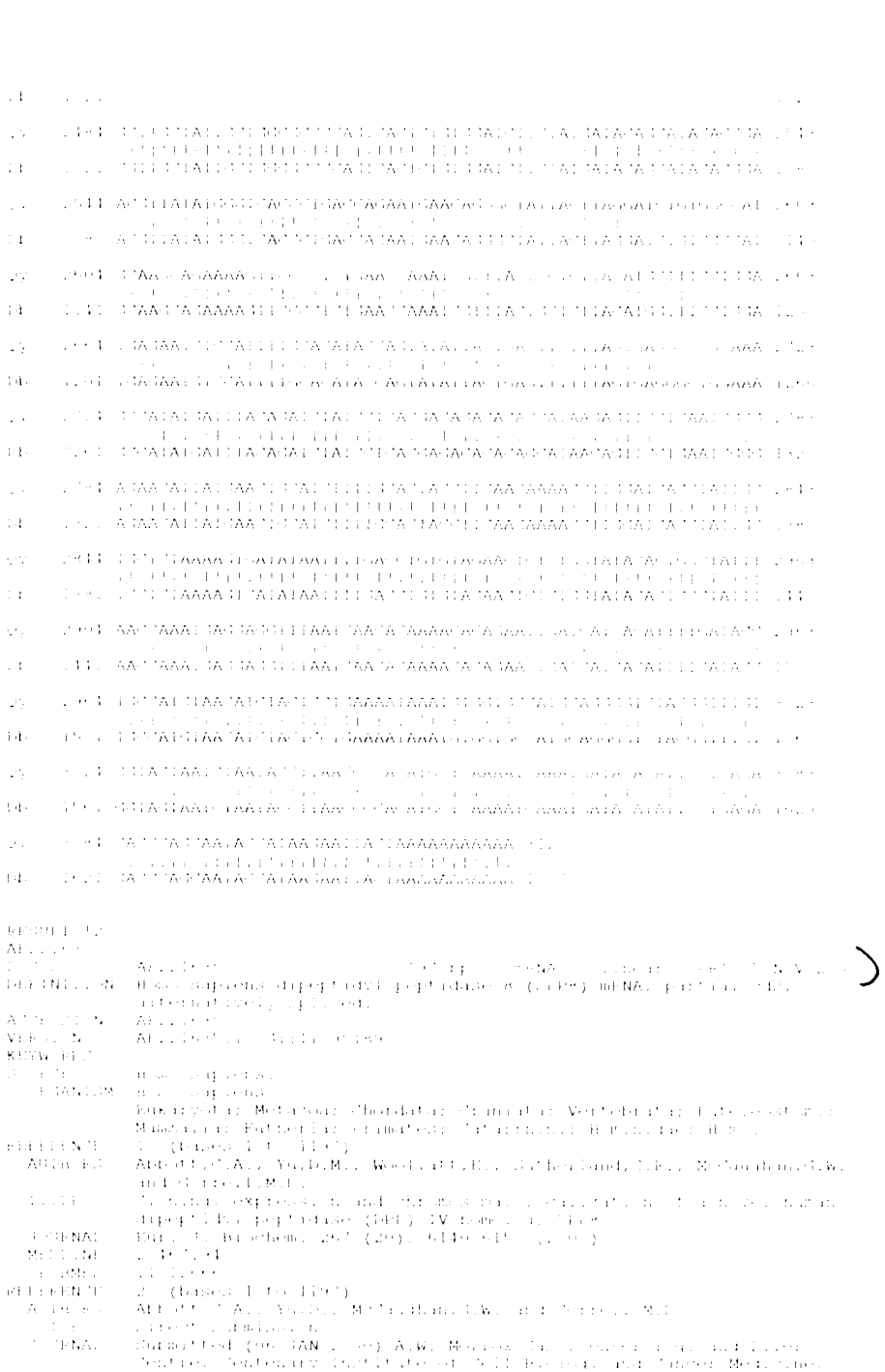


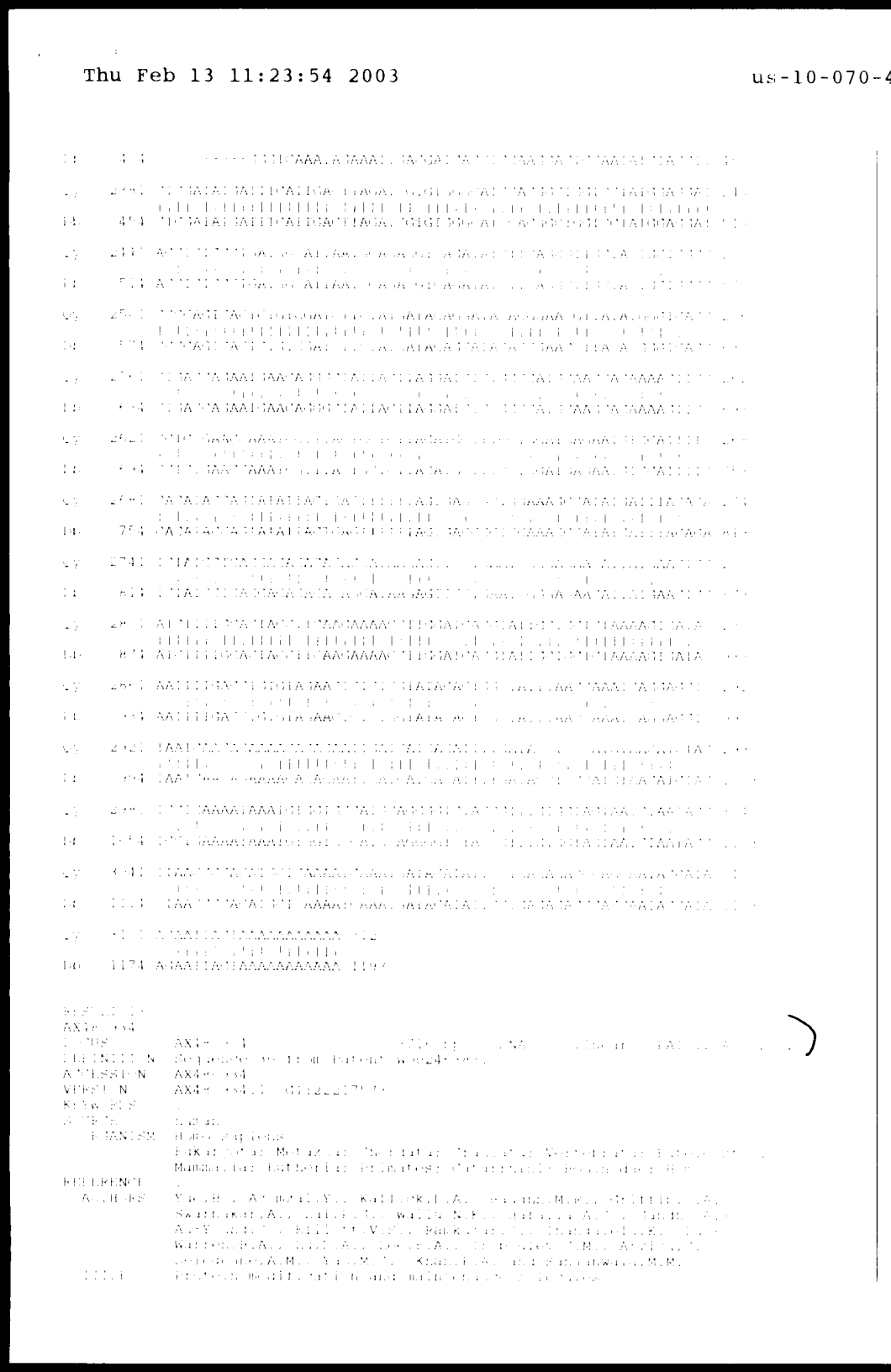


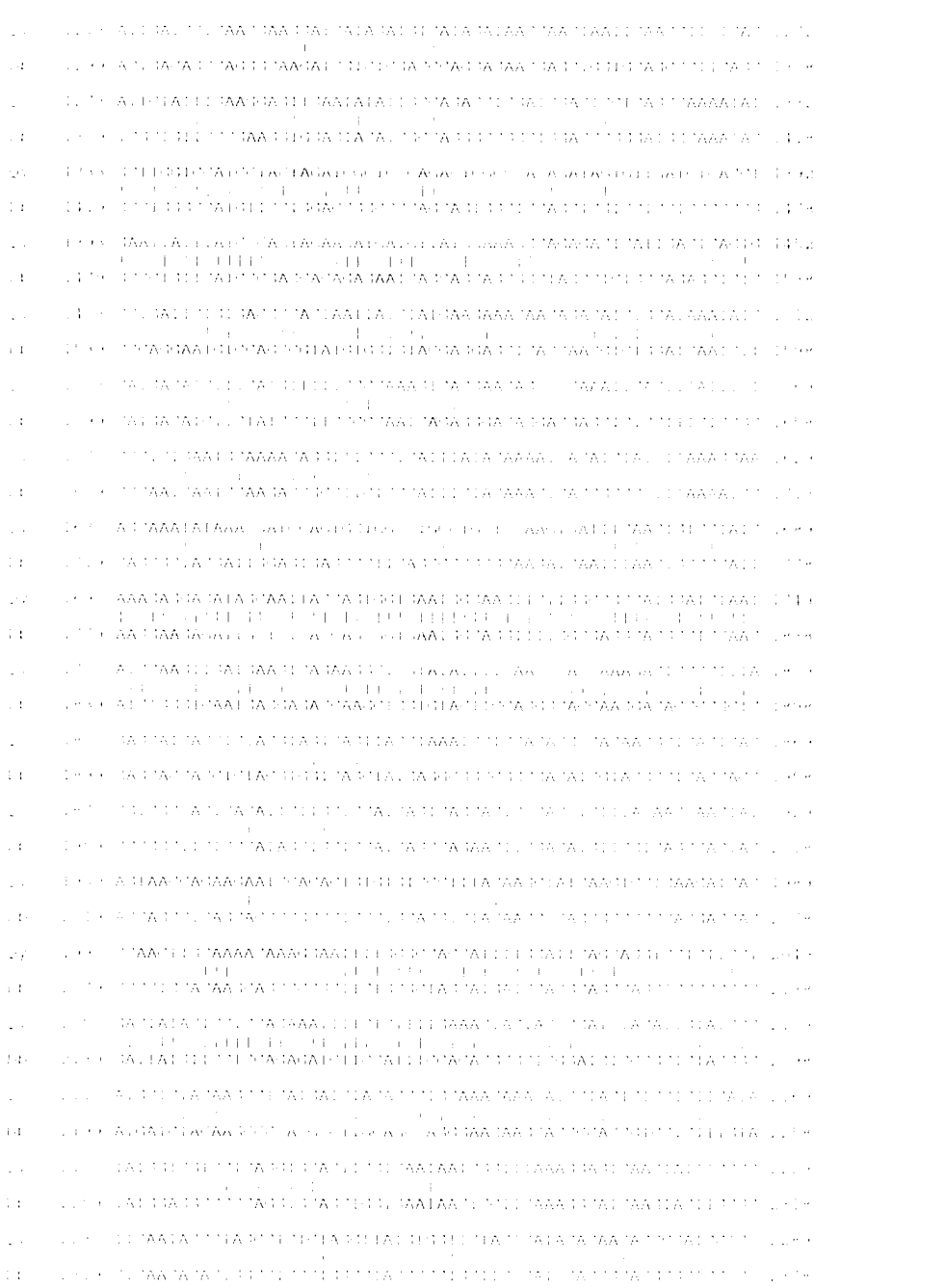


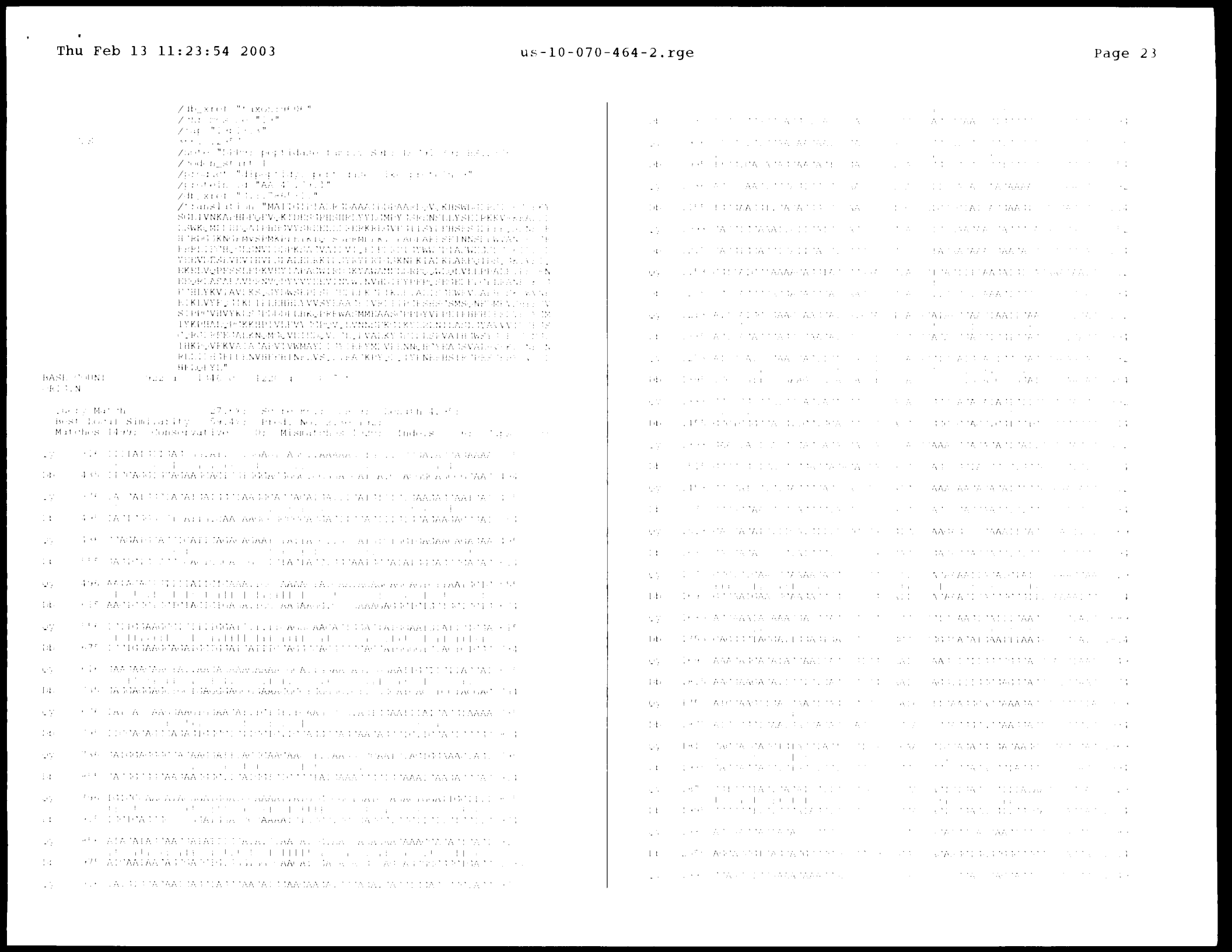


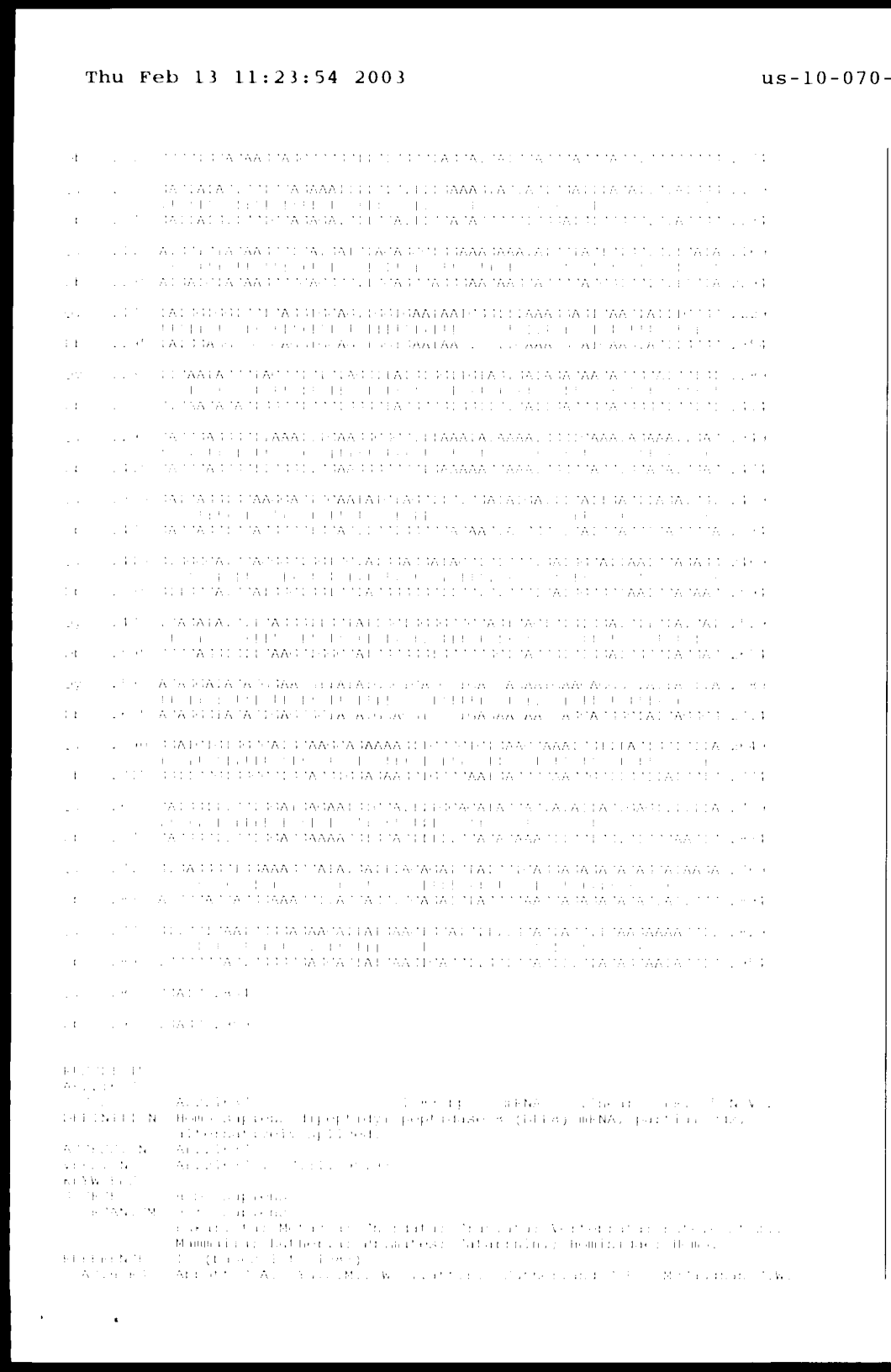


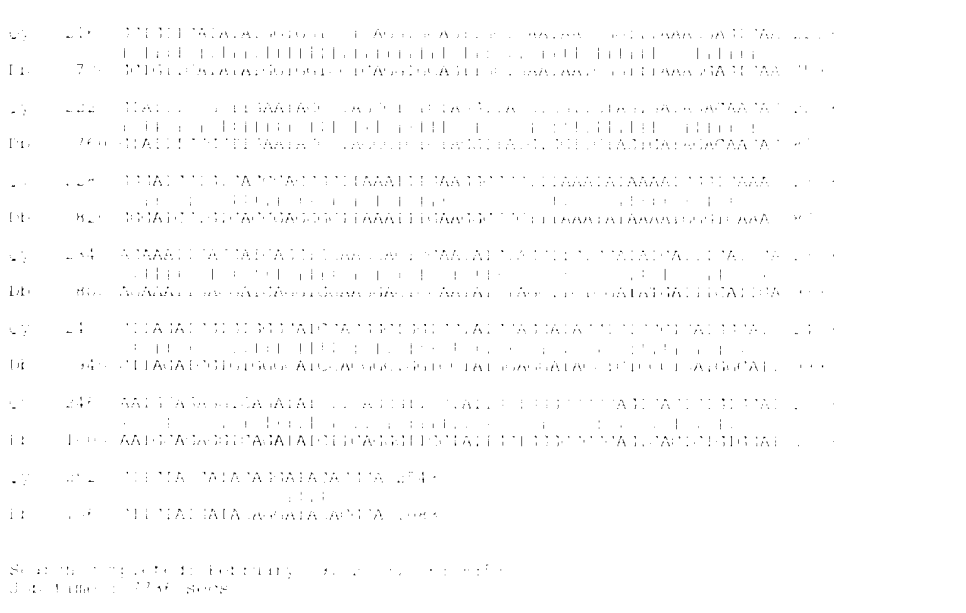


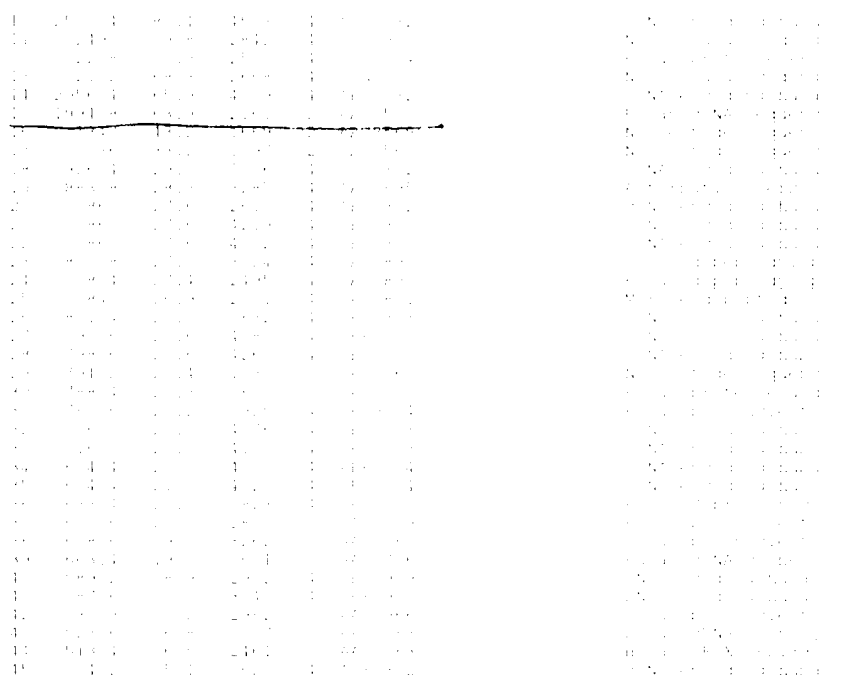


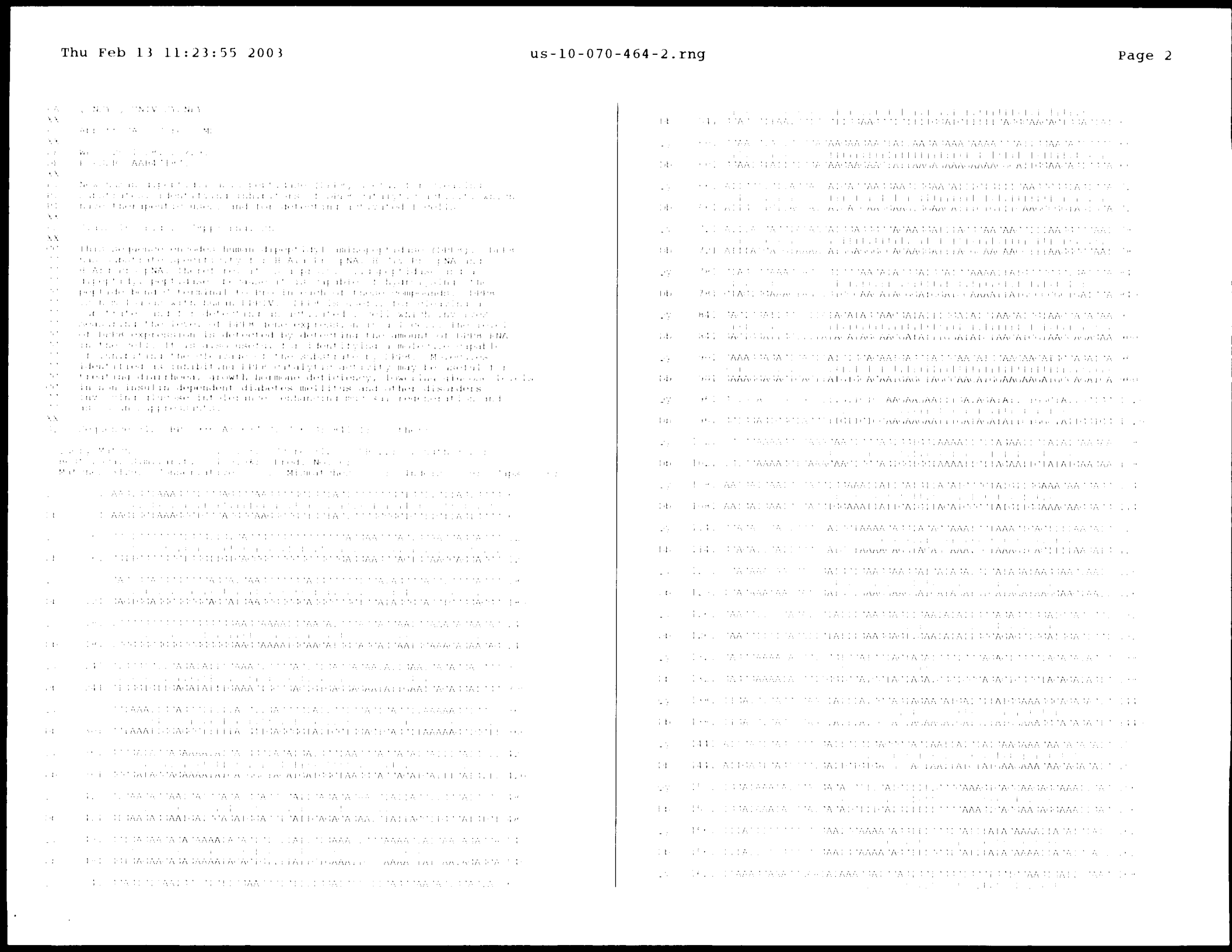


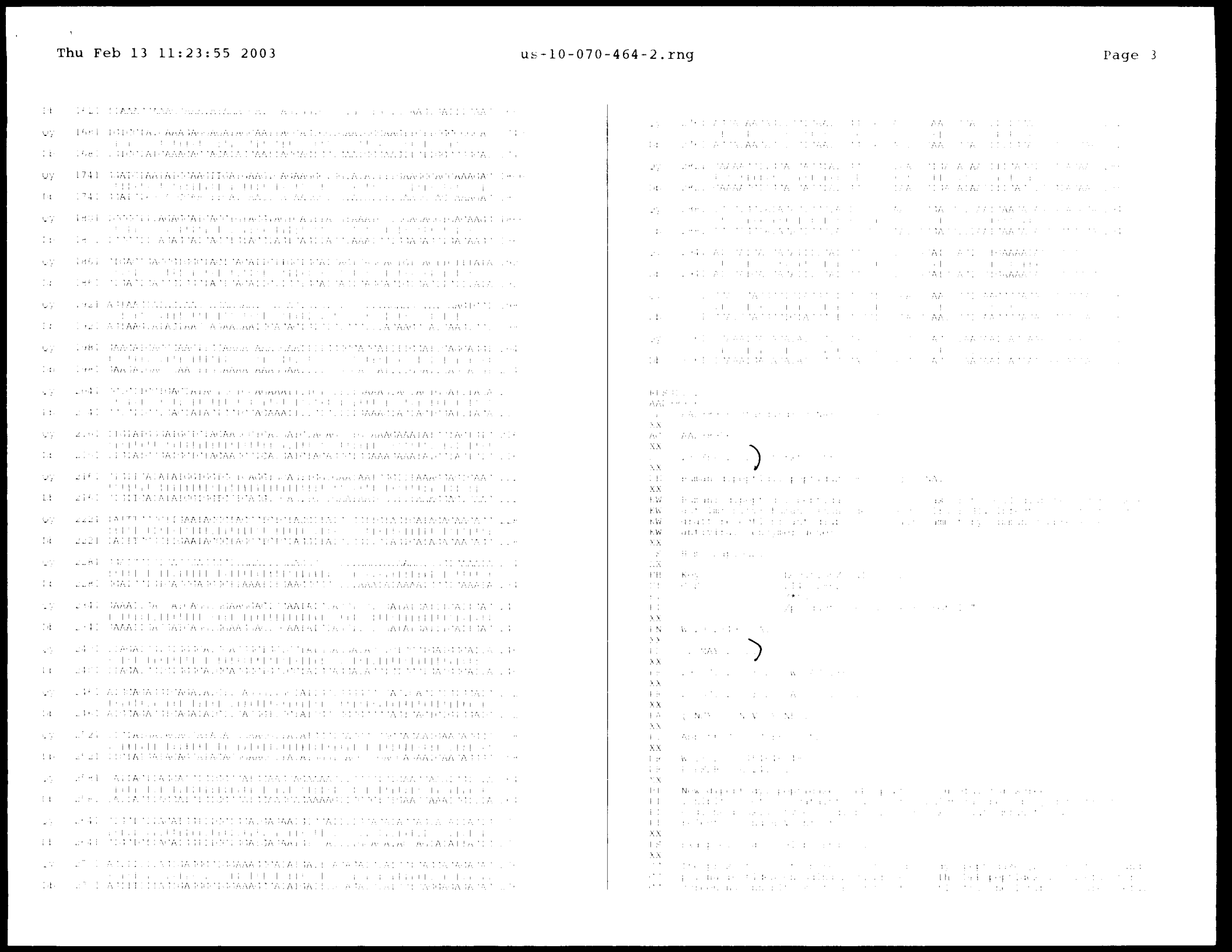


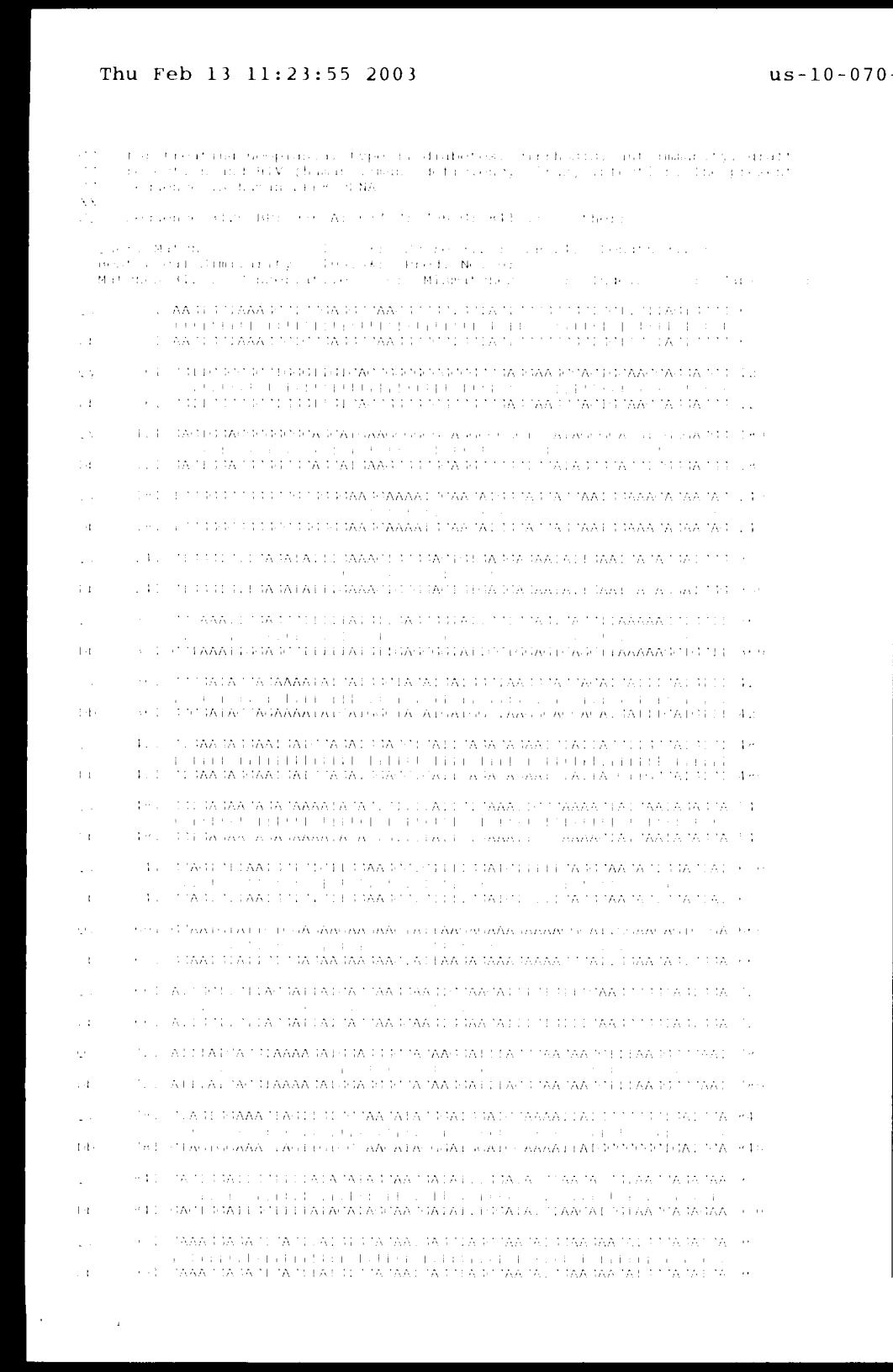


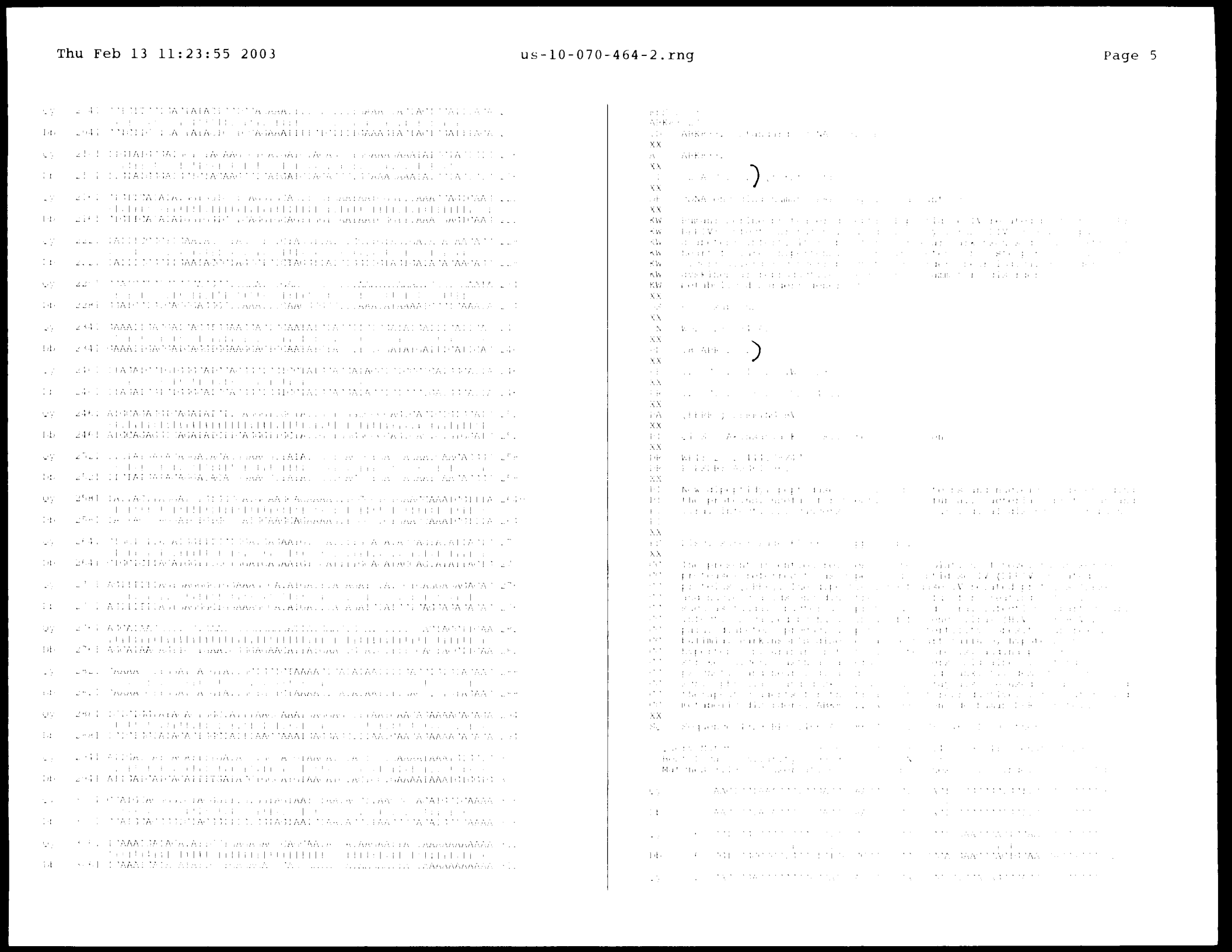


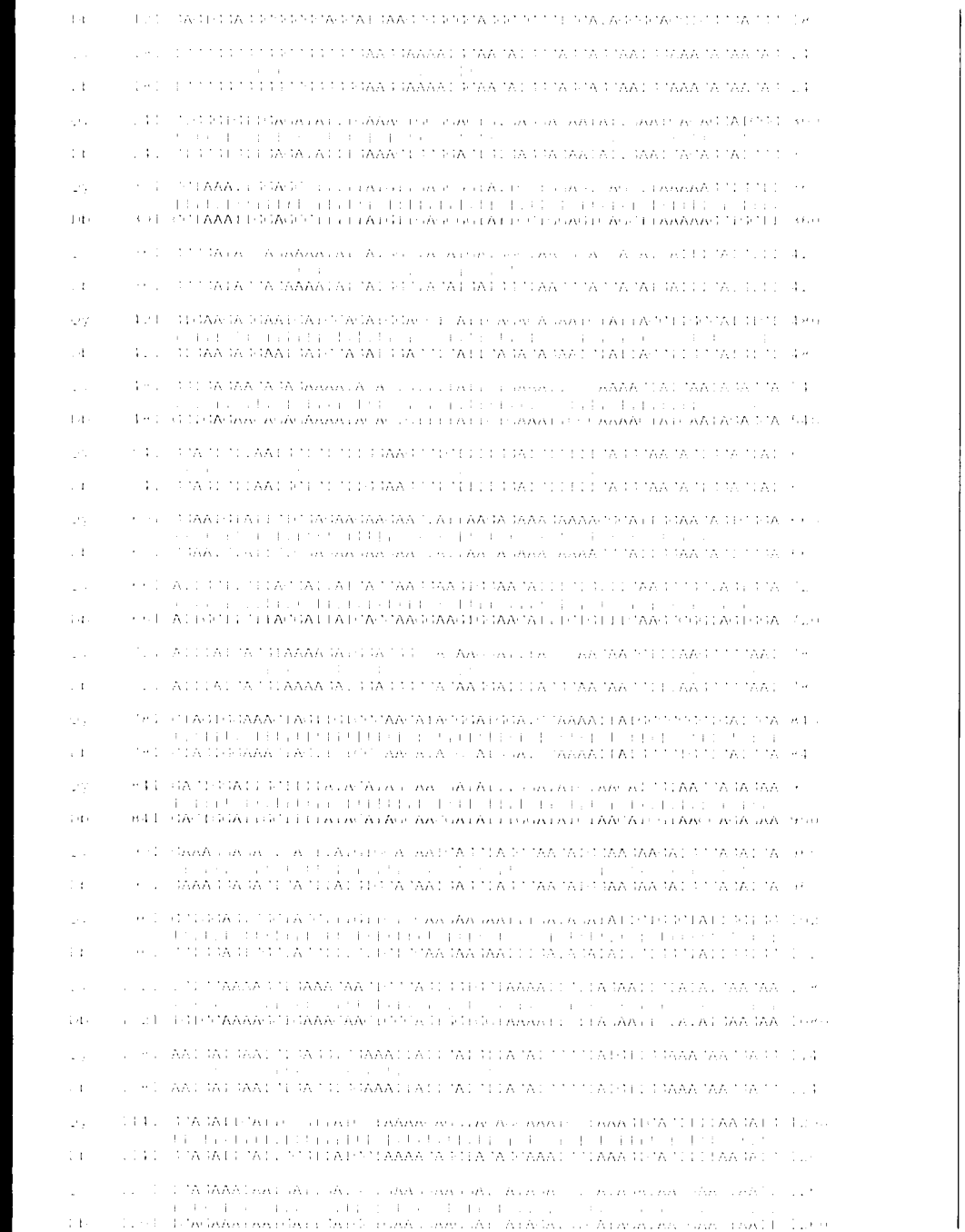


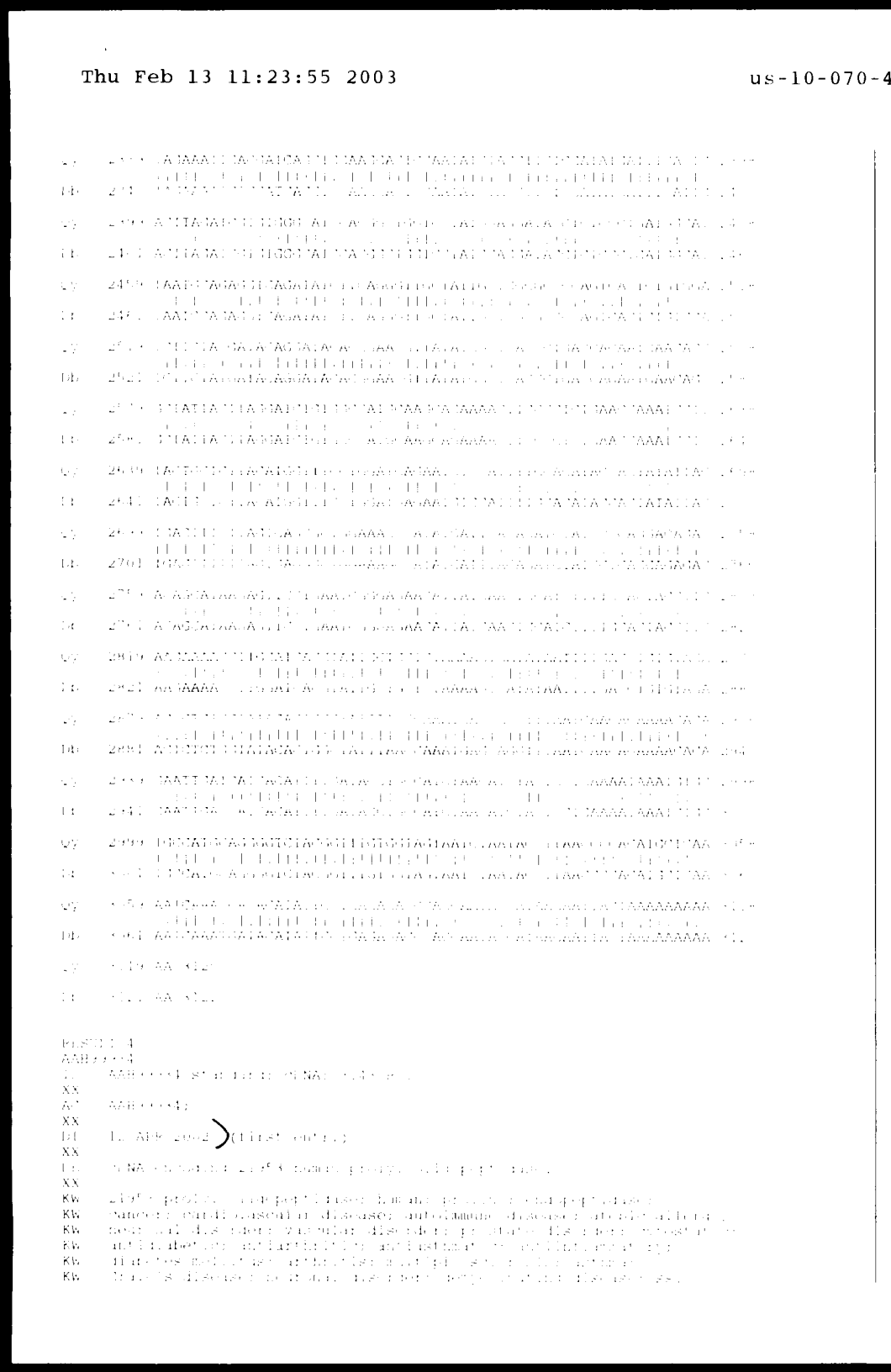


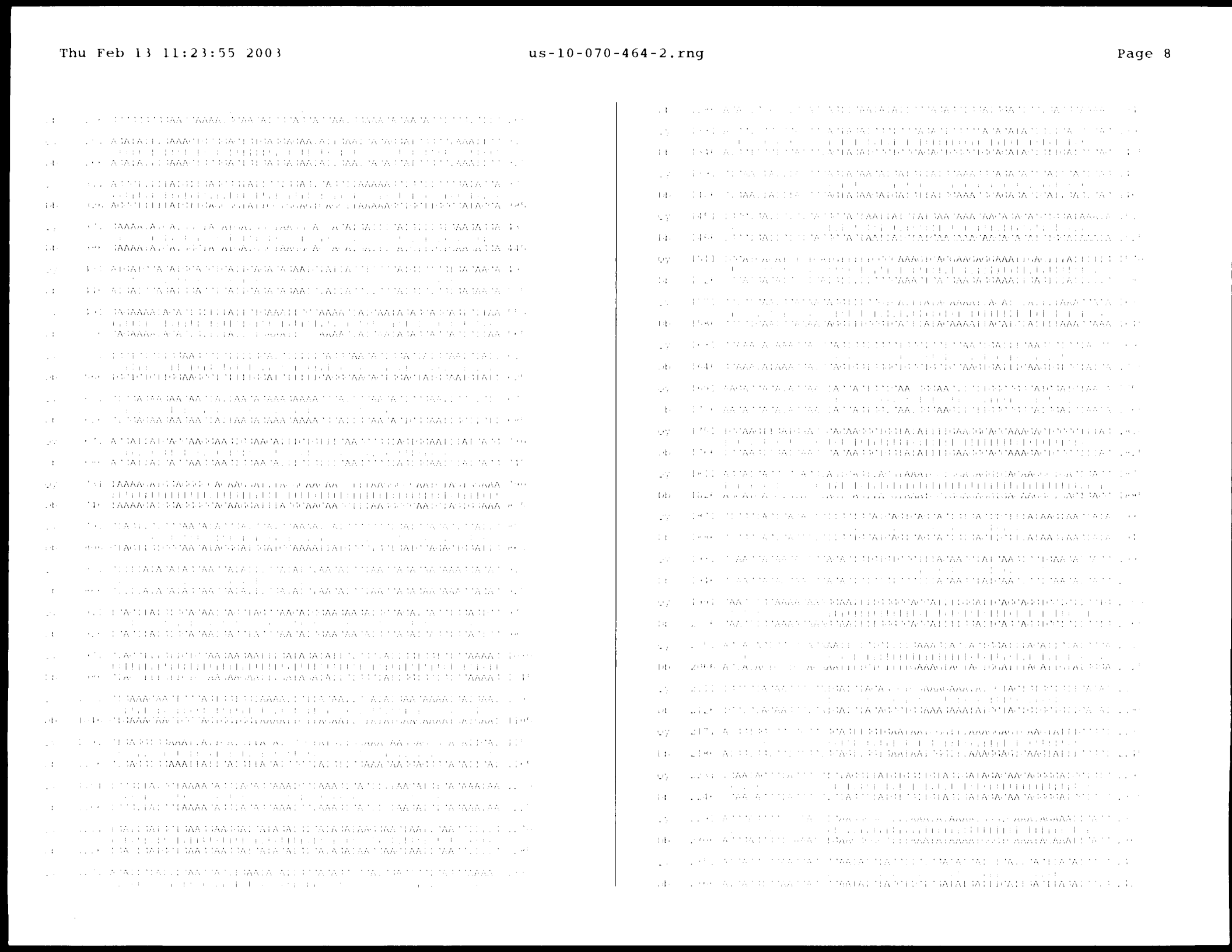


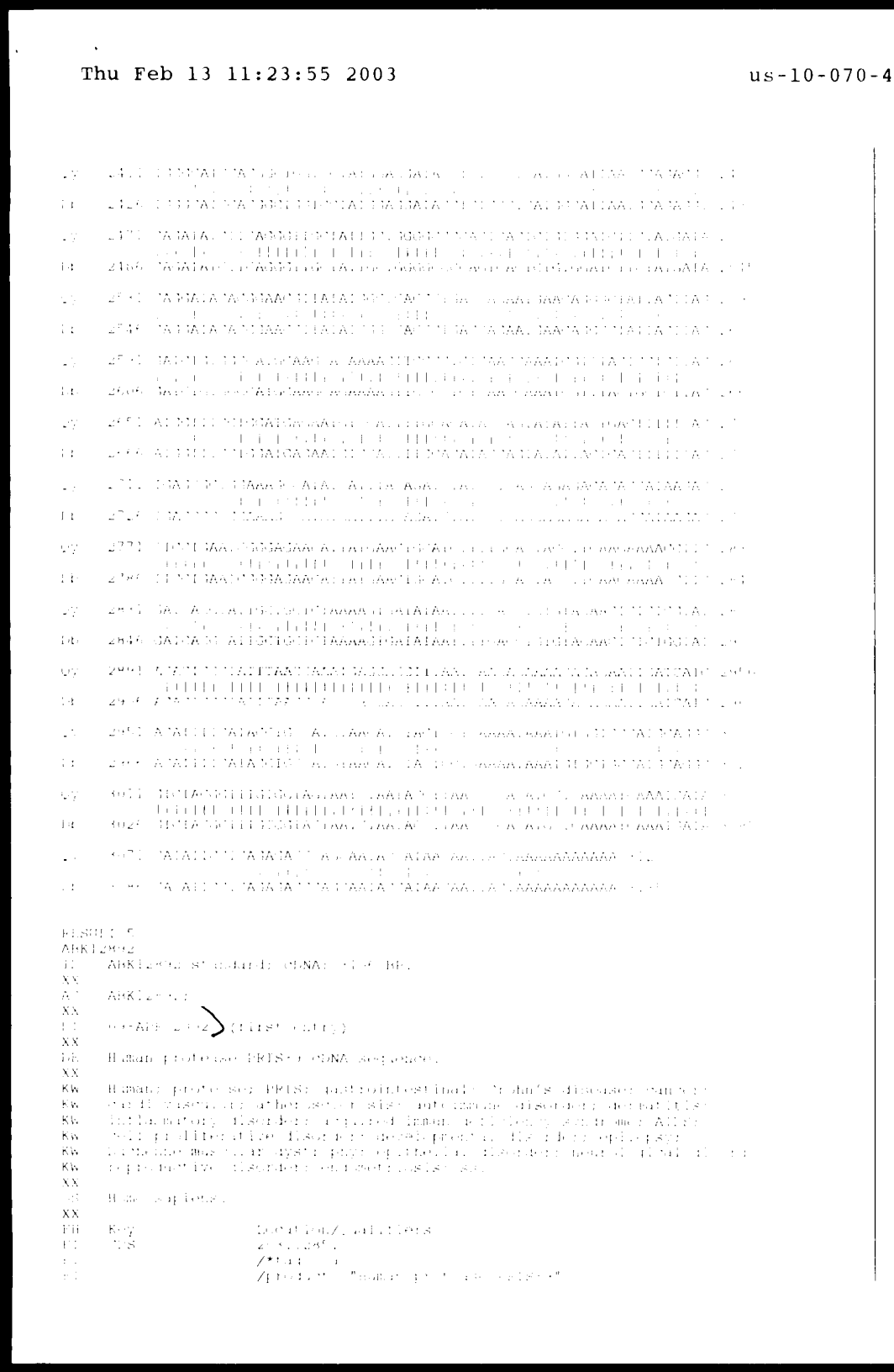


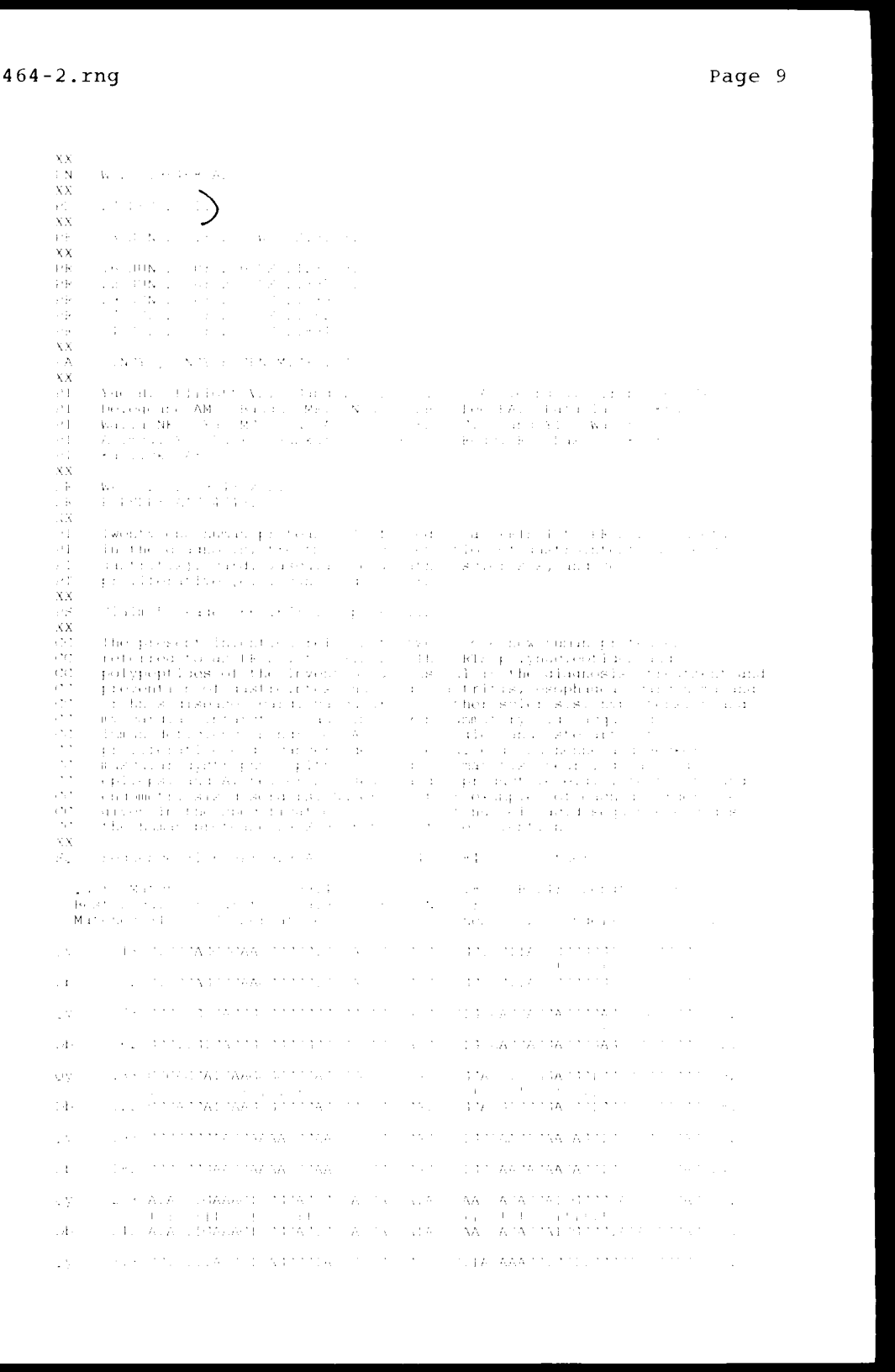


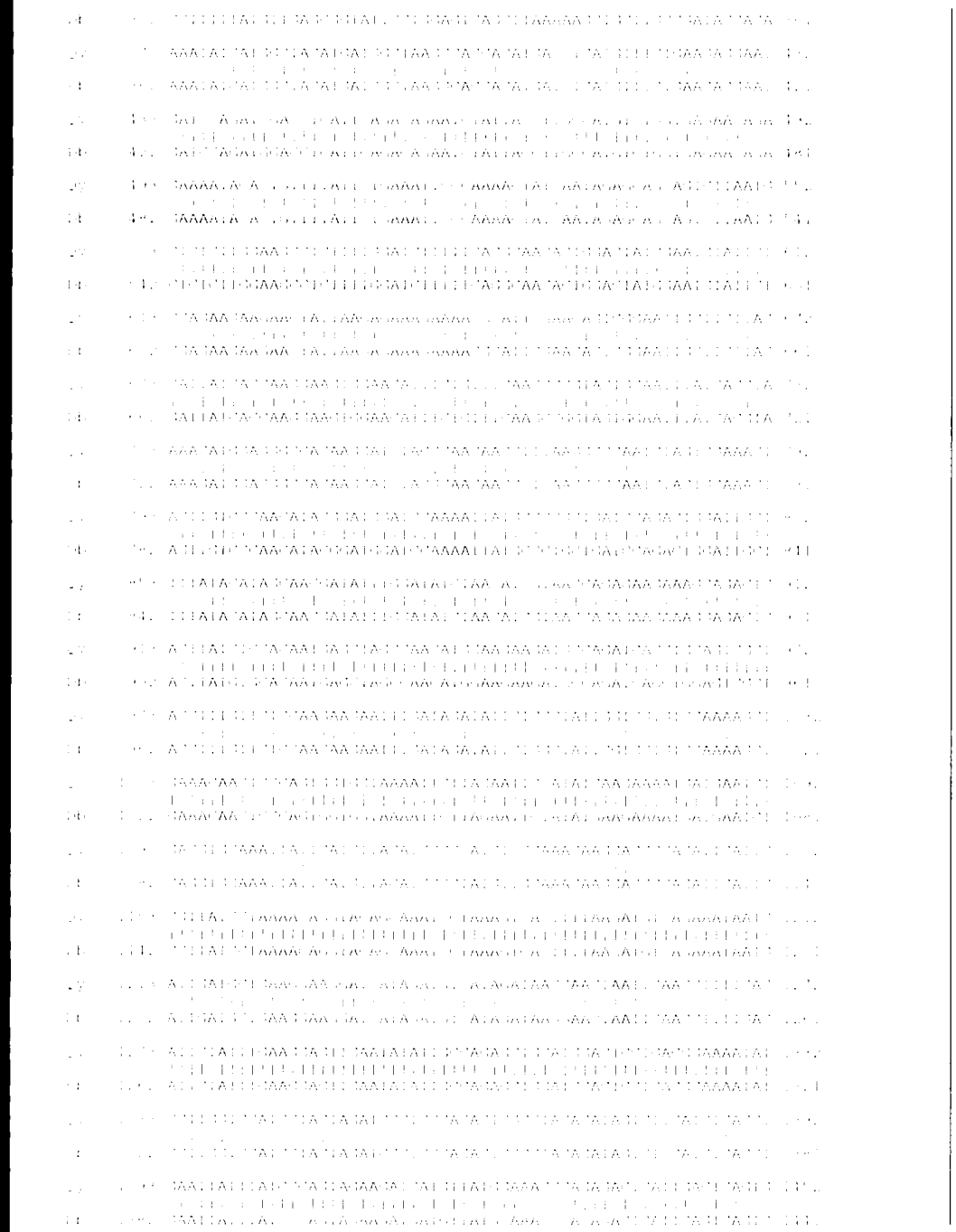


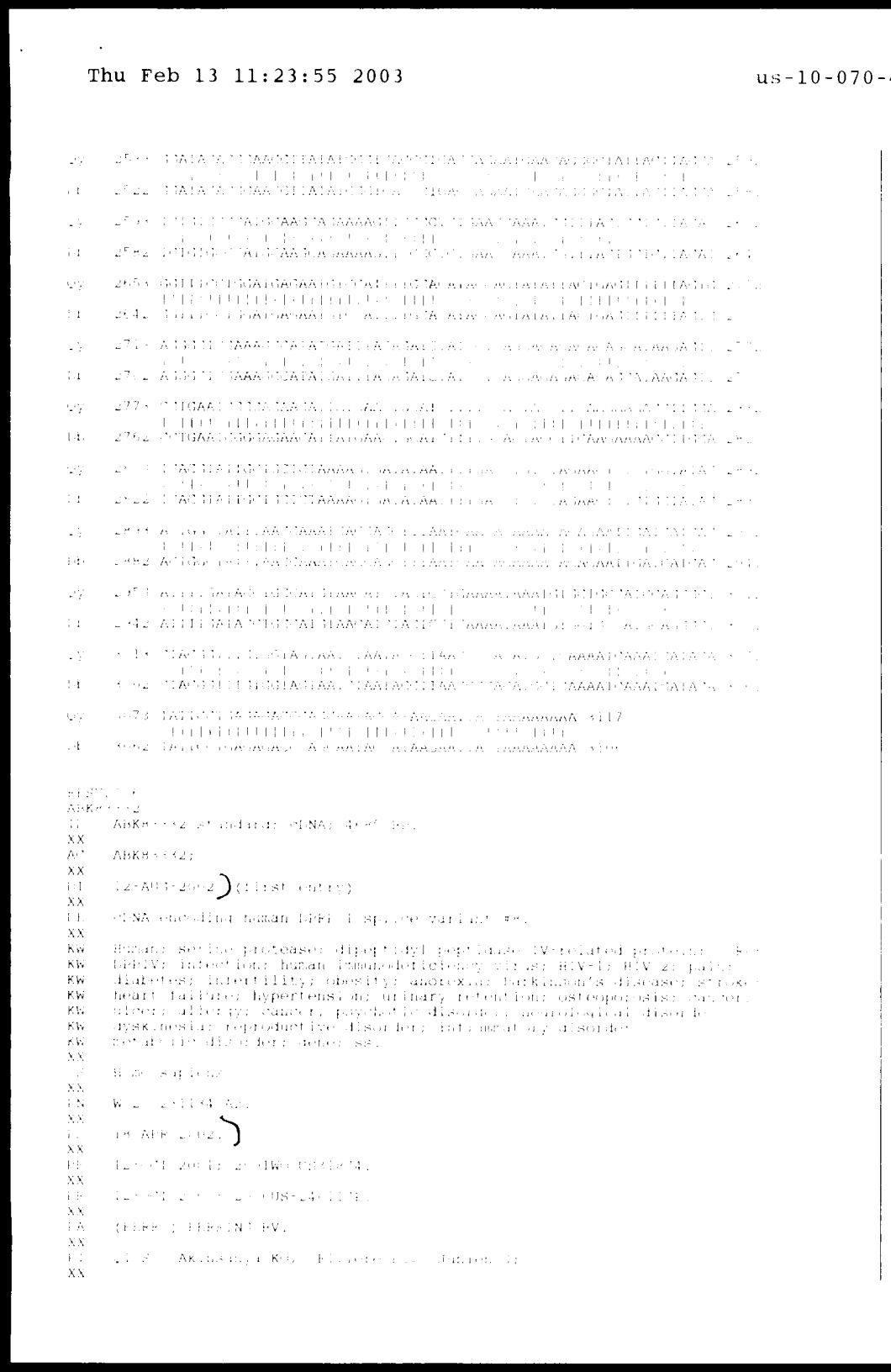


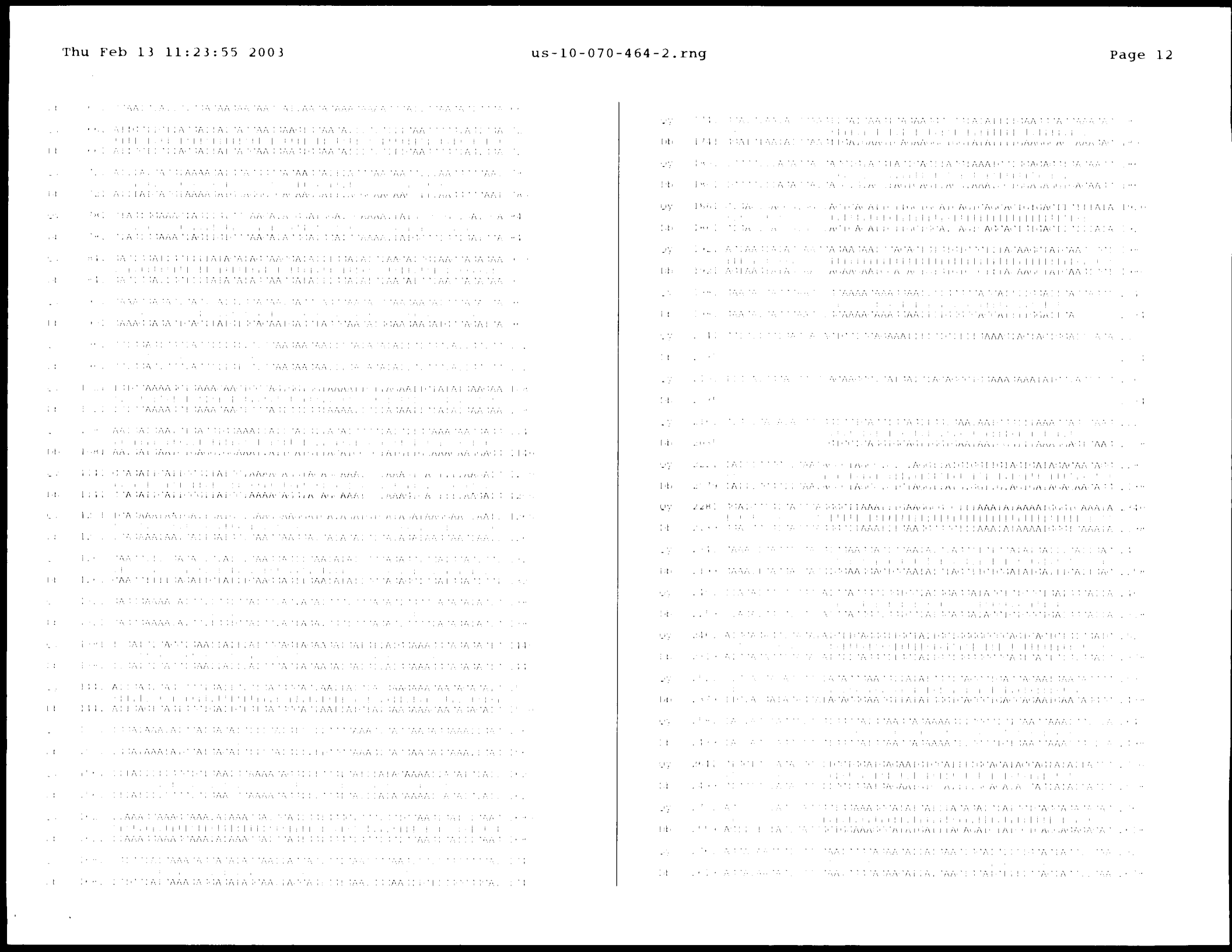


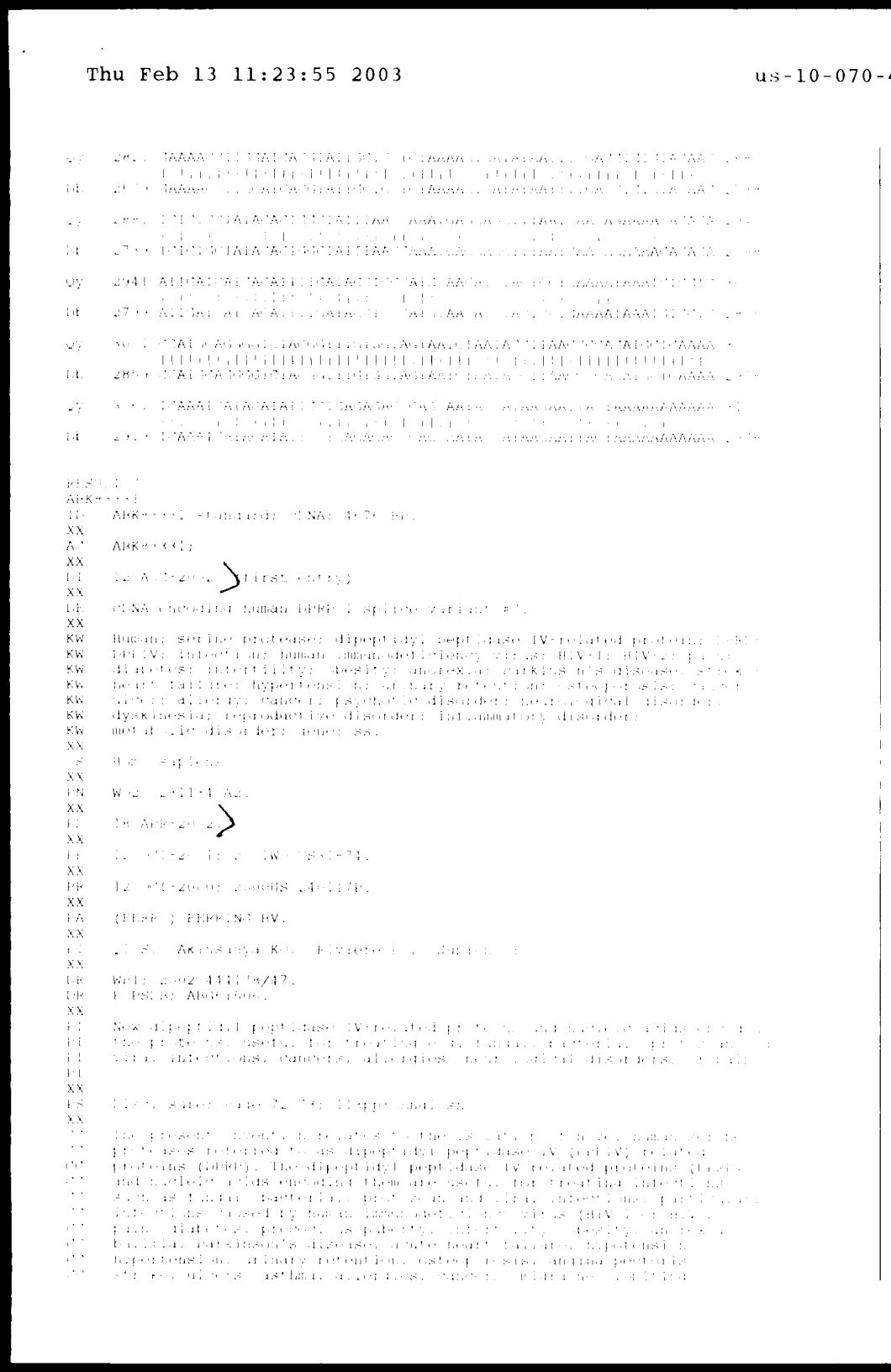


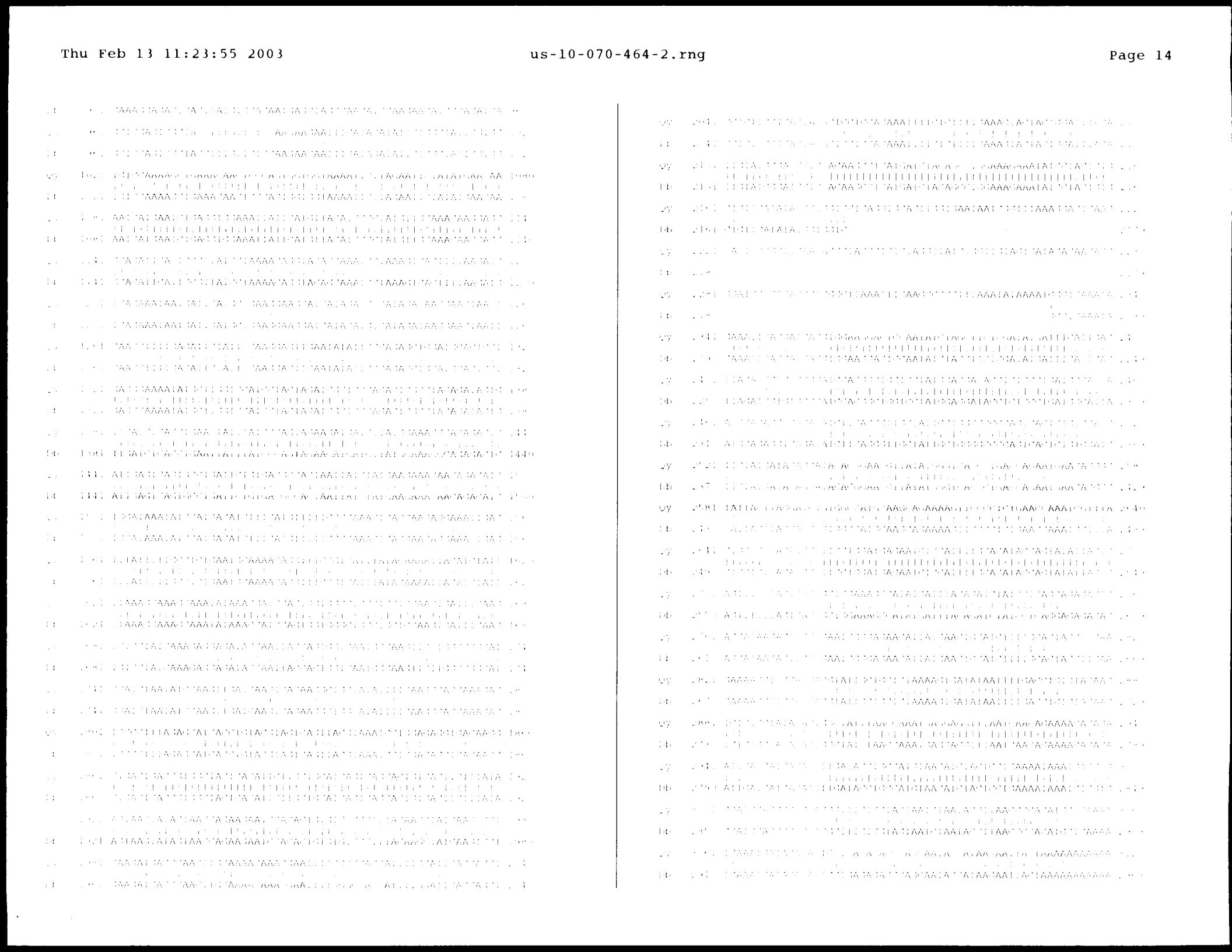












```
RESULT 9
ABK83422
ID   ABK83422 standard; cDNA; 2671 BP.
XX
AC   ABK83422;
XX
DT   12-APR-2002 (first entry)
XX
DE   cDNA encoding human DPPIV related serine protease DPP8-1.
XX
KW   Human; serine protease; dipeptidyl peptidase IV related protein; DPP8;
KW   DPPIV; infection; human immunodeficiency virus; HIV-1; HIV-2; pain;
KW   diabetes; infertility; obesity; anorexia; Parkinson's disease; acute
KW   heart failure; hypertension; urinary retention; osteoporosis; cancer;
KW   ulcer; allergy; cancer; psychotic disorder; neurological disorder;
KW   dyskinesia; reproductive disorder; inflammatory disorder;
KW   metabolic disorder; gene; cs.
XX
OS   Homo sapiens.
XX
PN   WO200241874-A2.
XX
PD   30-MAY-2002.
XX
PF   12-NOV-2001; 2001WO-US51874.
XX
PR   13-NOV-2000; 2000US-248117P.
XX
PA   (FERR ) FERRING BV.
XX
PI   Li S, Akinsanya KO, Bleicher KB, Lazarus JJ;
XX
DR   WPI; 2002-441178/47.
DR   P-PSDB; ABQ15591.
XX
PT   New dipeptidyl peptidase IV related proteins and nucleic acids encoding
PT   the proteins, useful for treating e.g. fungal, bacterial, protozoan and
PT   viral infections, cancers, allergies, neurological disorders, or pain
PT   -
XX
PS   Claim 1; Page 54-54; 113pp; English.
XX
CC   The present invention relates to the isolation of novel human serine
CC   proteases referred to as dipeptidyl peptidase IV (DPPIV)-related
CC   proteins (DPRP). The dipeptidyl peptidase IV-related proteins (DPRP)
CC   and nucleic acids encoding them are useful for treating infections
CC   such as fungal, bacterial, protozoan and viral infections, particularly
CC   infections caused by human immunodeficiency virus (HIV-1 or HIV-2),
CC   pain, diabetes, precocious puberty, infertility, obesity, anorexia,
CC   bulimia, parkinson's disease, acute heart failure, hypotension,
CC   hypertension, urinary retention, osteoporosis, angina pectoris,
CC   stroke, ulcers, asthma, allergies, cancers, migraine, vomition,
CC   psychotic and neurological disorders (e.g. anxiety, dementia, a
CC   schizophrenia), and dyskinesias. These may also be used in discovering
CC   therapeutic agents for the treatment of reproductive, inflammatory, and
CC   metabolic disorders. ABK83422-ABK83471 encode human DPRP proteins.
XX
SQ   Sequence 2671 BP; 805 A; 524 C; 594 G; 748 T; 0 other;

  Query Match             84.8%;  Score 2643;  DB 24;  Length 2671;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 2648;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

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Qy     501 GACATCGACGCCTTCAAGAACAAGGAGGTGCACATCGAGTTCCACCTCATCAAGAAC 560
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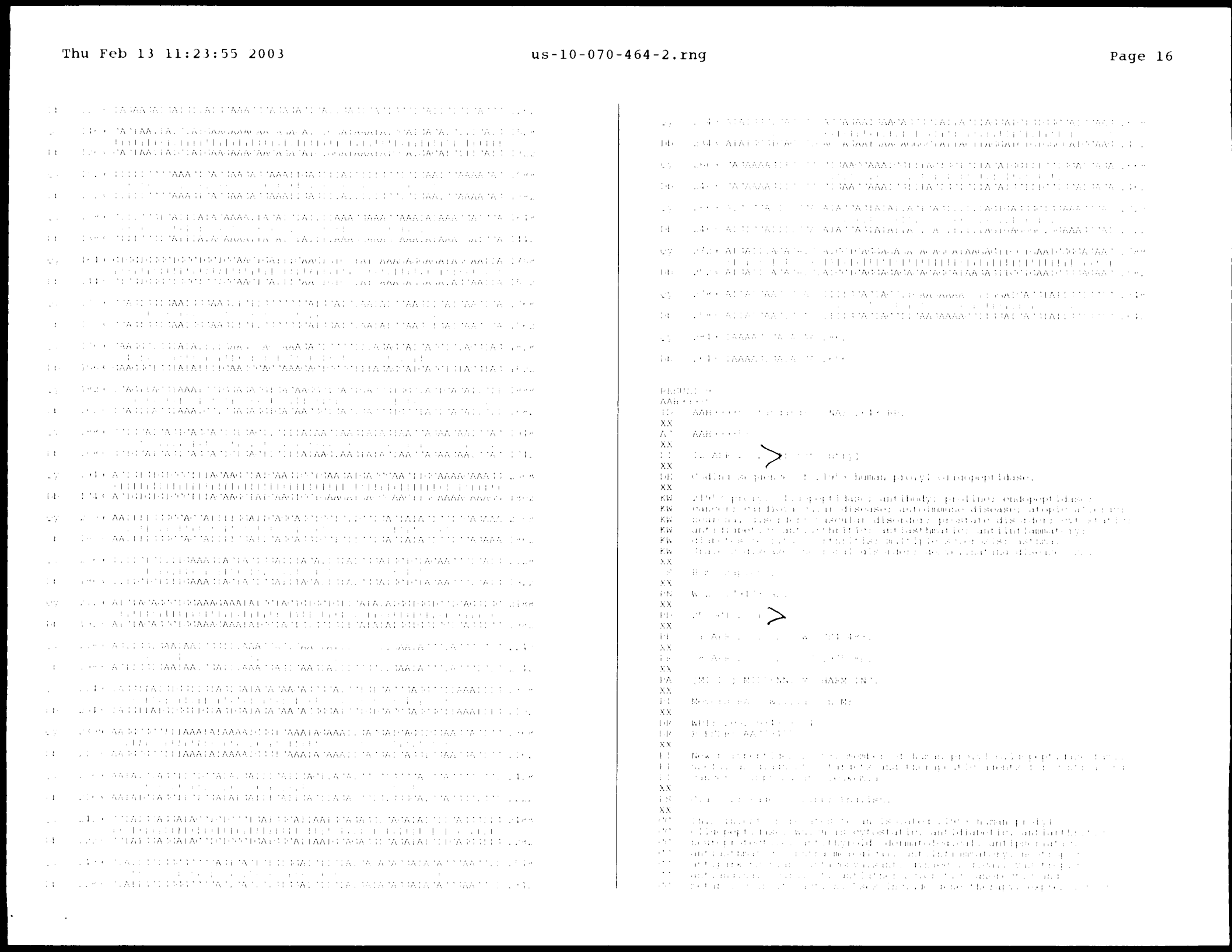
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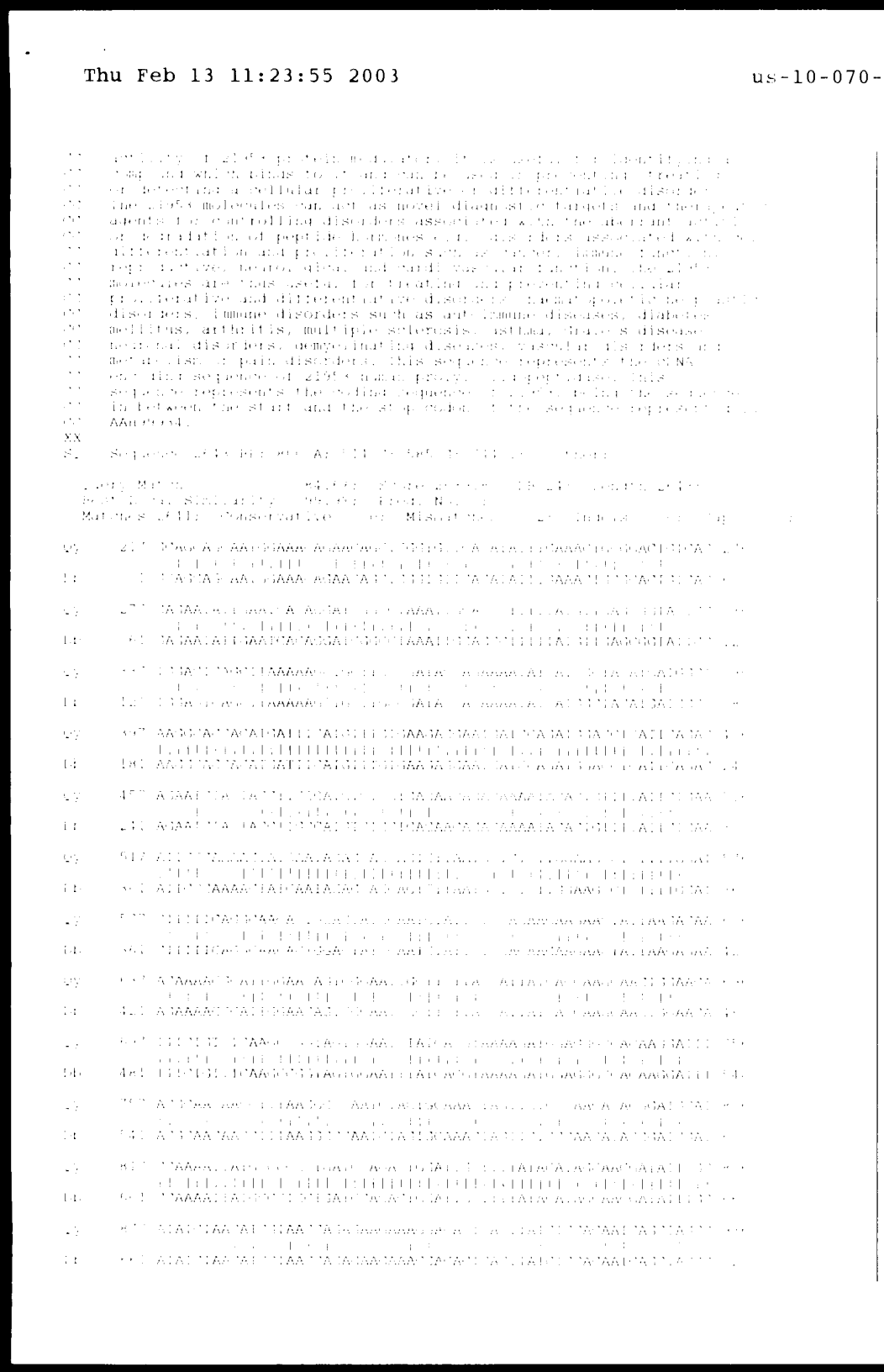
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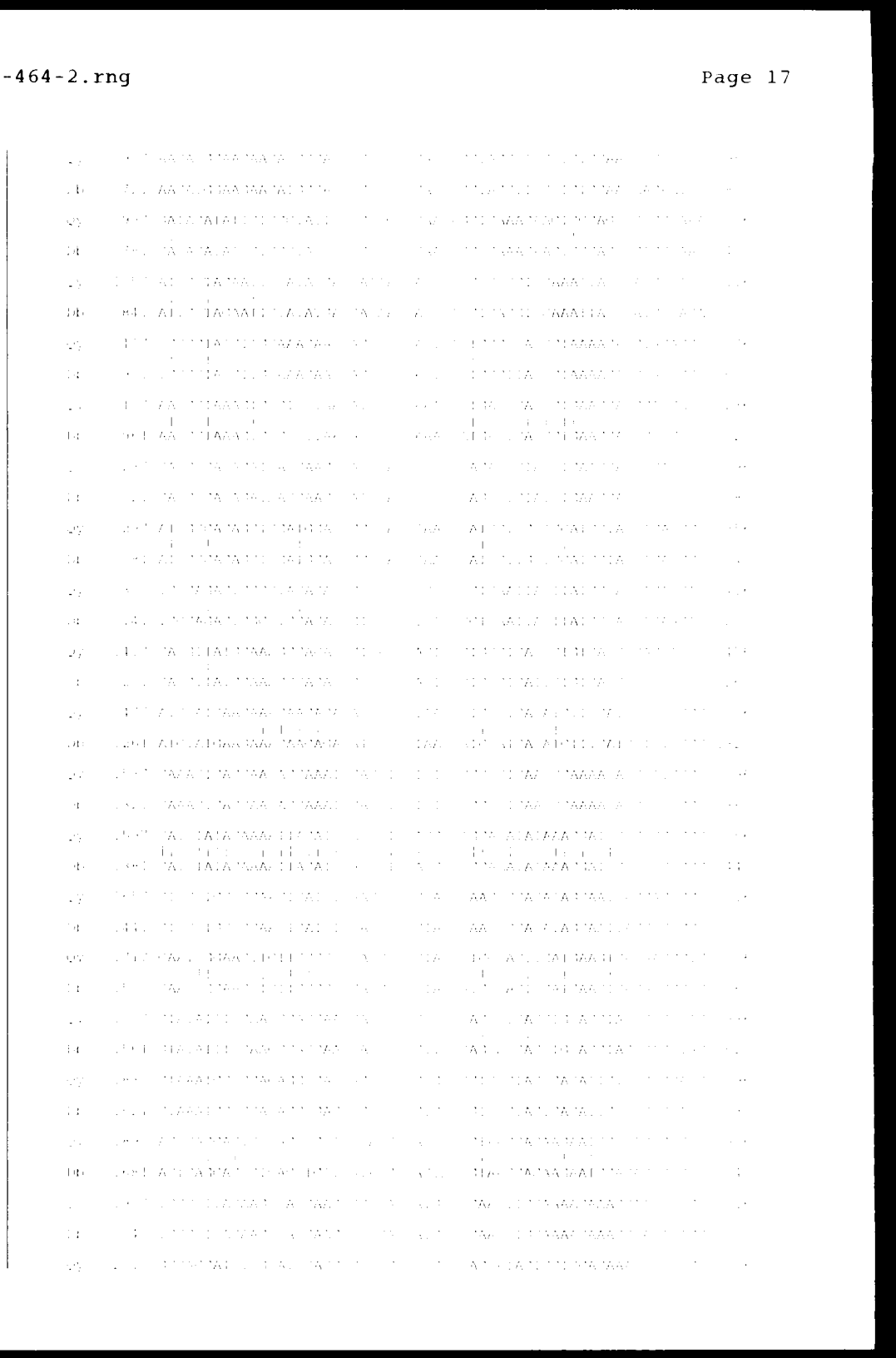
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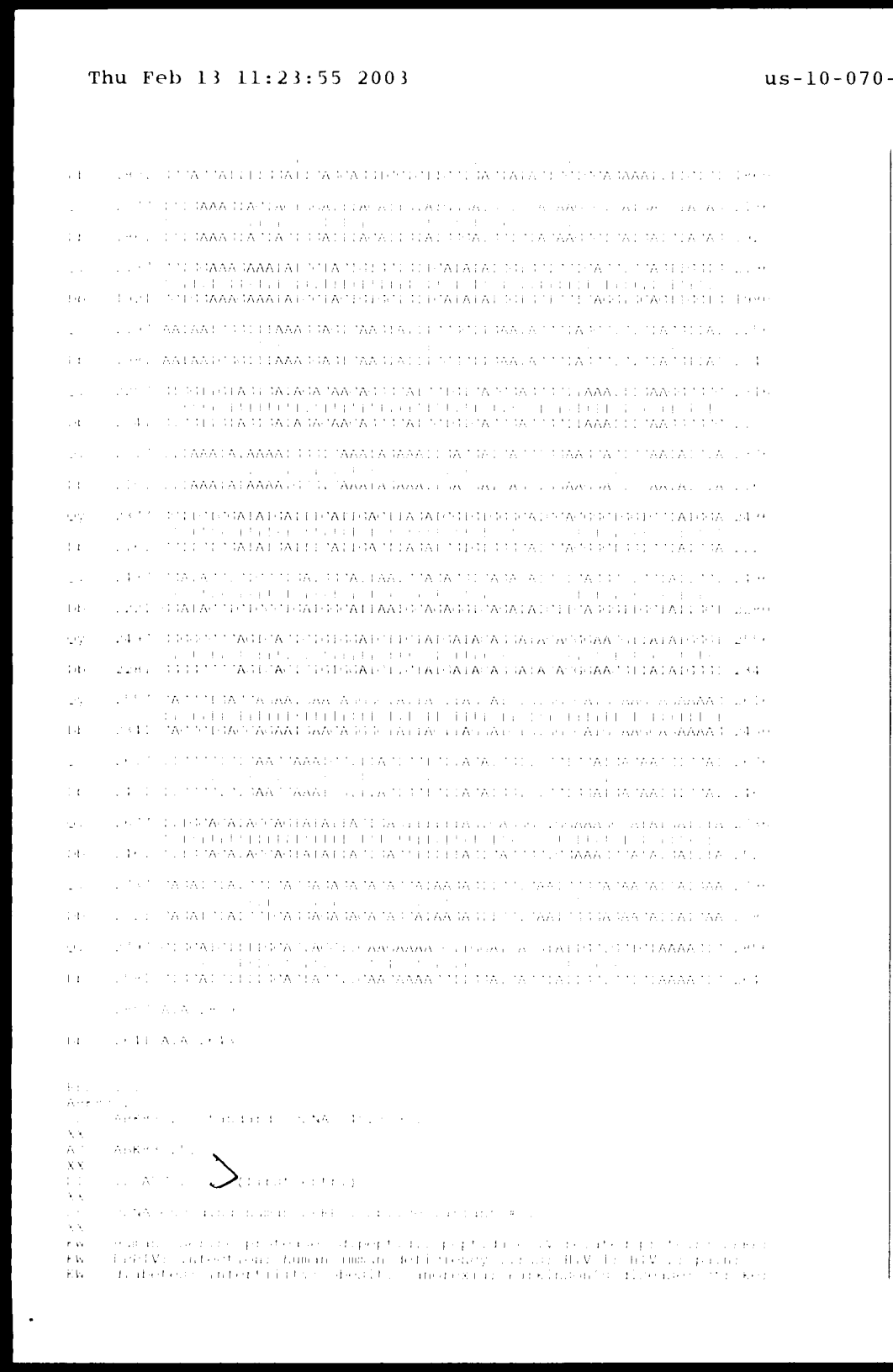
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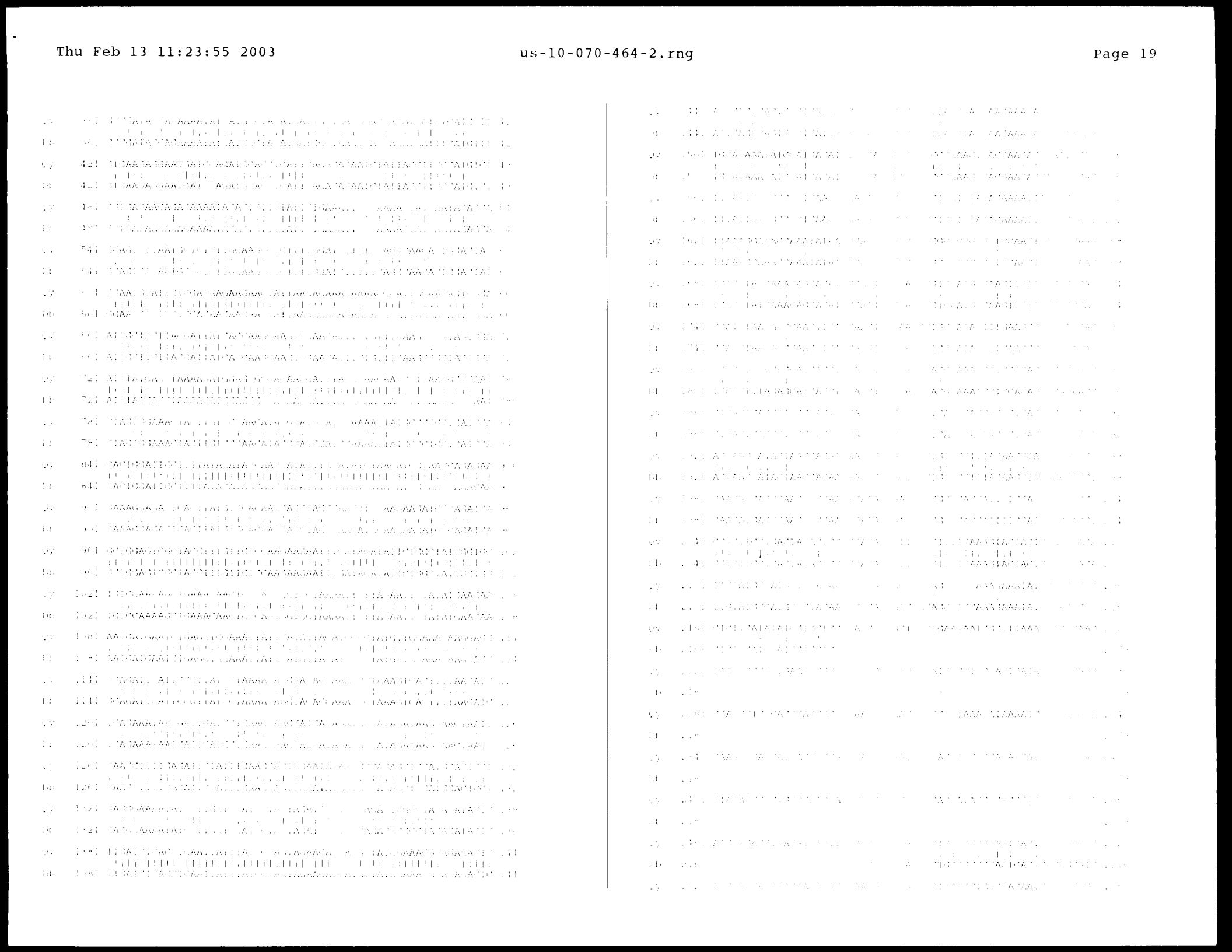
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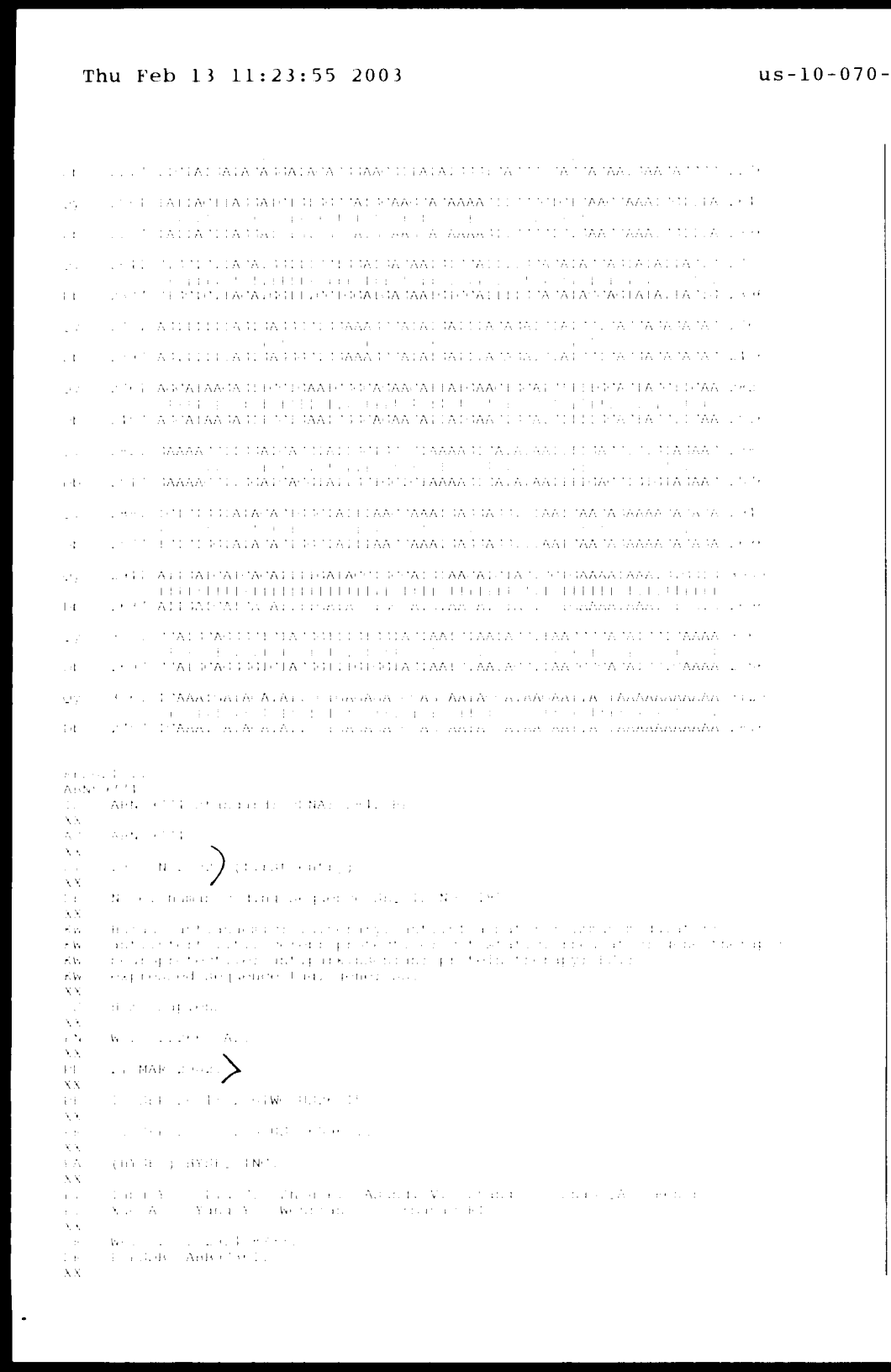


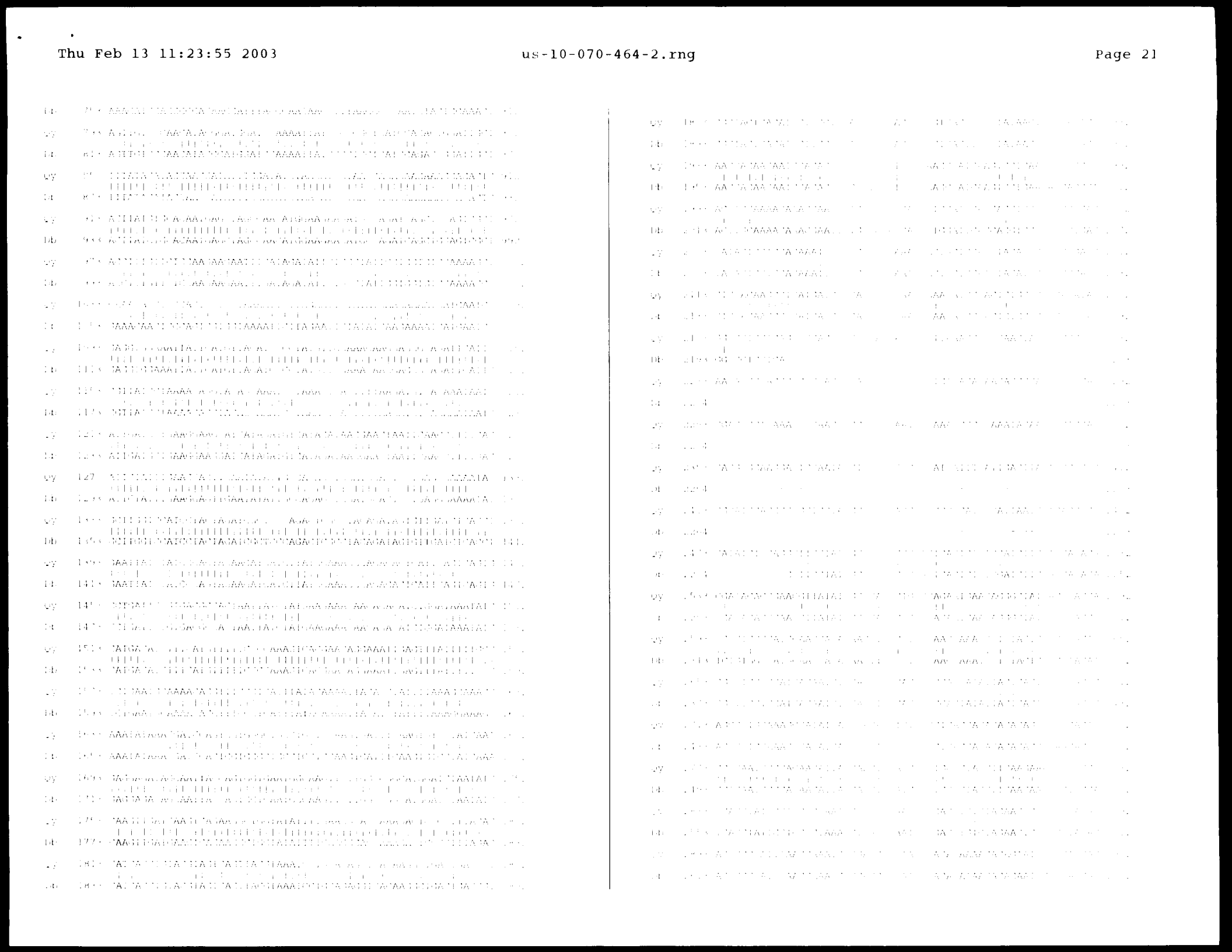


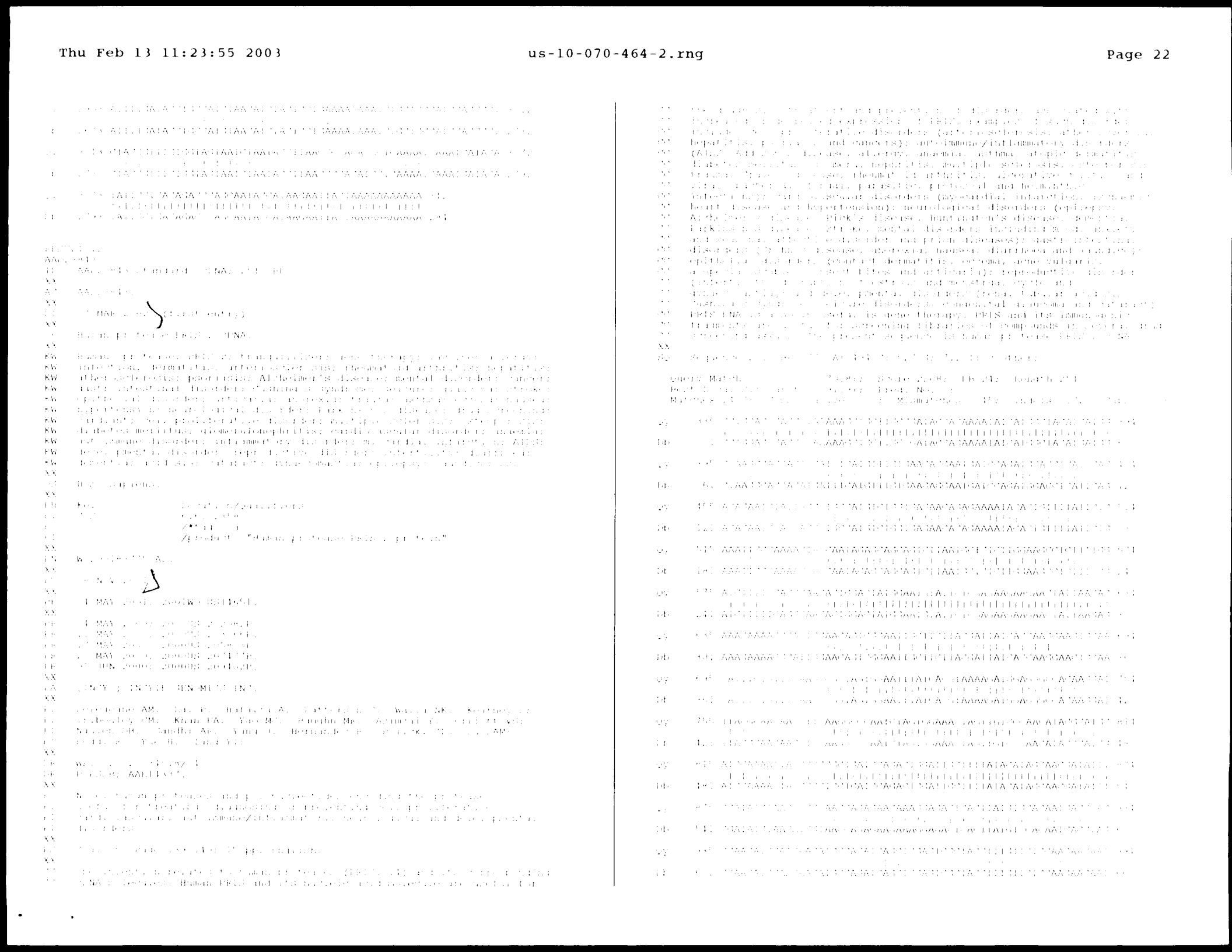


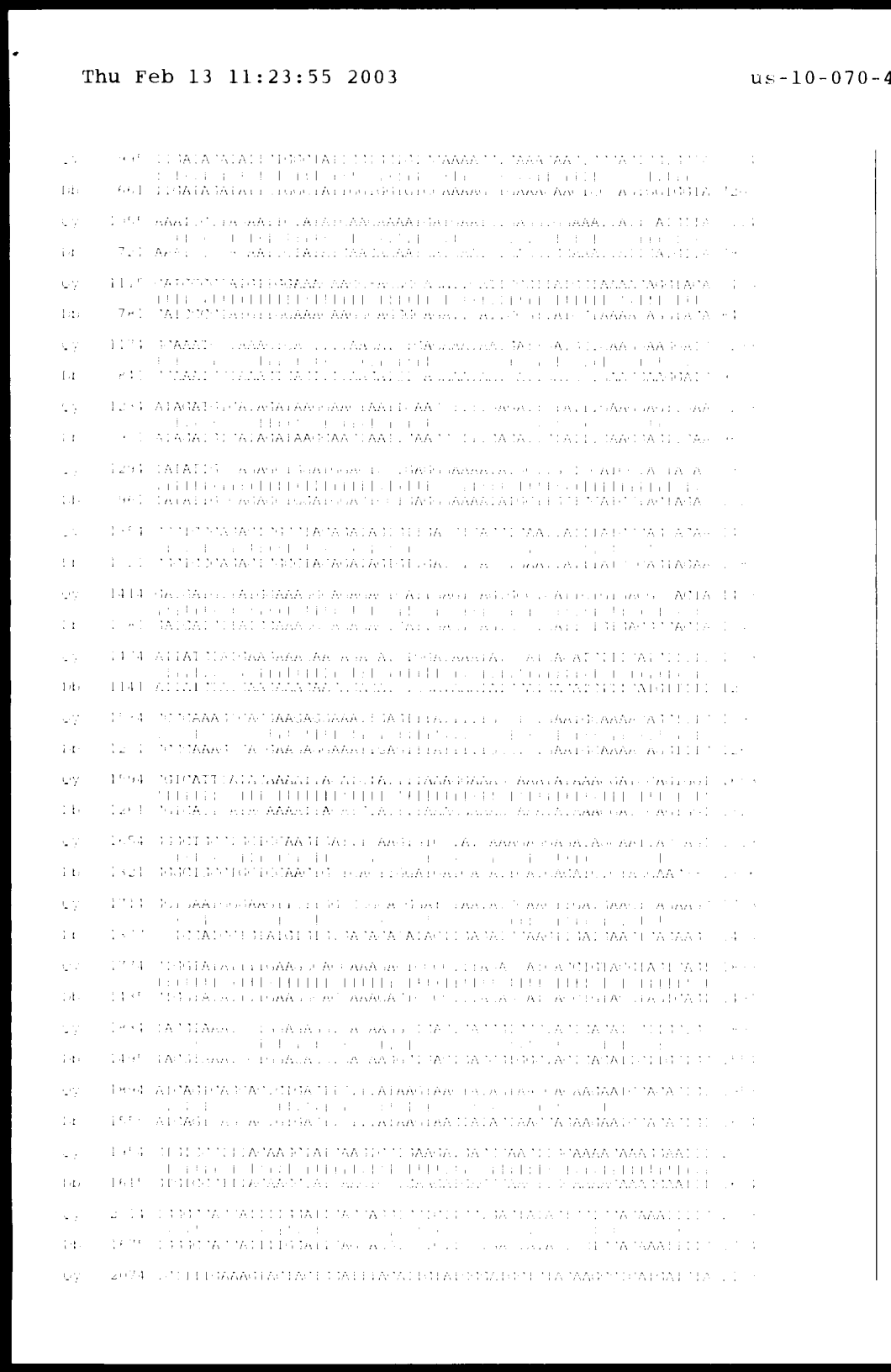


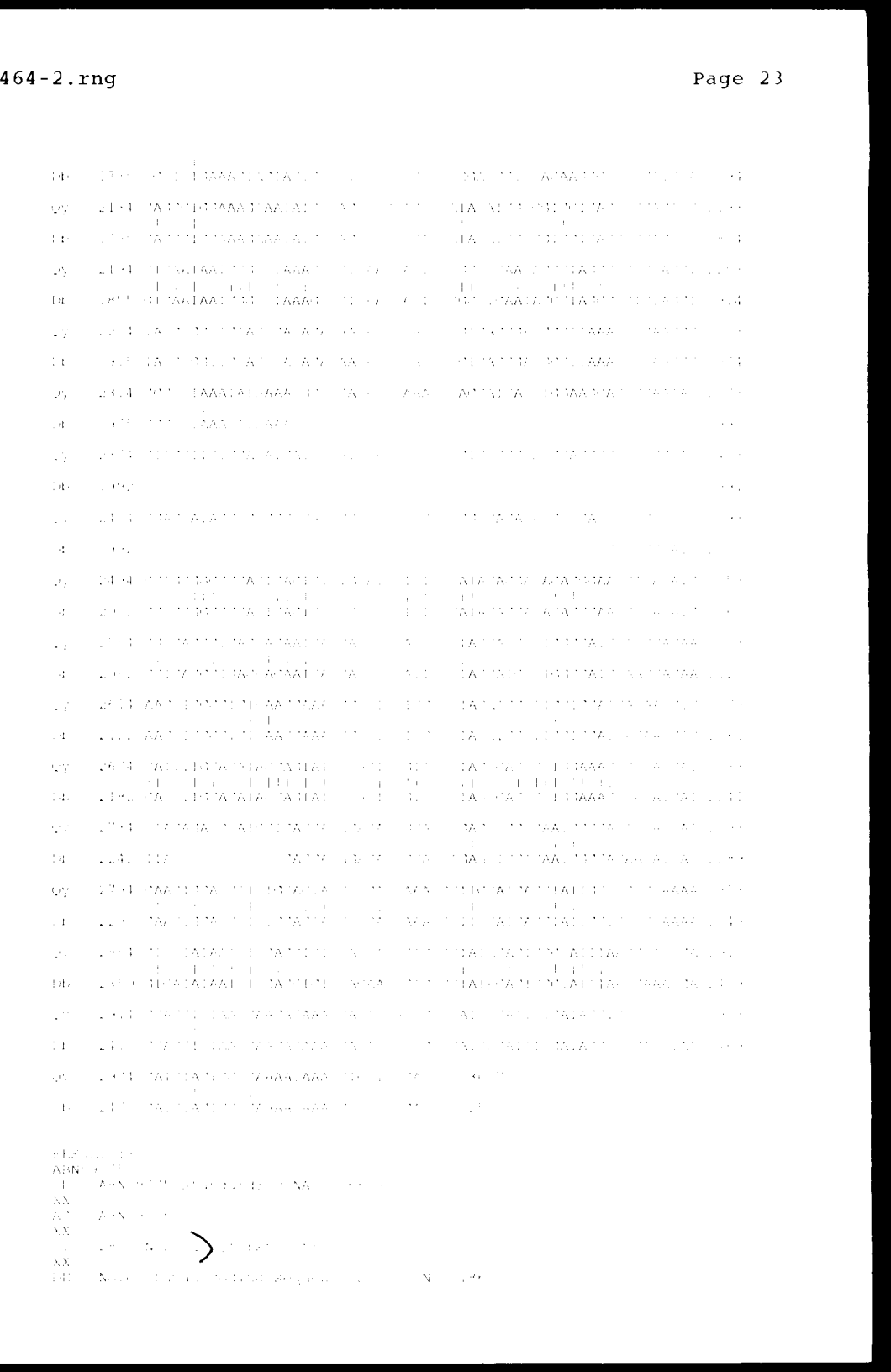


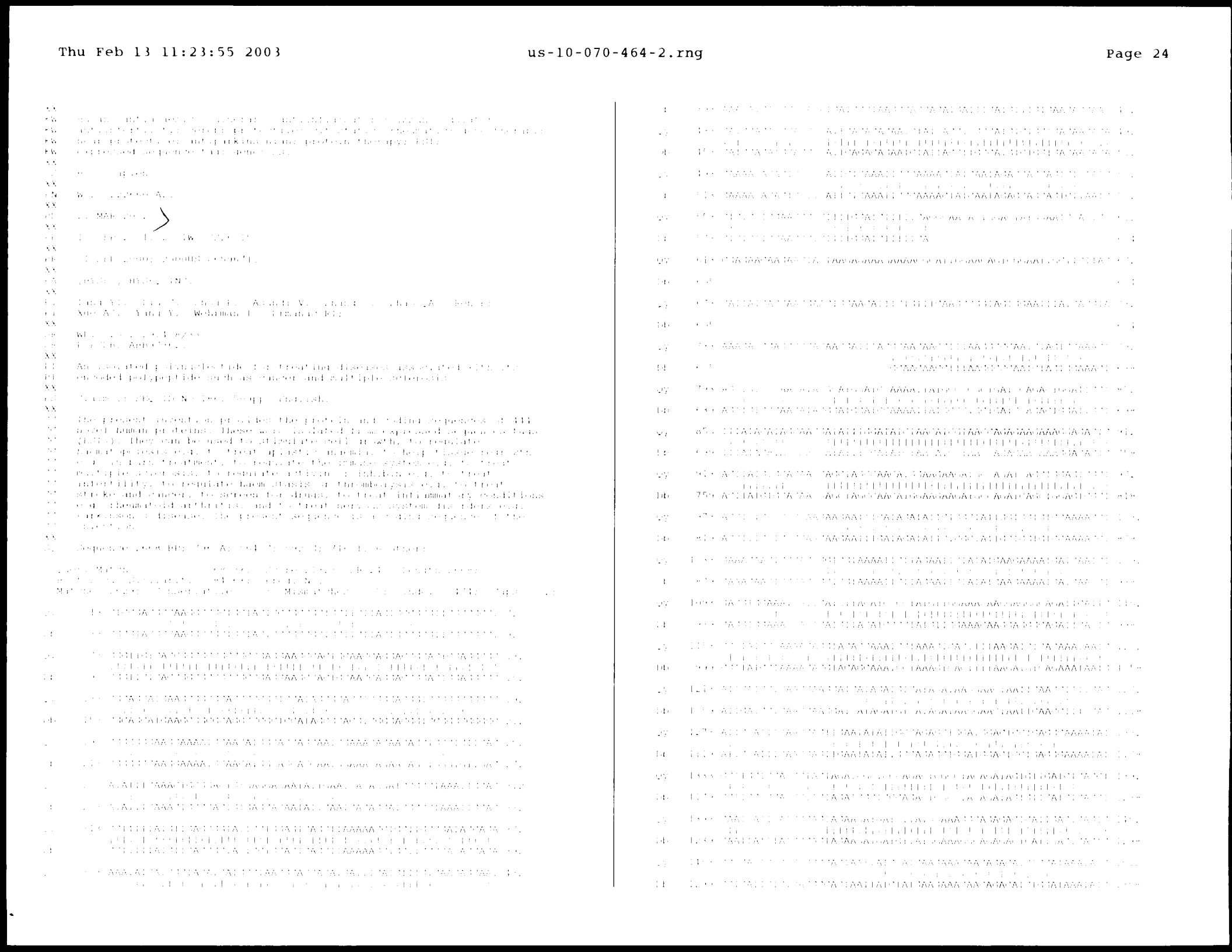


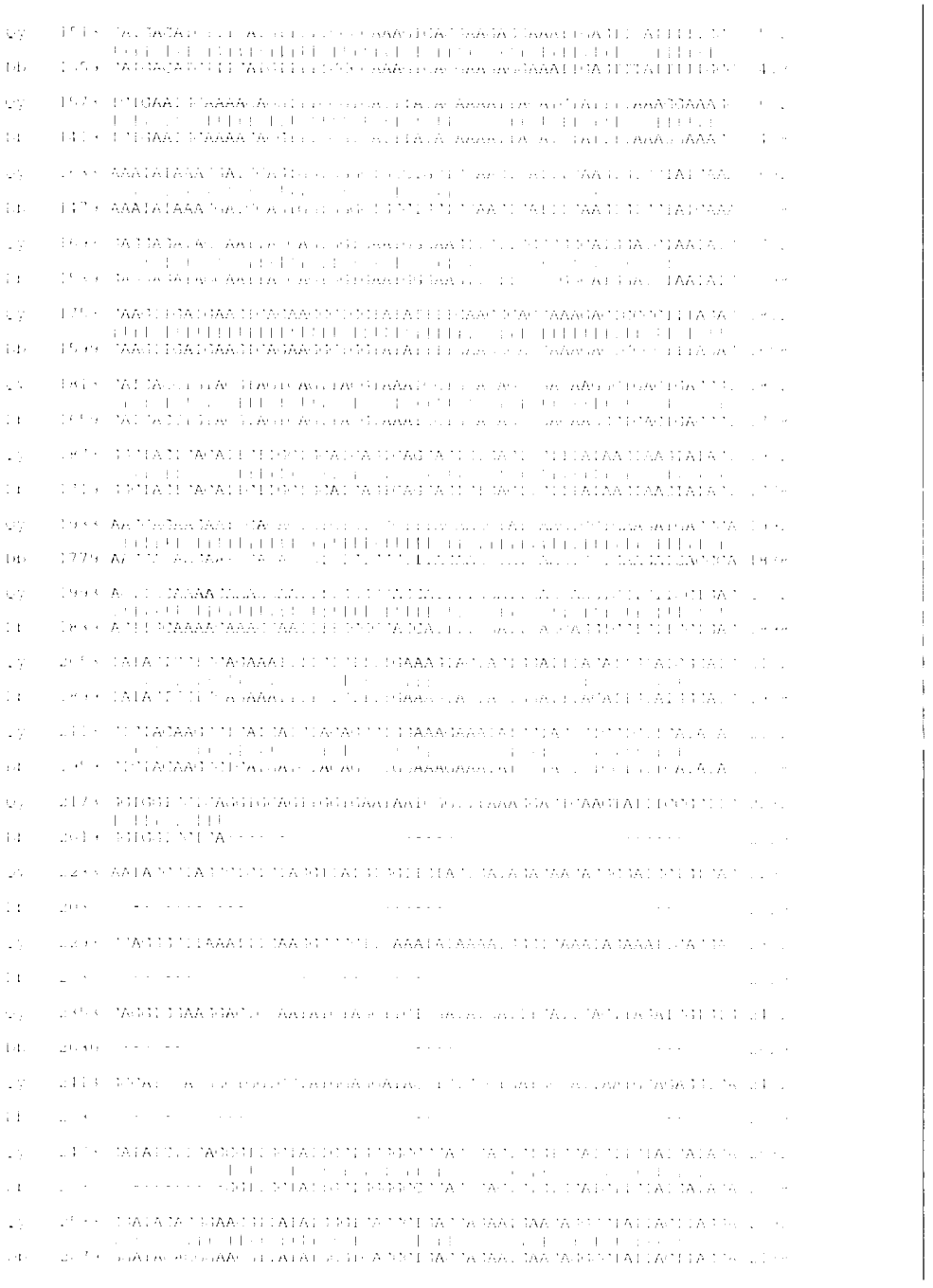


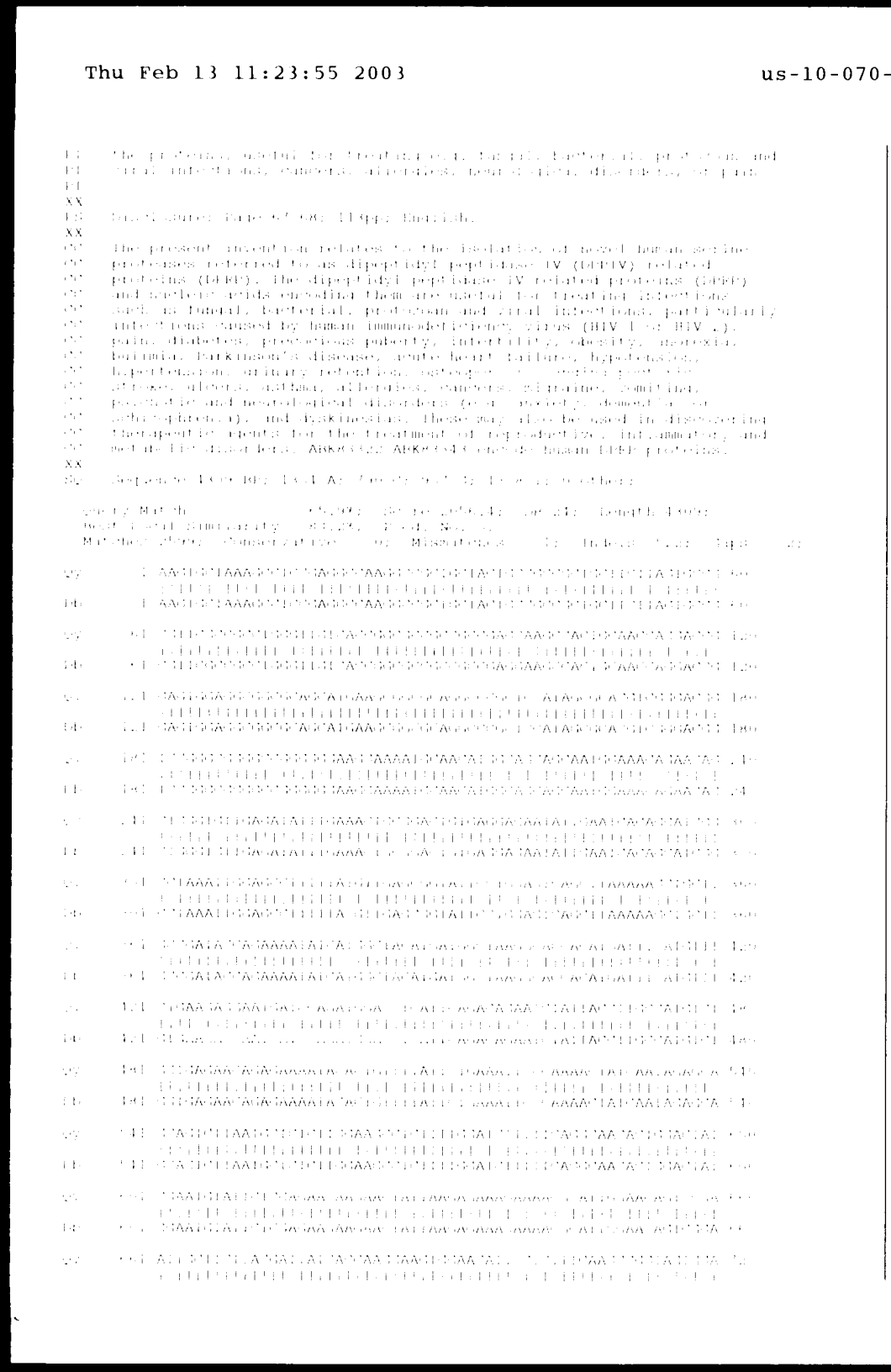


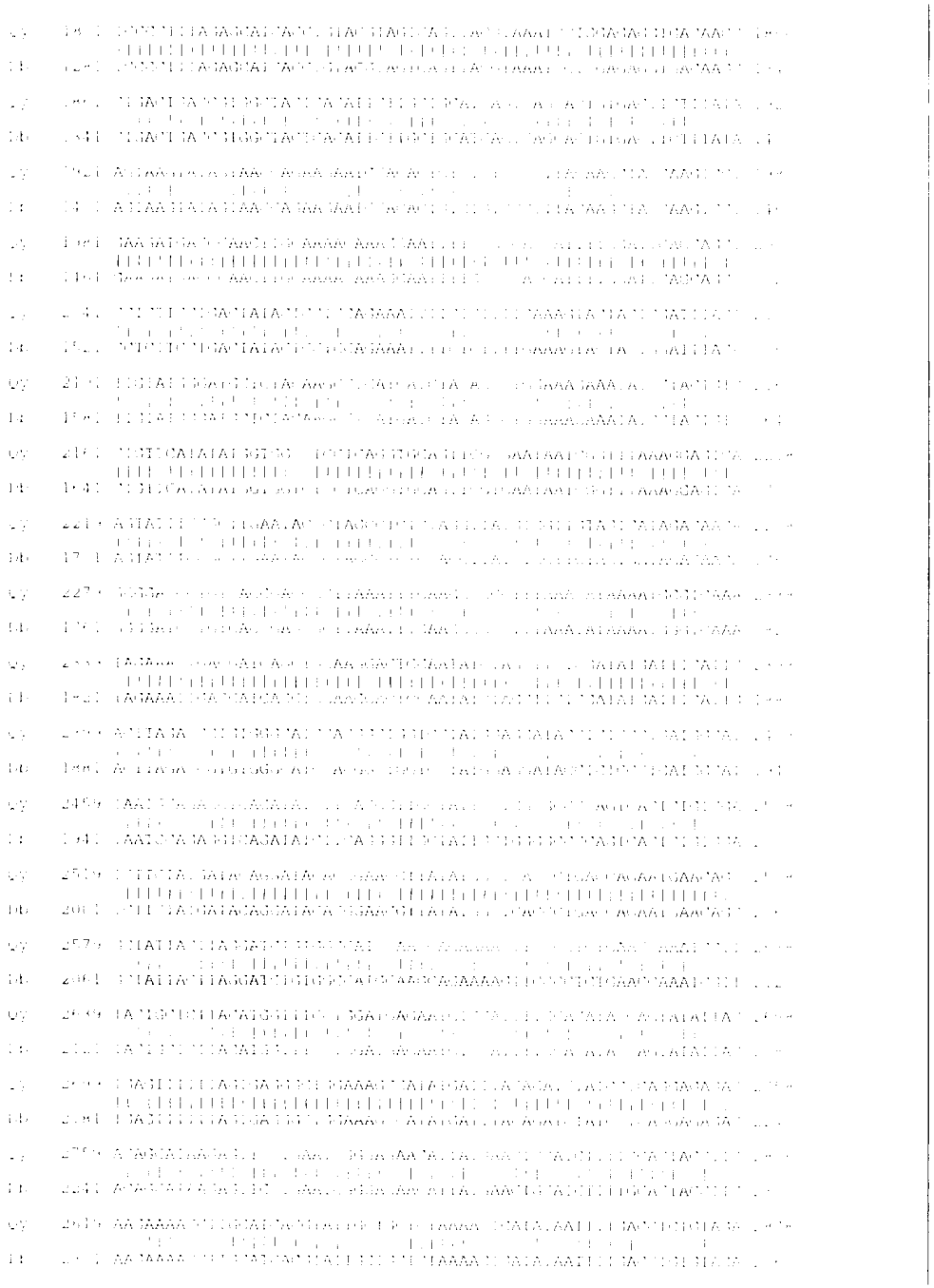


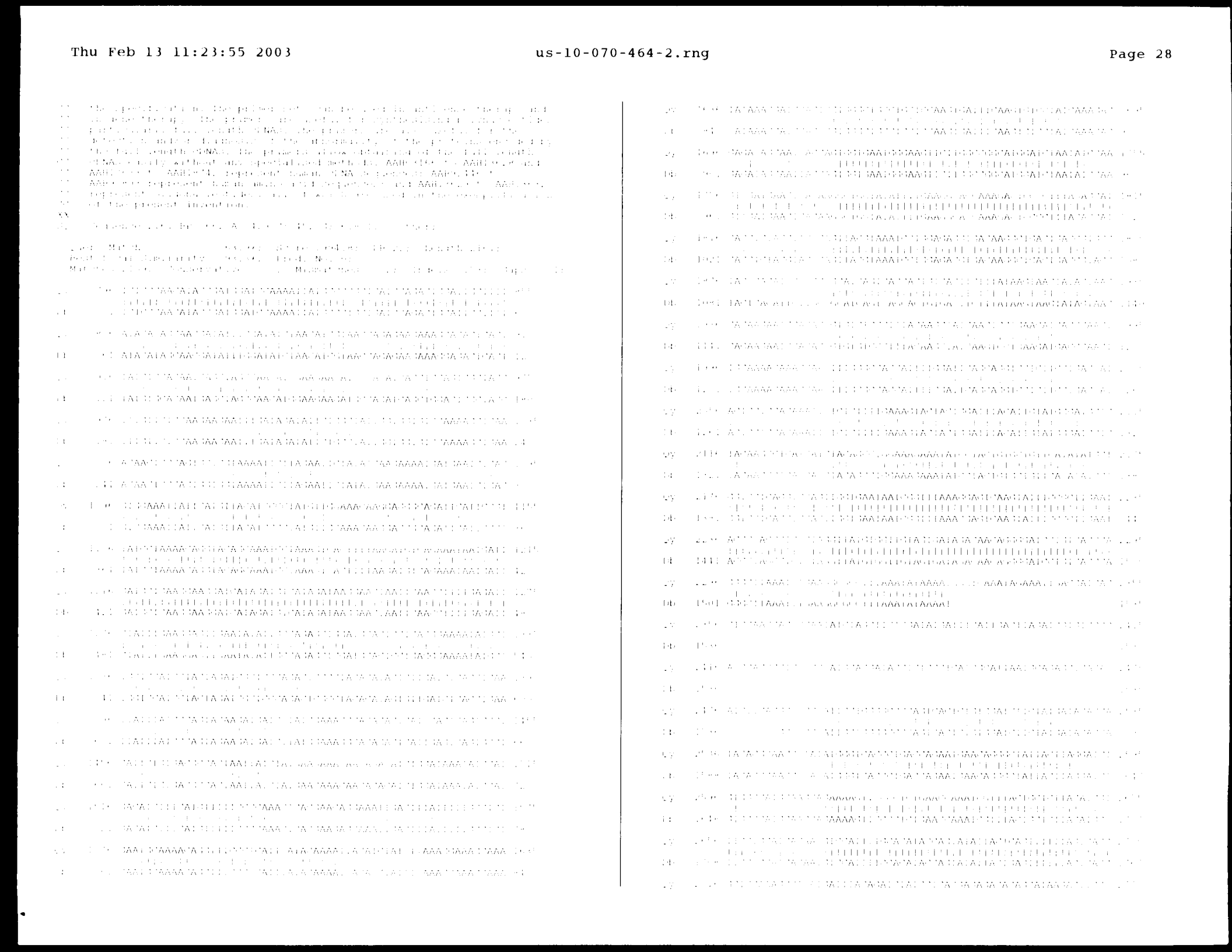












Search Completed: February 9, 2003, 04:39:21

Copyright (c) 1993 - 2003 Compugen Ltd.

Run on: February [illegible] 2003 [illegible]

Title: US-10-070-464-2

Sequence: [illegible]

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Listing first [illegible] summaries

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3: om_estlbc:*
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7: om_estlv:*
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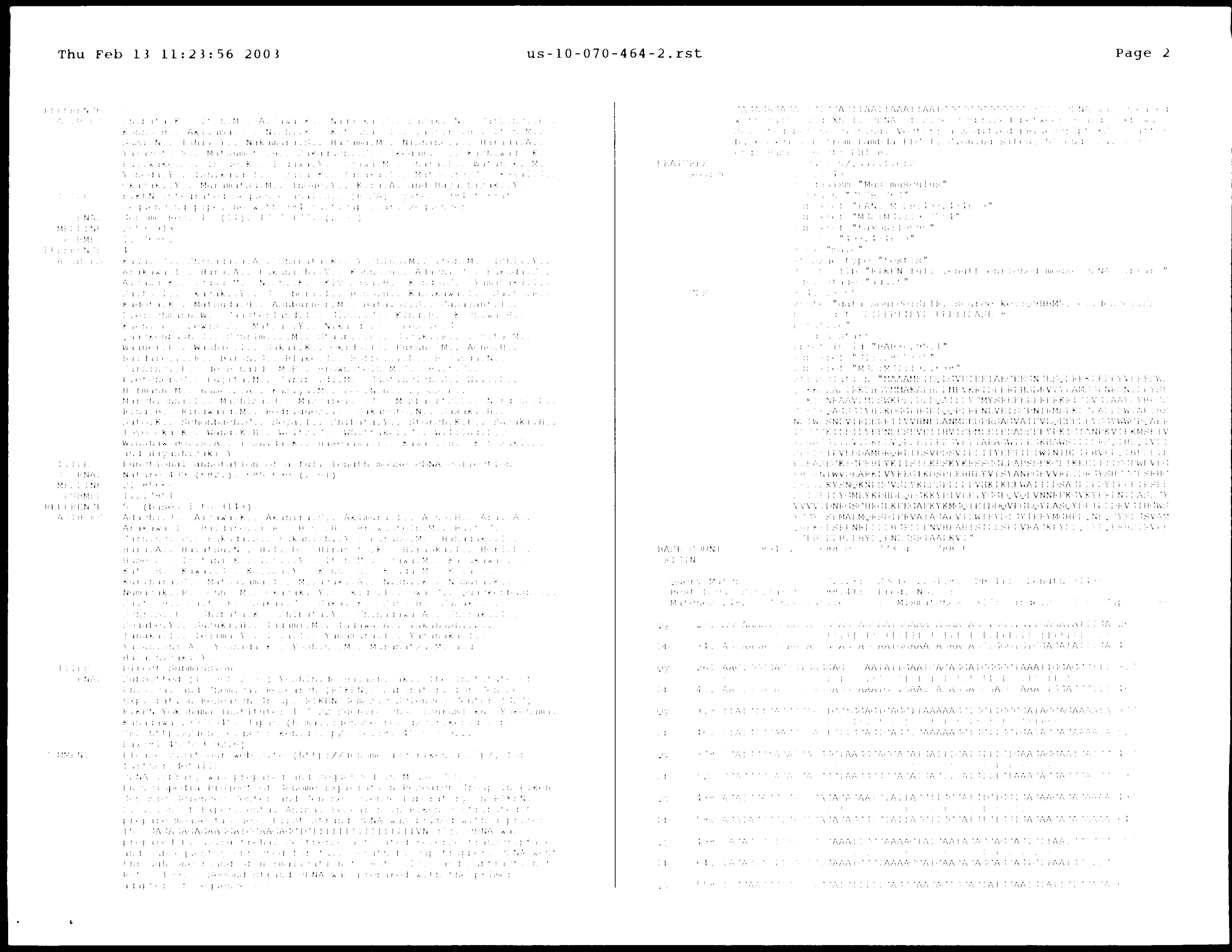
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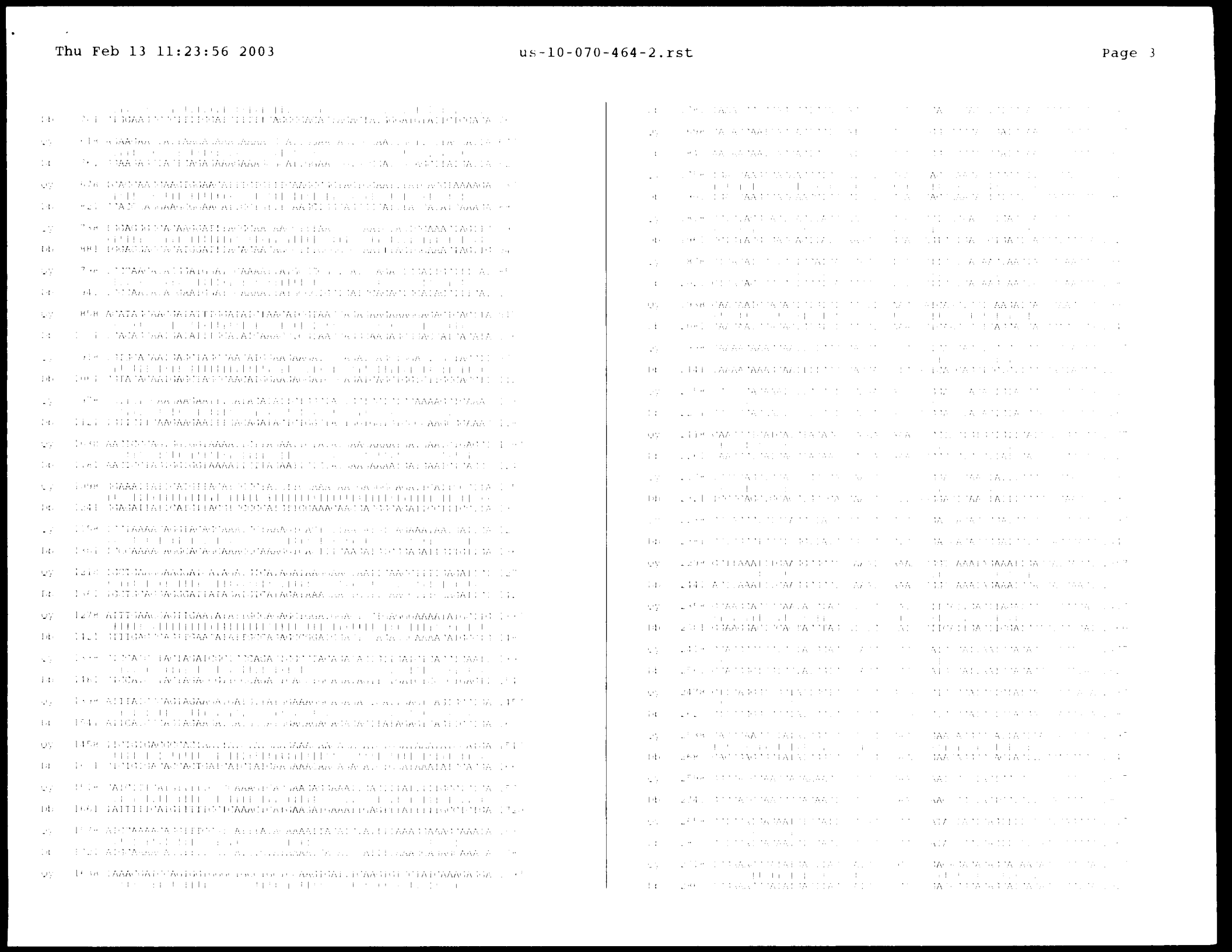
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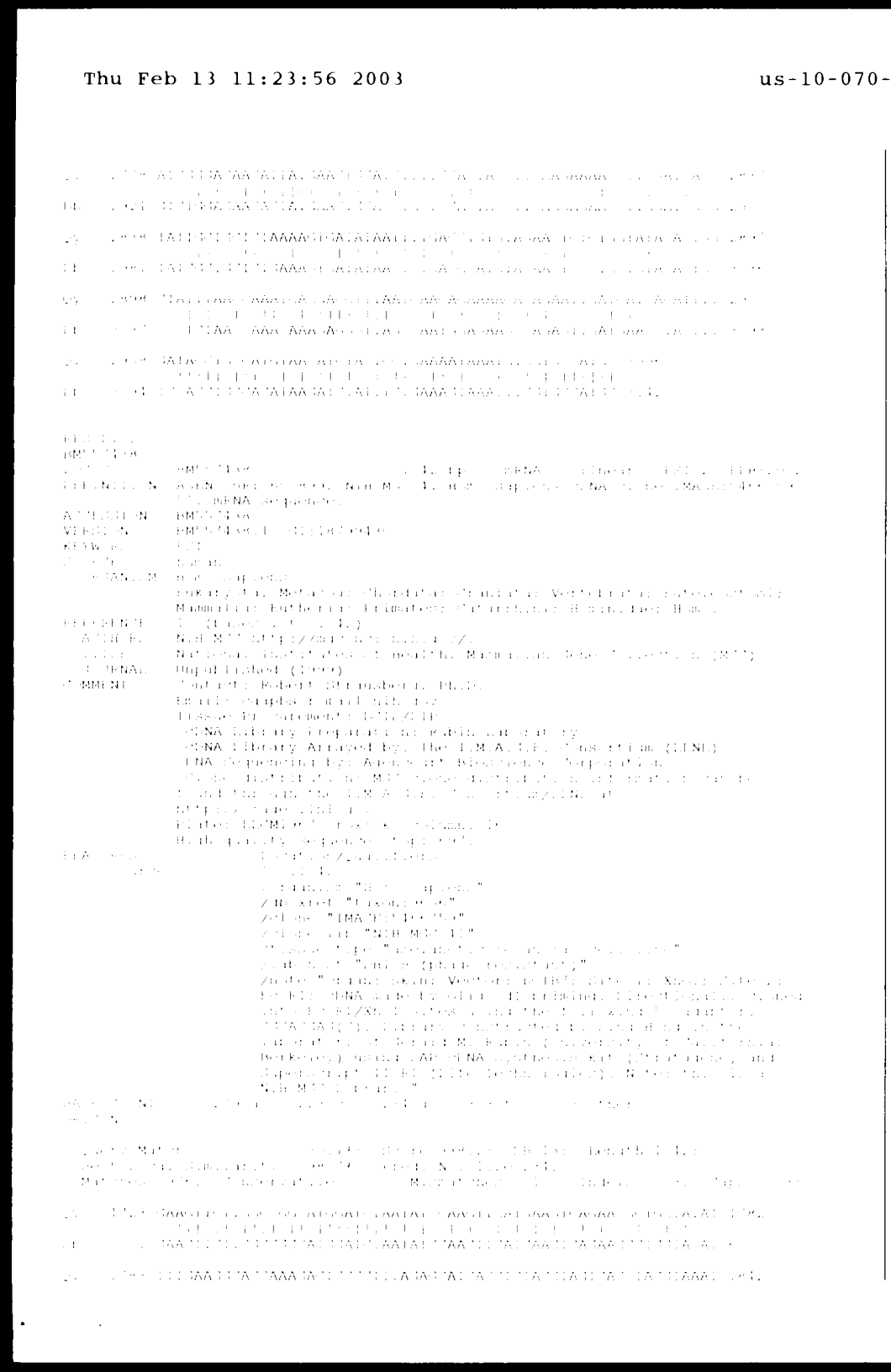
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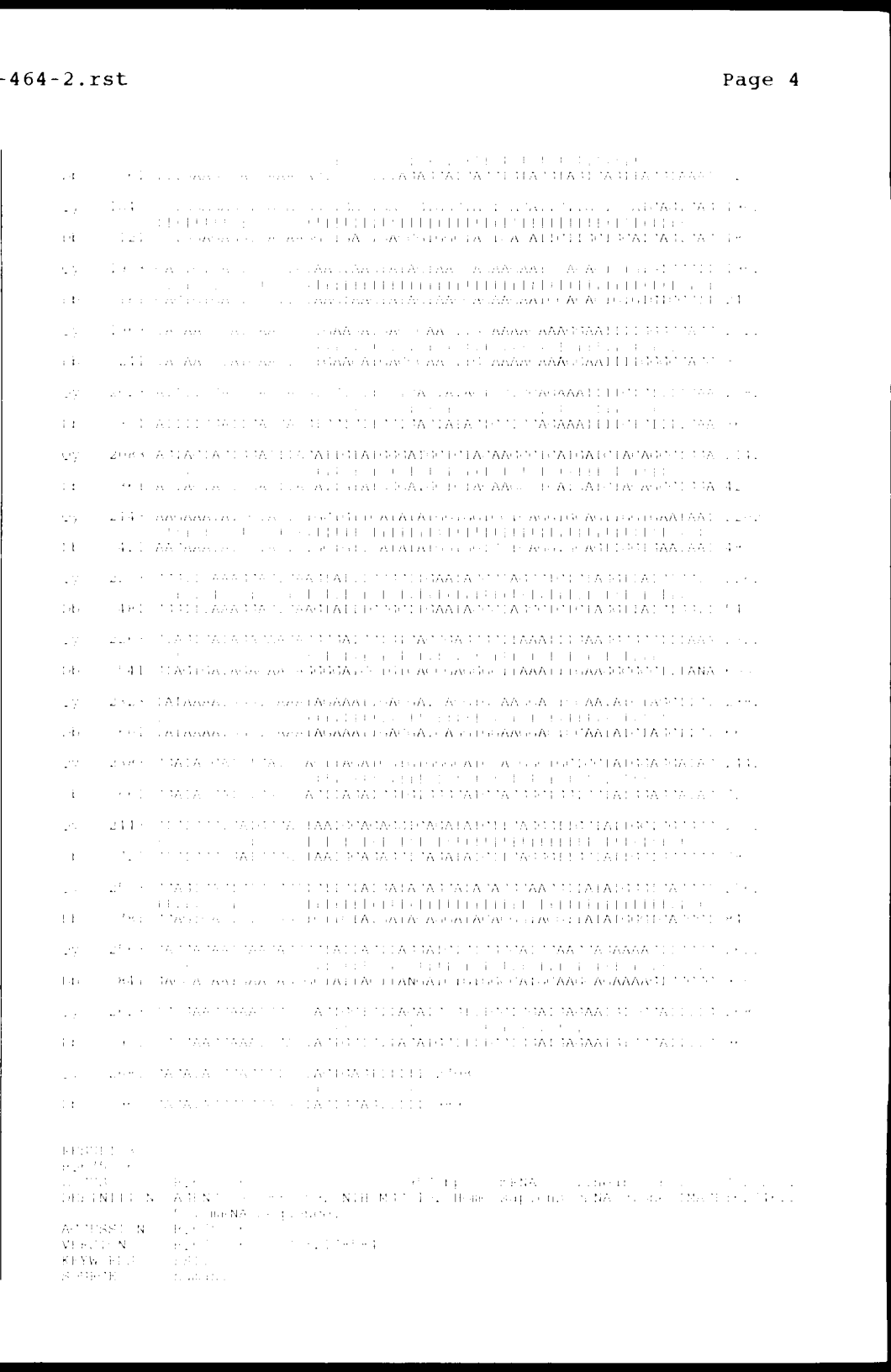
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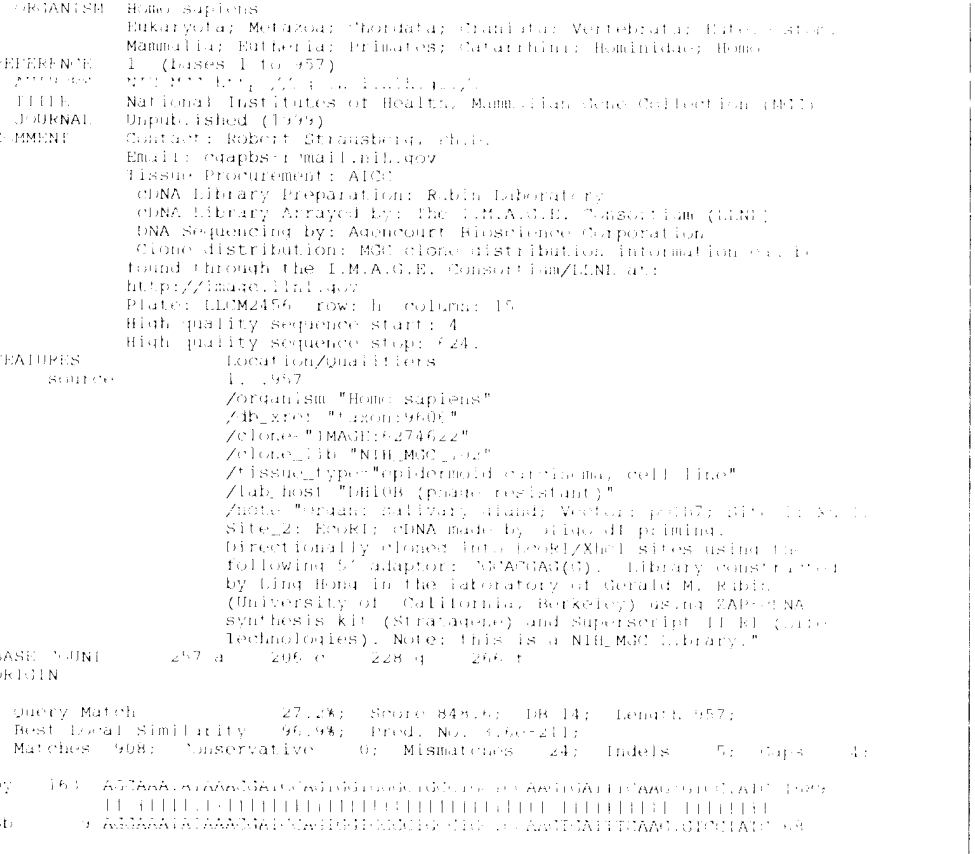


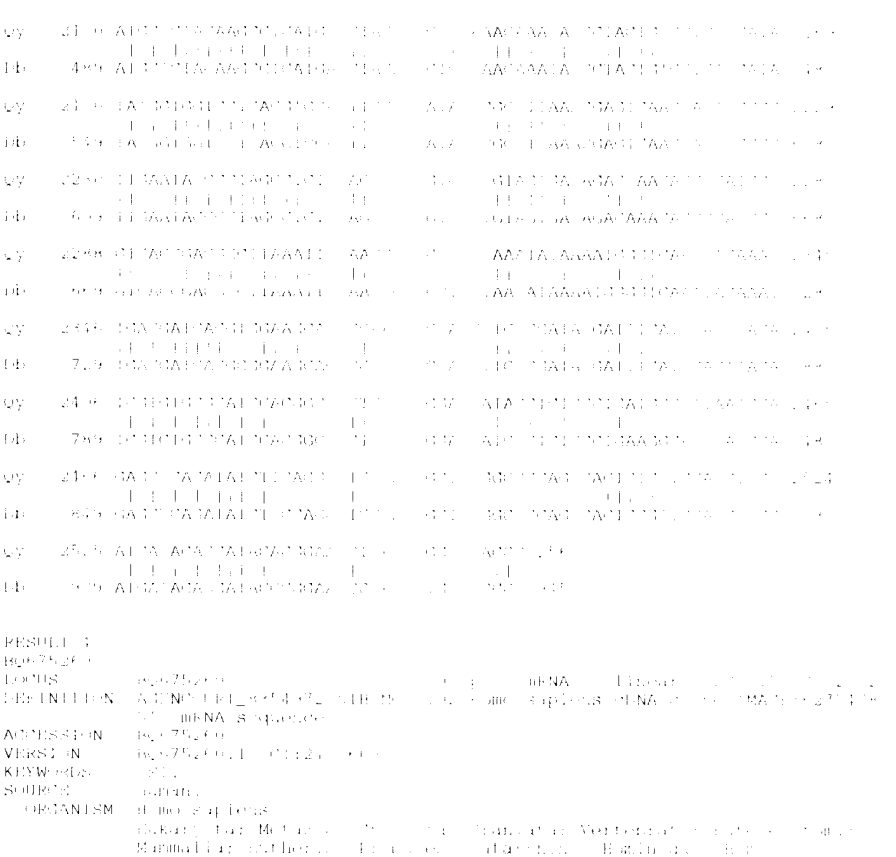


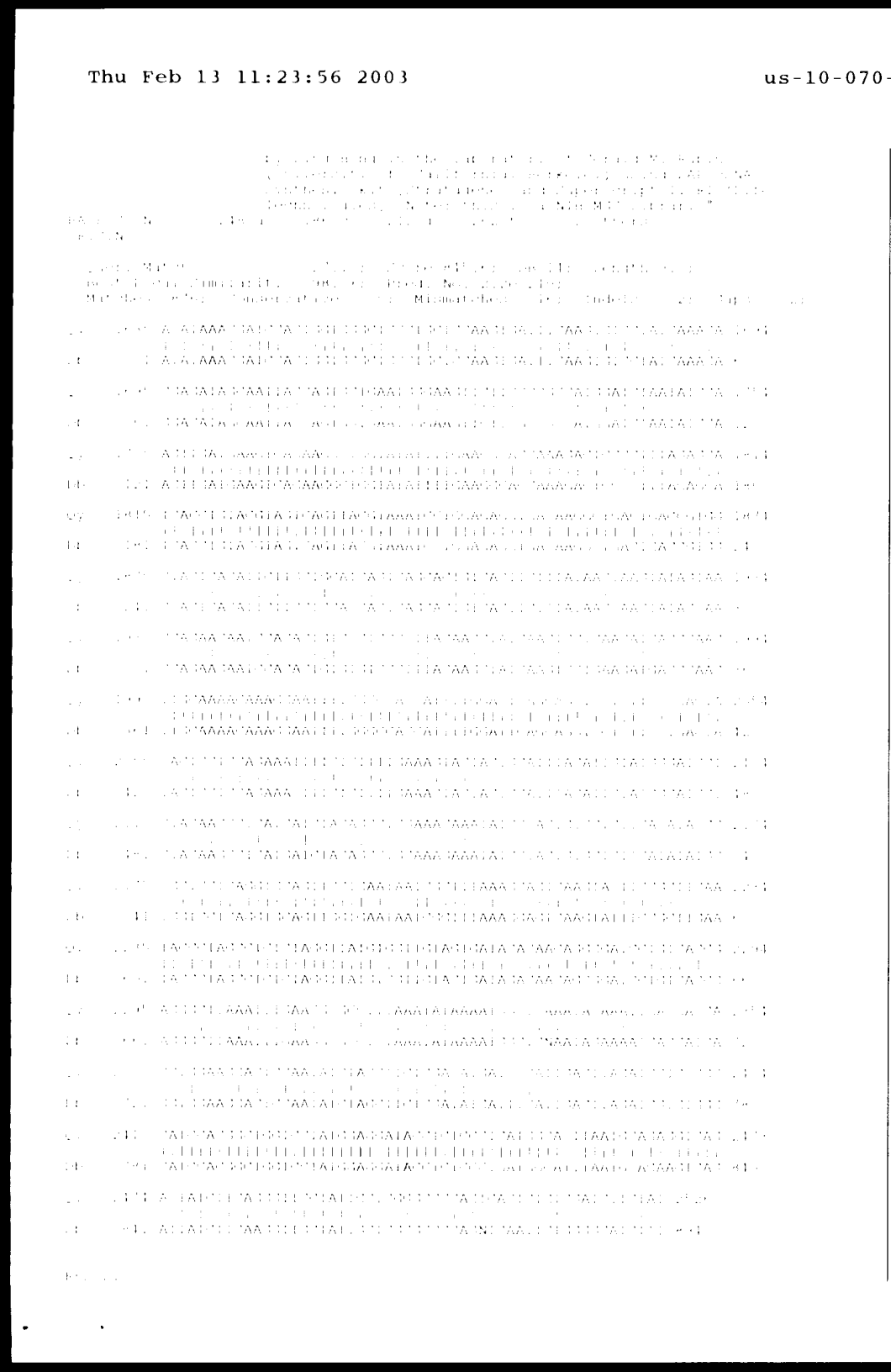


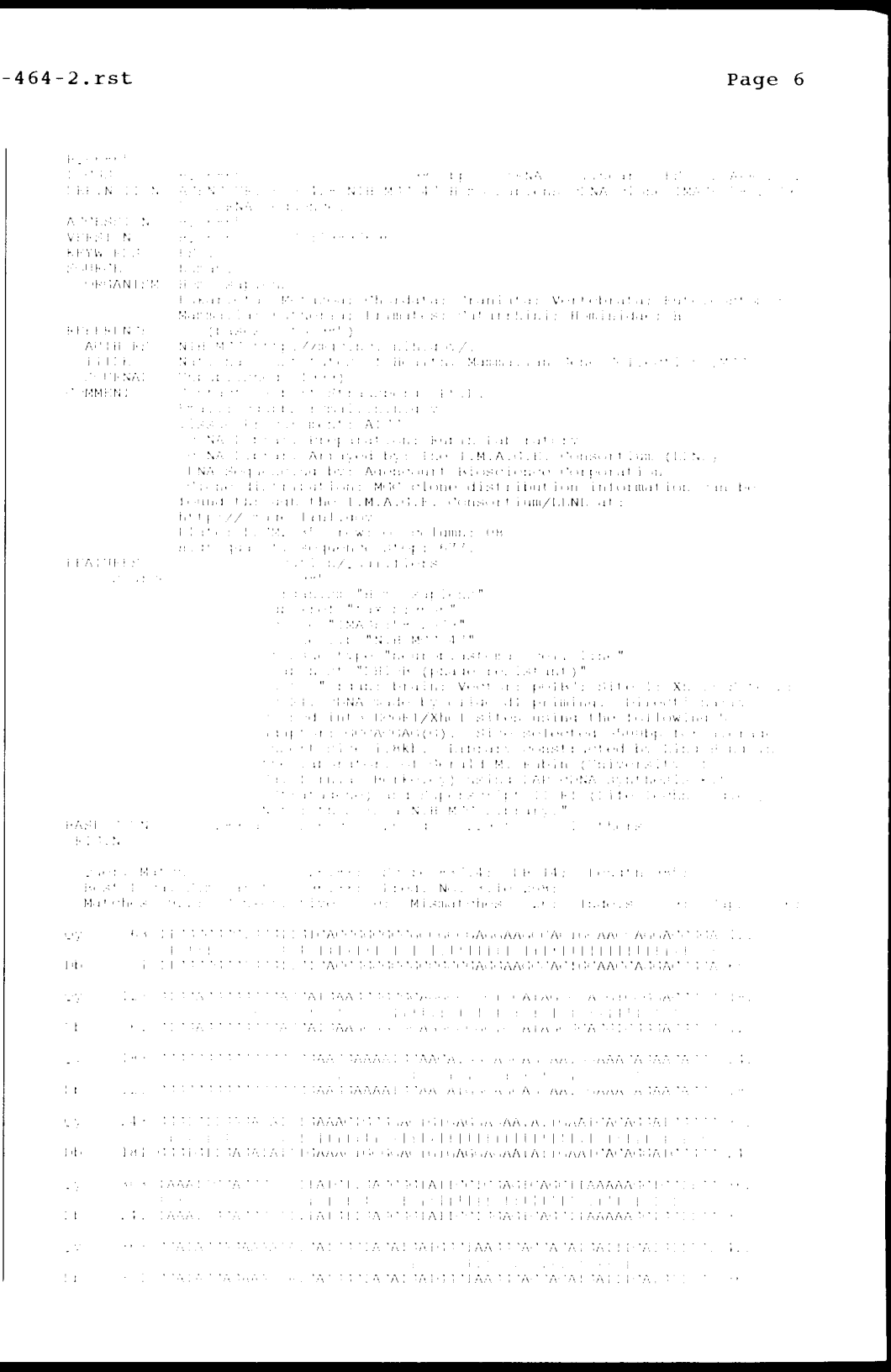
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE   1  (bases 1 to 957)
  AUTHORS   [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Robin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2456  row: h  column: 15
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                     /note="organ: salivary gland; Vector: pcDNA; Site_1:
                     Site_2: EcoRI; cDNA made by oligo dT priming;
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: 5'CACGAG(G). Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II kit (Life
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BASE COUNT      257 a    206 c    228 g    266 t
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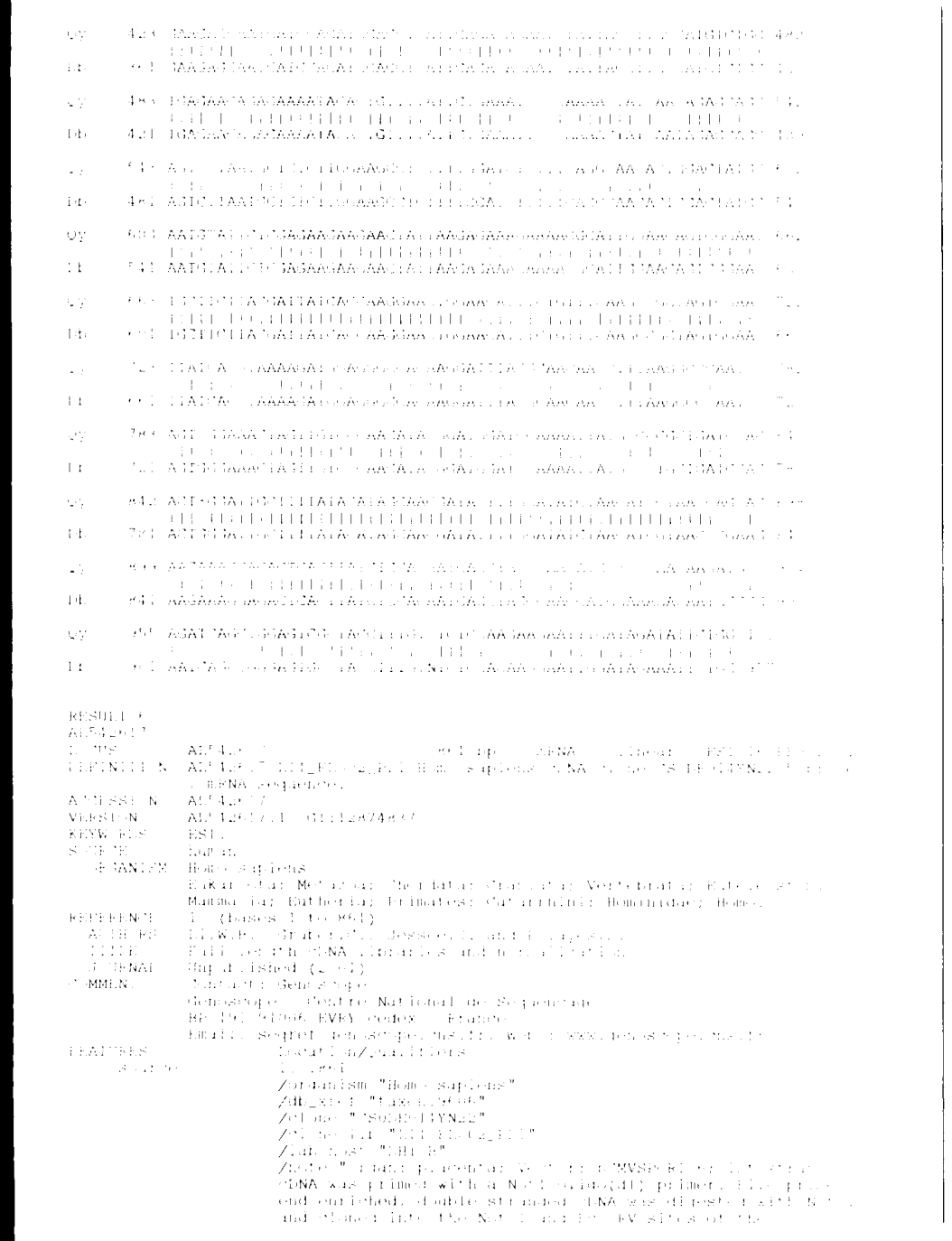
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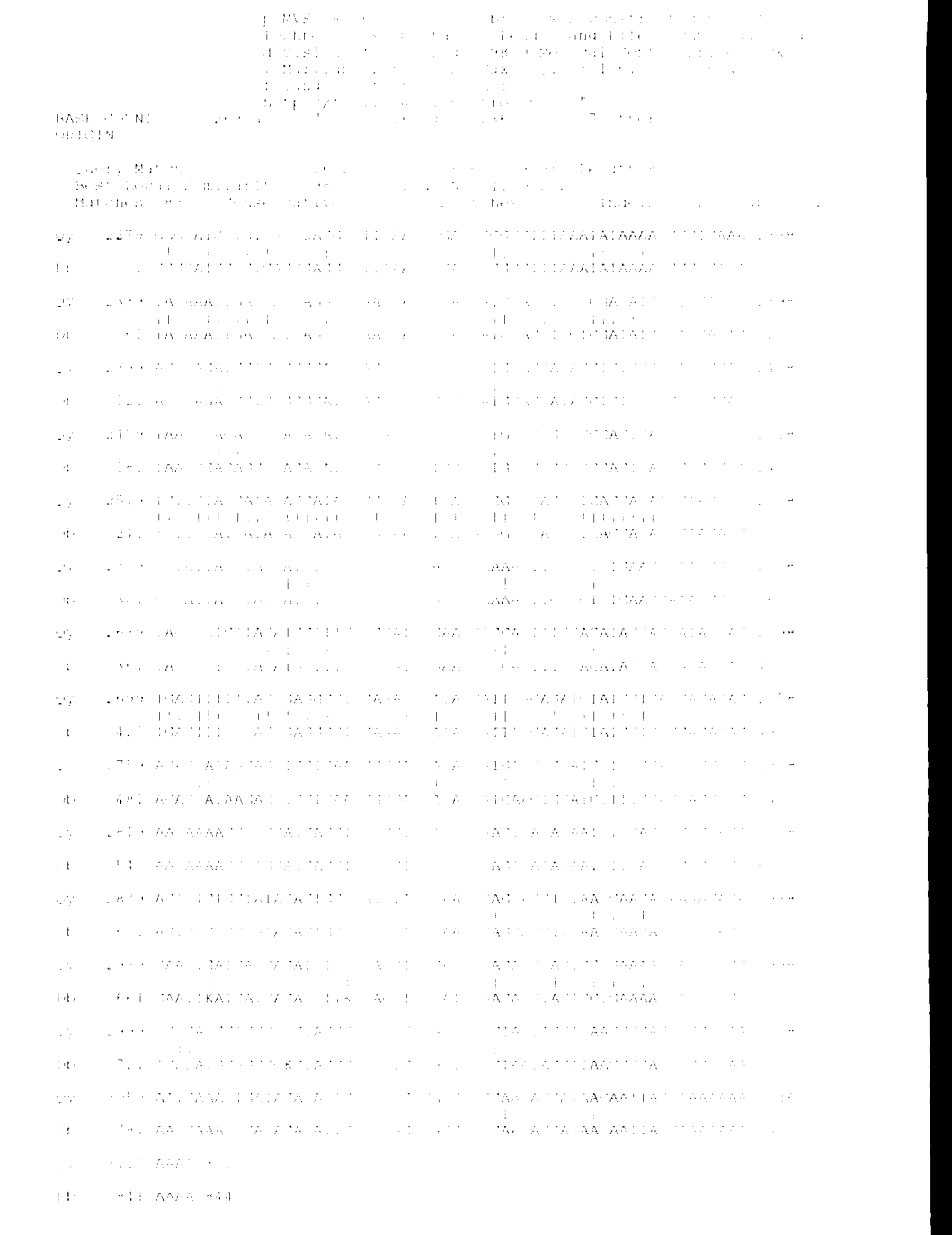


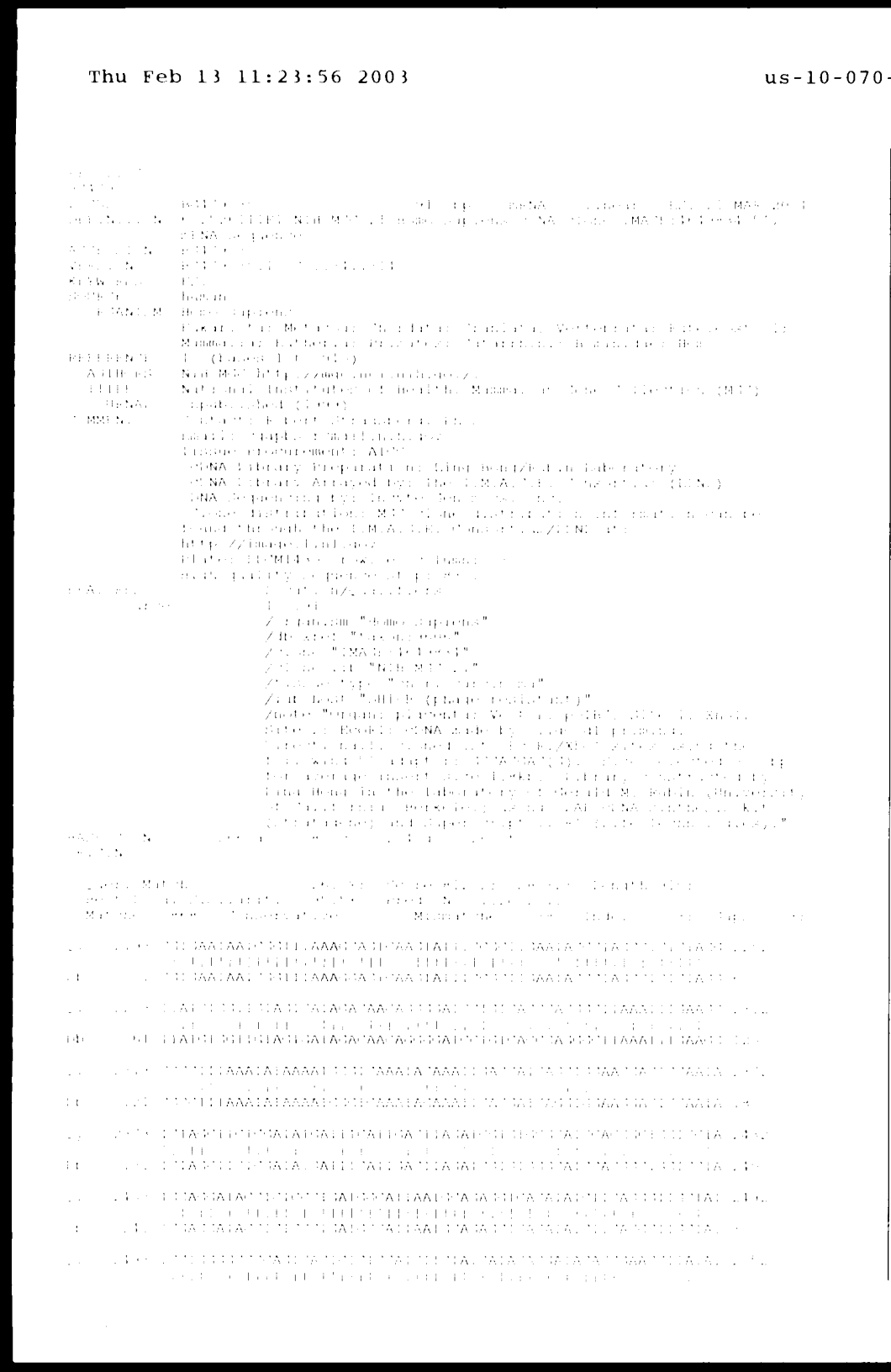


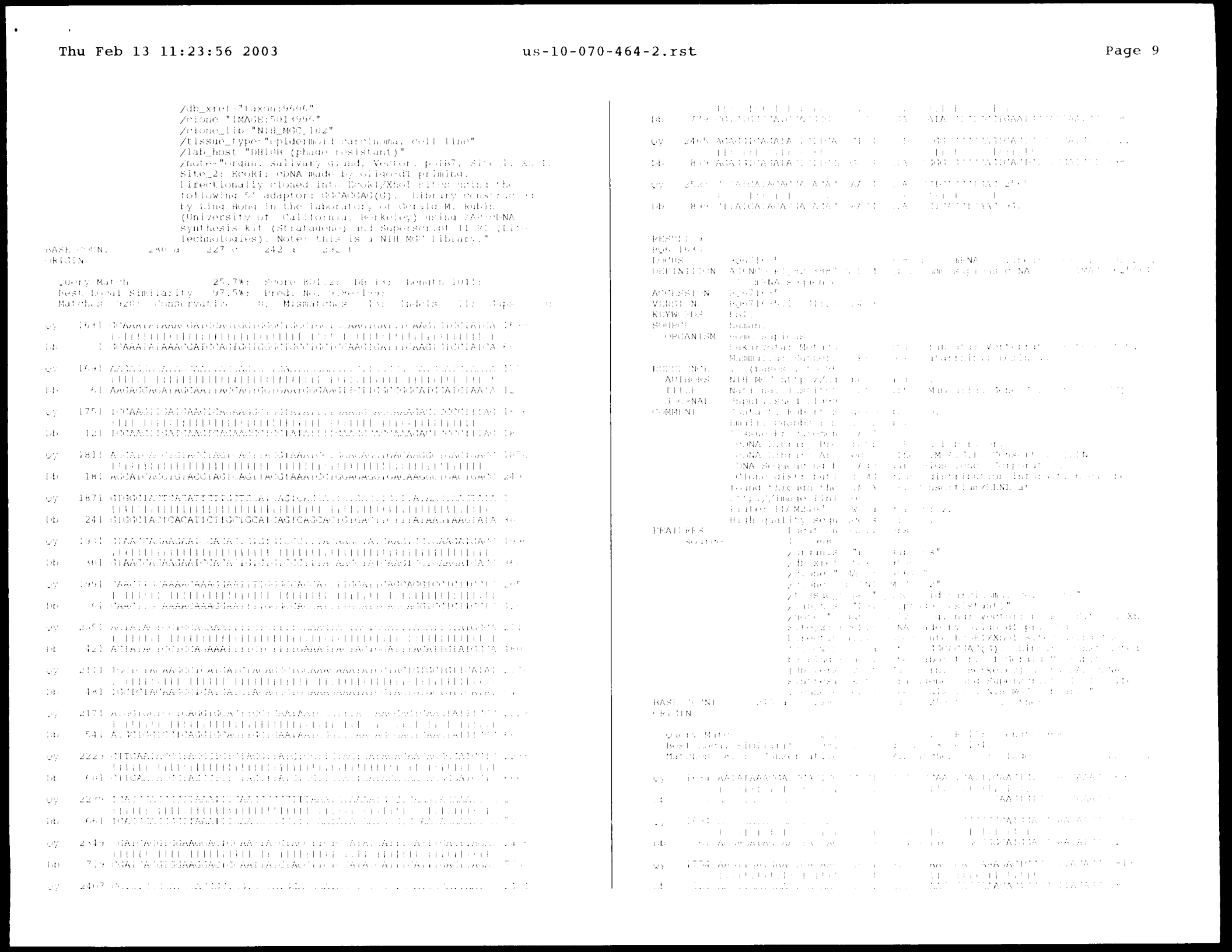


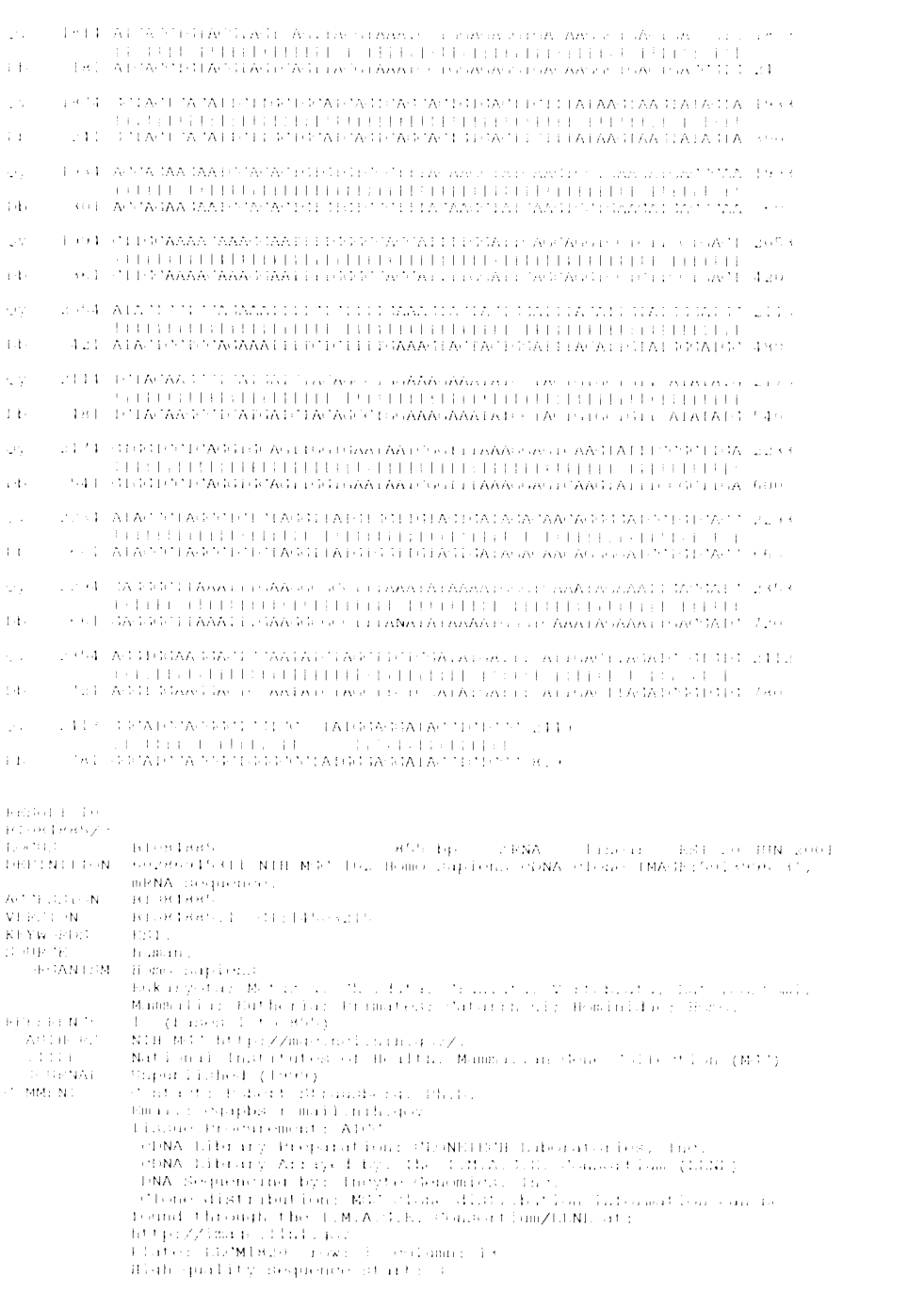


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XX
SV AL541017.1
XX
DT 12-MAR-2002 (Rel. 74, Created)
DT 12-MAR-2002 (Rel. 74, Last updated, Version 1)
XX
DE Homo sapiens
XX
KW EST.
XX
OS Homo sapiens
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN [1] (bases 1 to 961)
RA Wilson R.;
RT "Finished sequence of human DNA for chromosome 1";
RL Submitted (12-MAR-2002) Genome Sequencing Center, Washington University
RL School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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FH Key Location/Qualifiers
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FT (CHORI)"
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FT /note="DNA was primed with a NotI adapter(21) primer, first strand
FT and second strand synthesis were performed, double stranded DNA was digested
FT with NotI, size selected into the NotI cloning vector, several



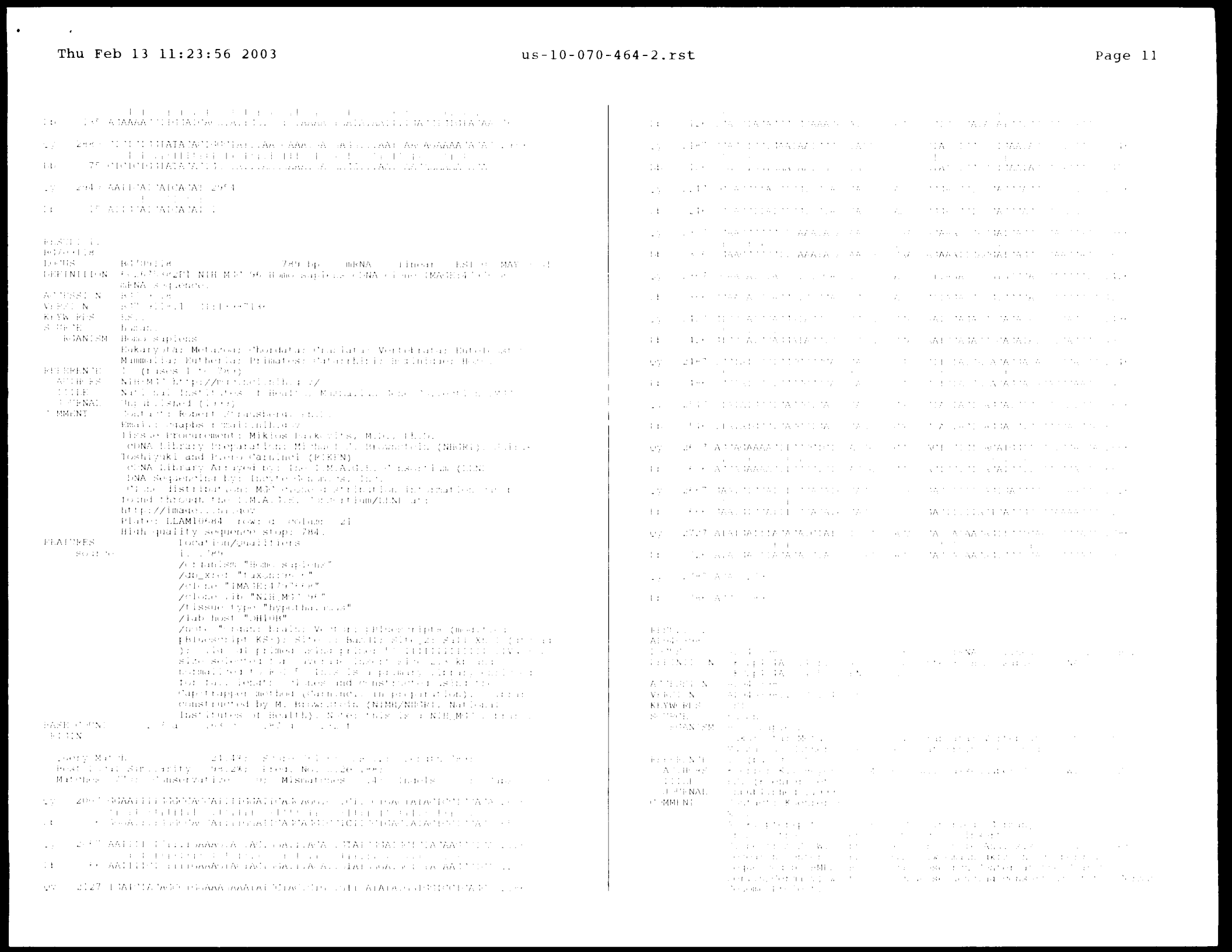


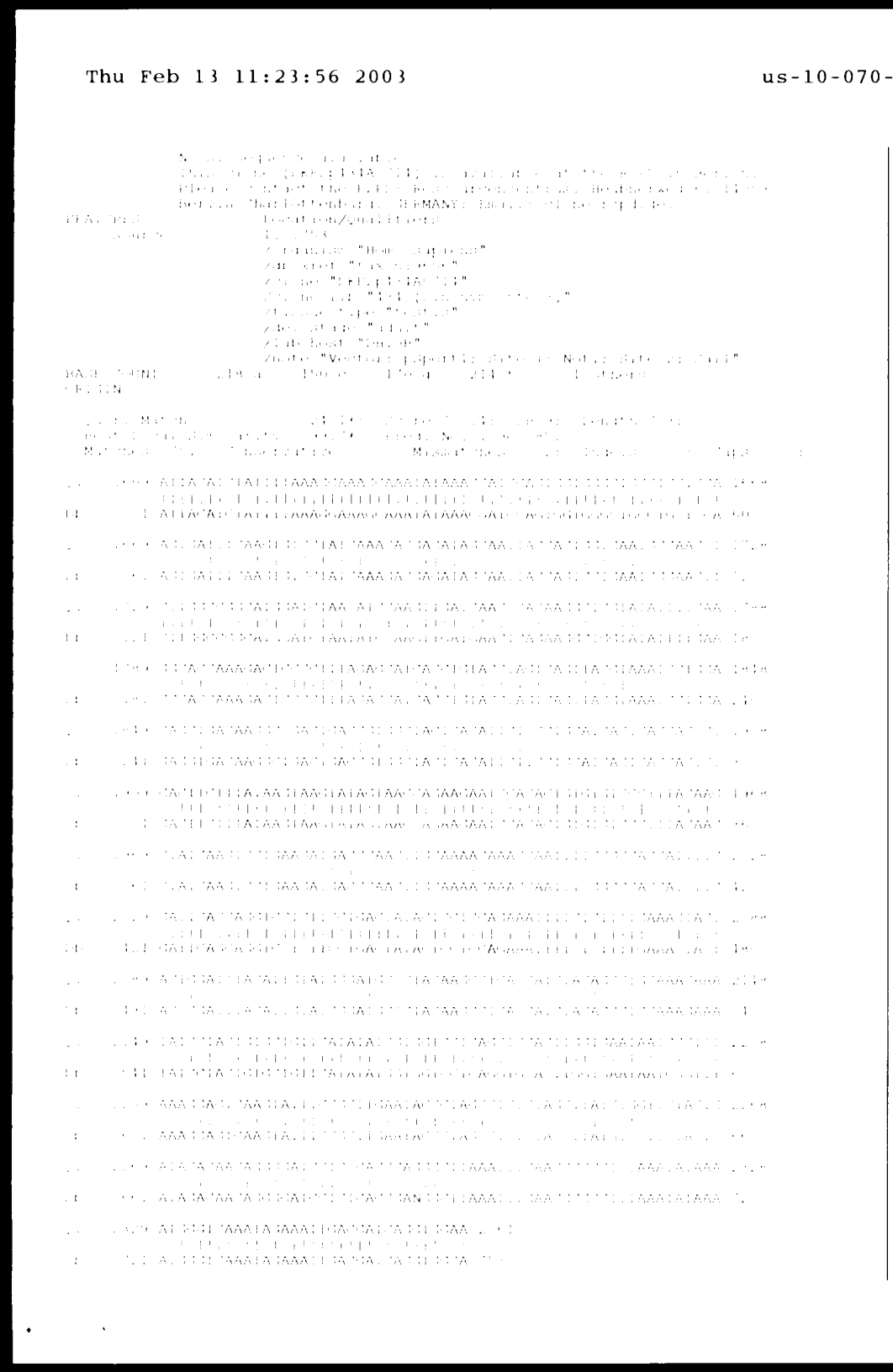




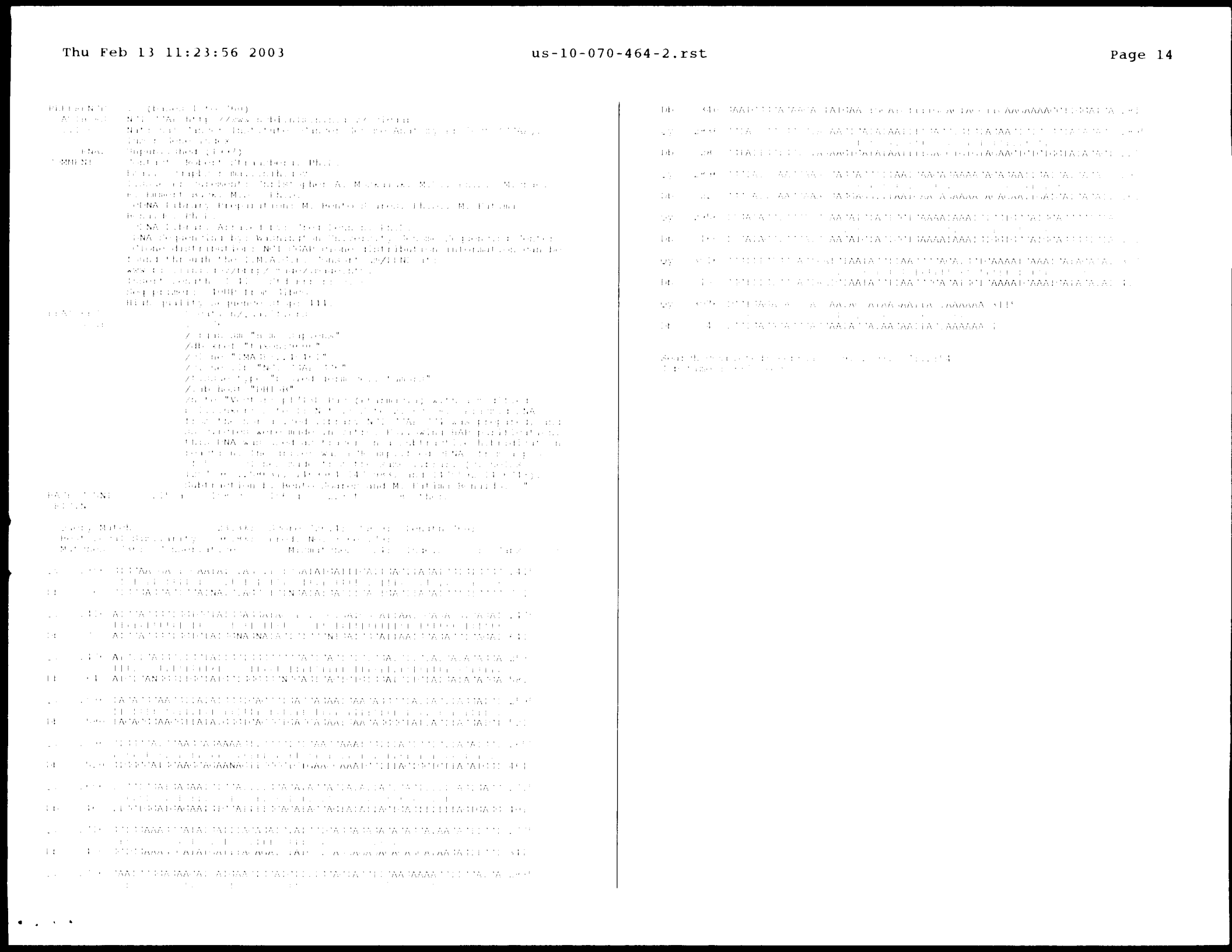
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DEFINITION  zq72e01f5.r1 NIH MGC Dog Bone Sapiens cDNA clone IMAGE:5005 5',
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ACCESSION   BI981895
VERSION     BI981895.1  GI:13115215
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Invitrogen Laboratories, Inc.
            cDNA Library Array by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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                     /note="Stratagene, Solicit, Grand, Vector, pcDNA, 2.1, Xho I,
                     Not I, 2: Double cDNA made by oligo dT priming.
                     Directionally cloned into EcoR I/Xho I sites using the
                     Not I-switch 5' adaptor: GGCACGAG(G). Library constructed
                     by Jim Bonfiglio in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH MGC library."
ORIGIN

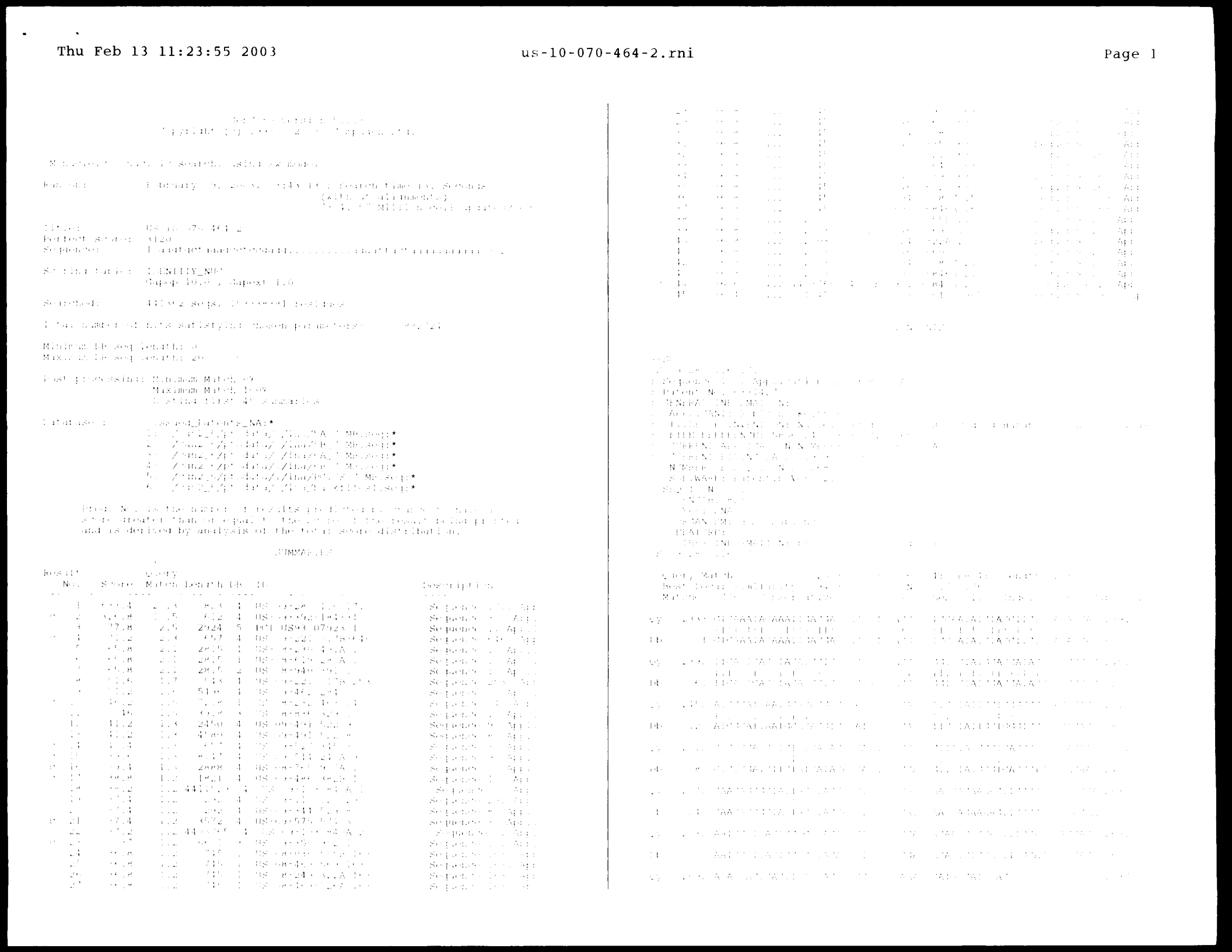
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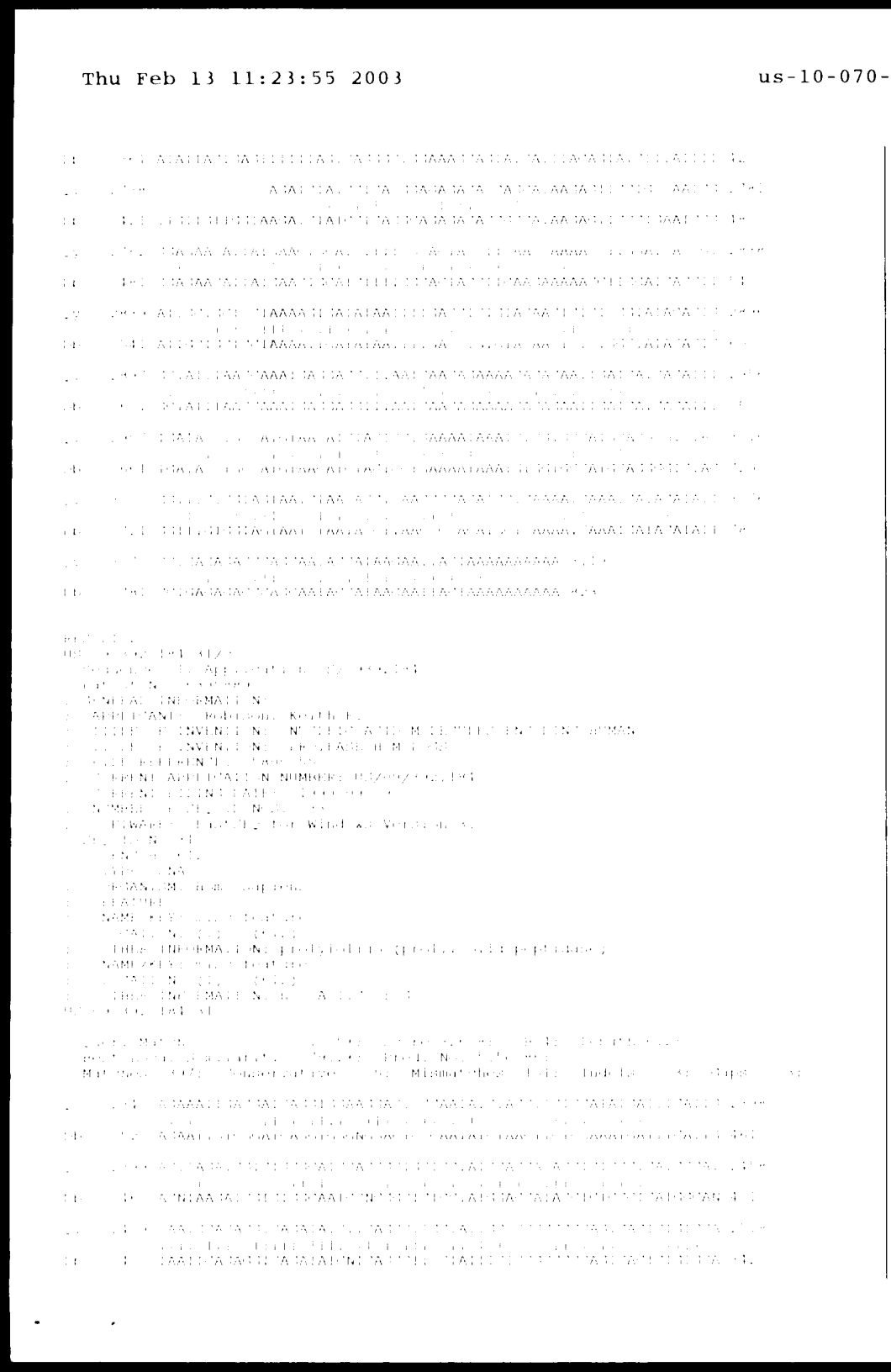


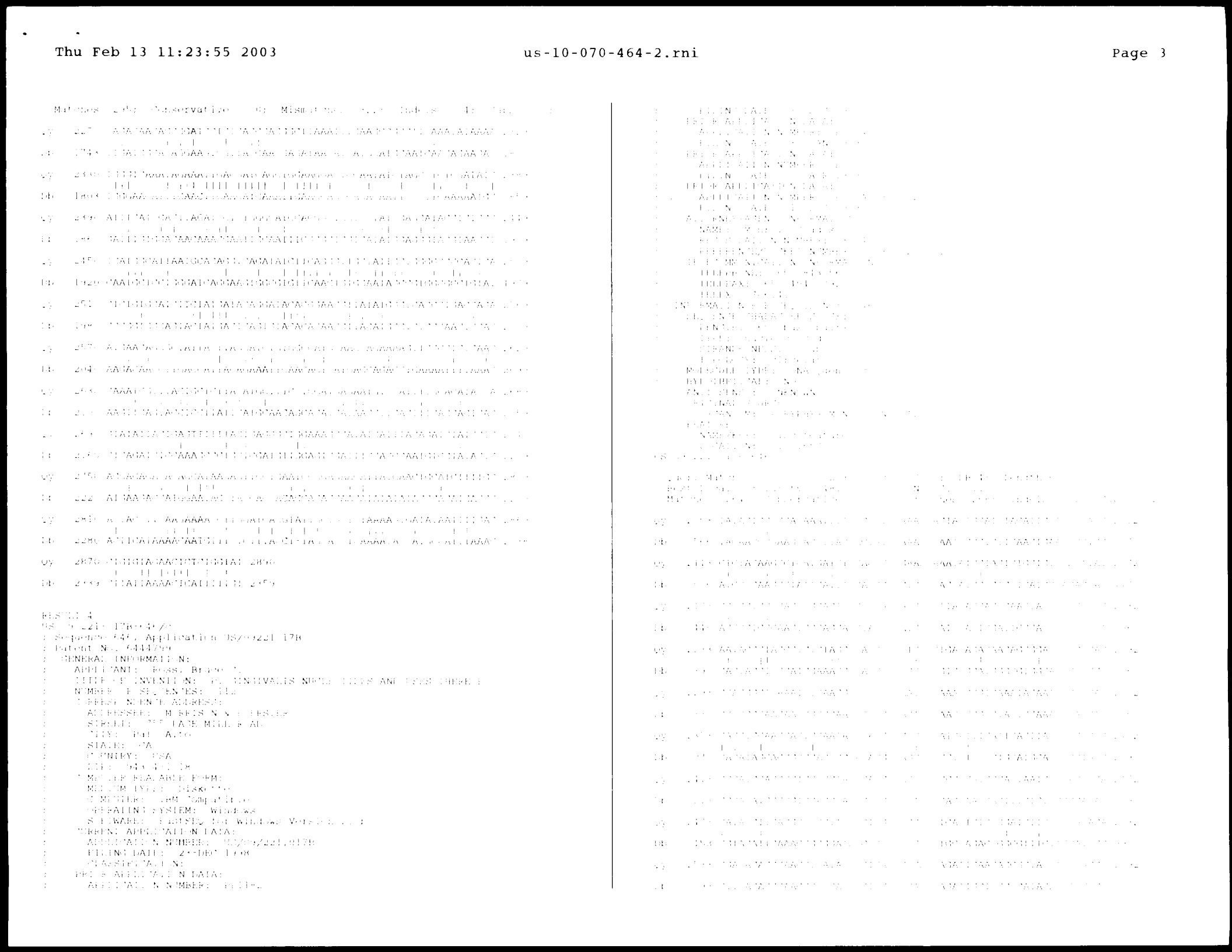


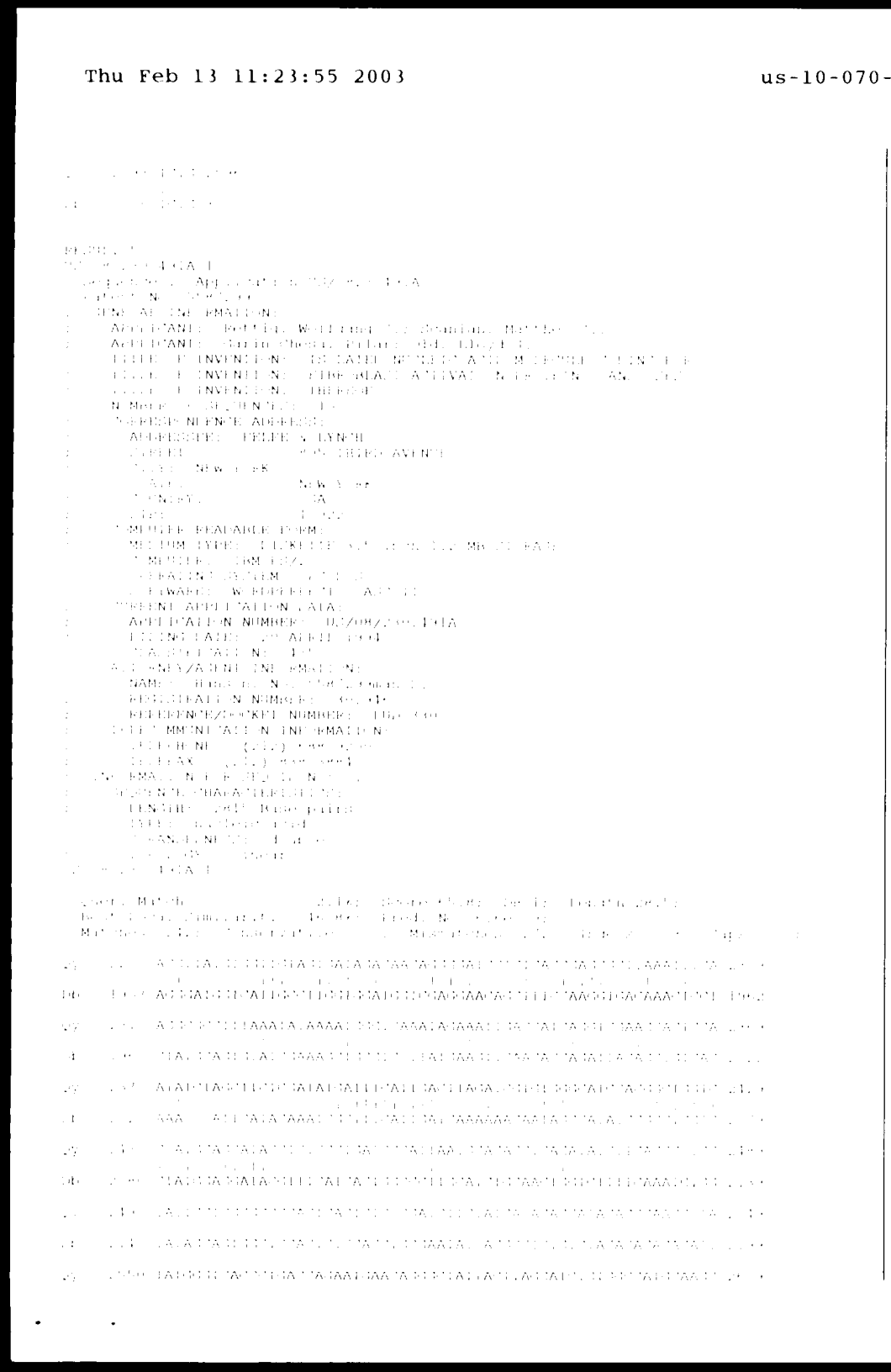
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ACCESSION   AL043338
VERSION     AL043338.1  GI:5422728
KEYWORDS    EST.
SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
REFERENCE   1  (bases 1 to 745)
  AUTHORS   Ansorge,W., Rosenthal,A., Monos,D., Lehrach,H., Radelof,U. and
            Stegner,J.
  TITLE     EST (30 Mbp of it)
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Ansorge W
            MIPS
            Max-Planck-Institute for Molecular Genetics
            Ihnestr. 73, 14195 Berlin
            Tel: +49-30-8413-1638, Fax: +49-30-8413-1385
            Email: ansorge@mpimg-berlin-dahlem.mpg.de
            Clone distributed by: Dr. W. Wiemann, Molecular Genetics of Cell
            Research Center (DKFZ); Email: w.wiemann@dkfz-heidelberg.de
            Sequenced by LMU (Ludwig Maximilians University
            Munich,Germany) within the cDNA sequencing activities of the German
            Human Genome Project.
            Seq primer: universal
            This clone (DKFZp434O0723) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum Deutschland
            Berlin-Charlottenburg, GERMANY; Email: service@rzpd.de.
FEATURES             Location/Qualifiers
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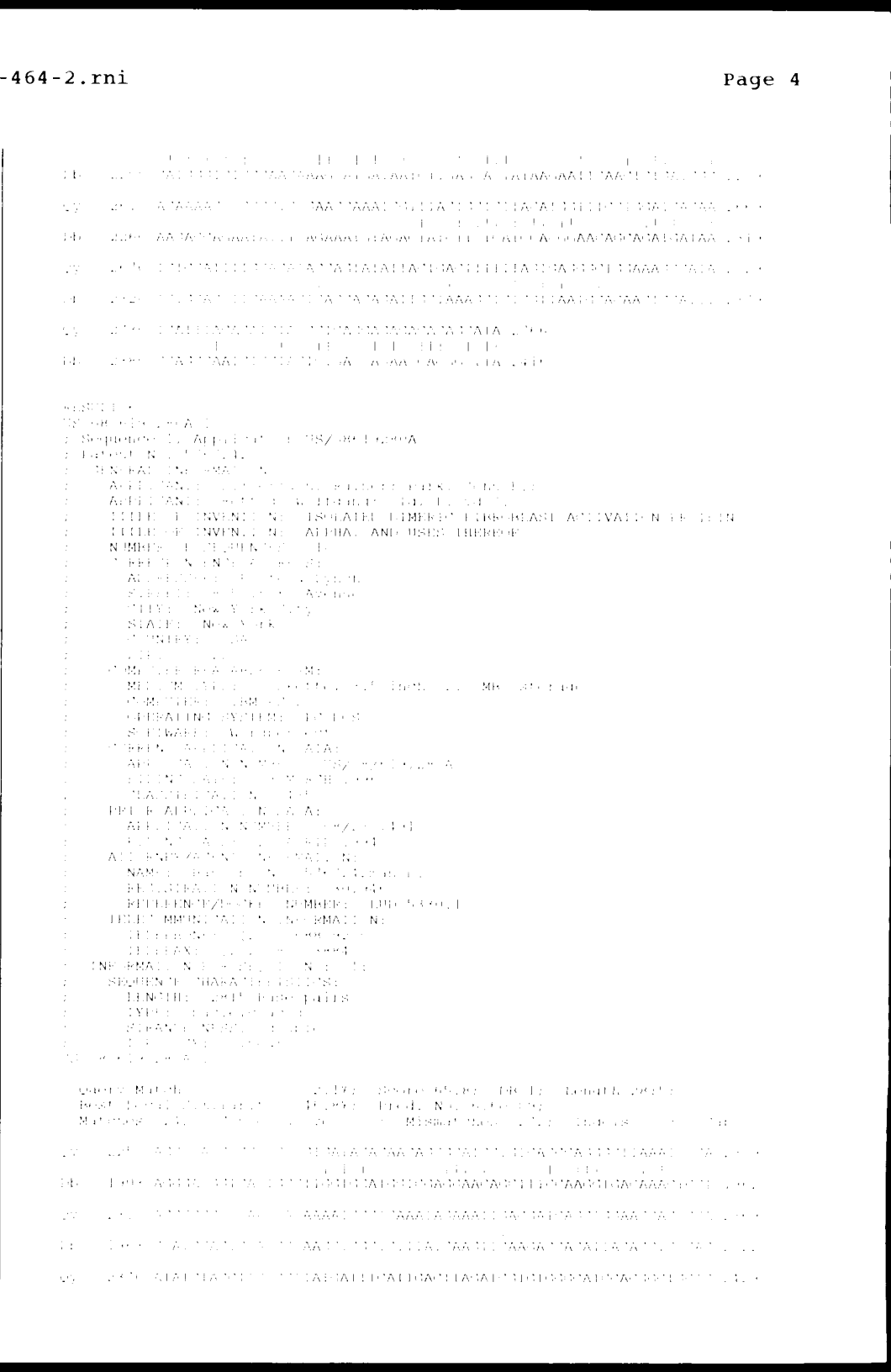


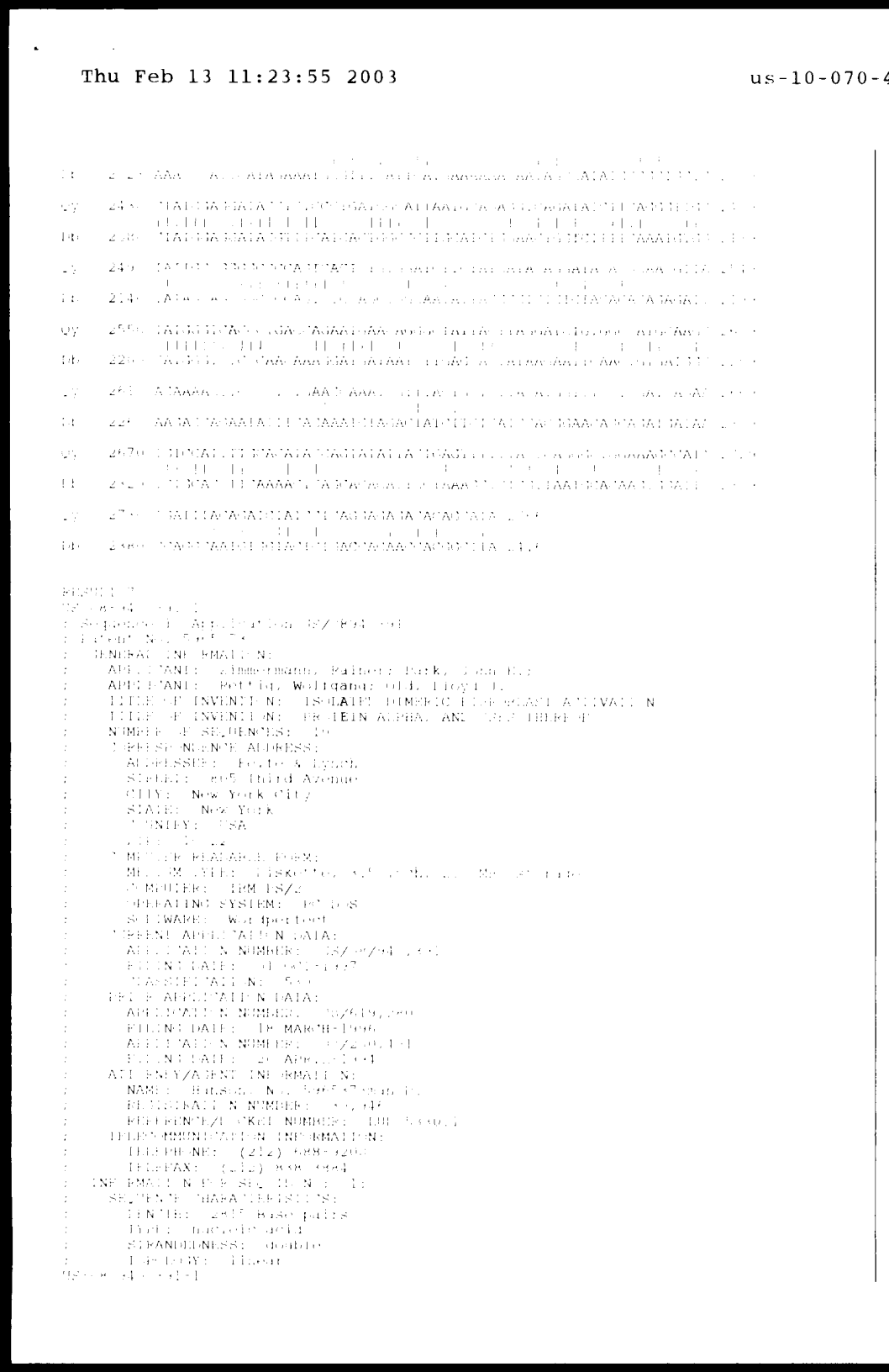


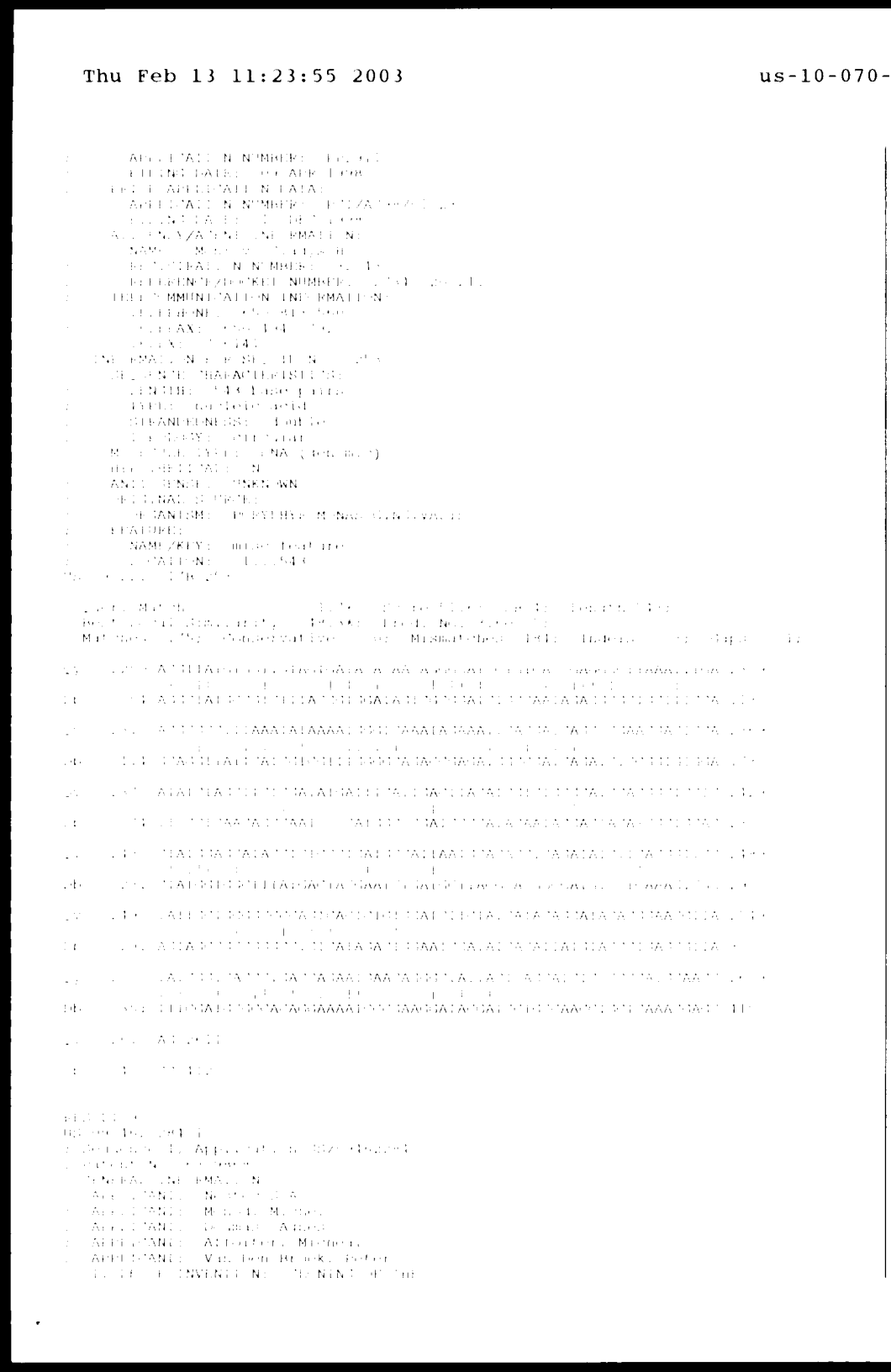


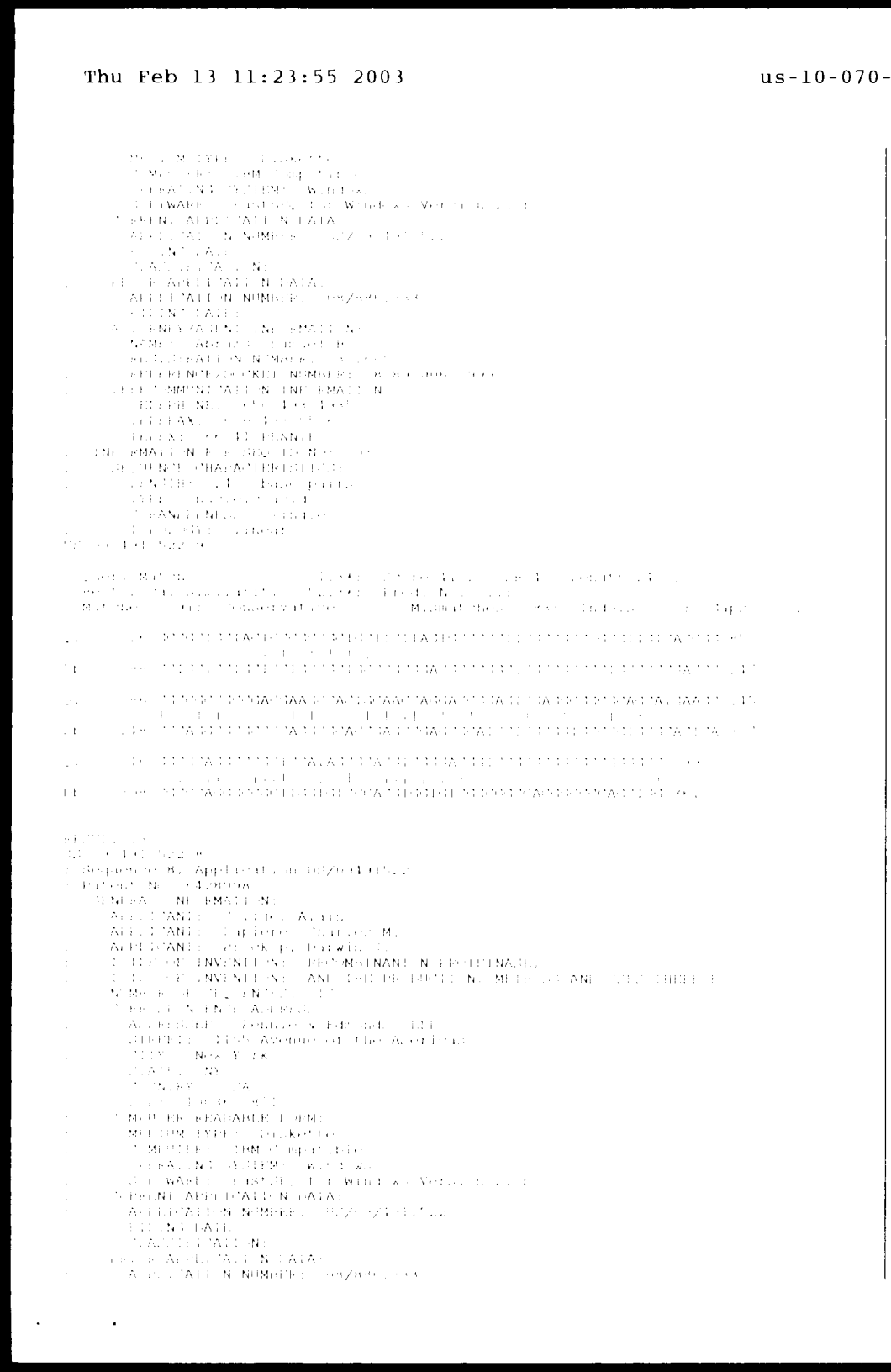


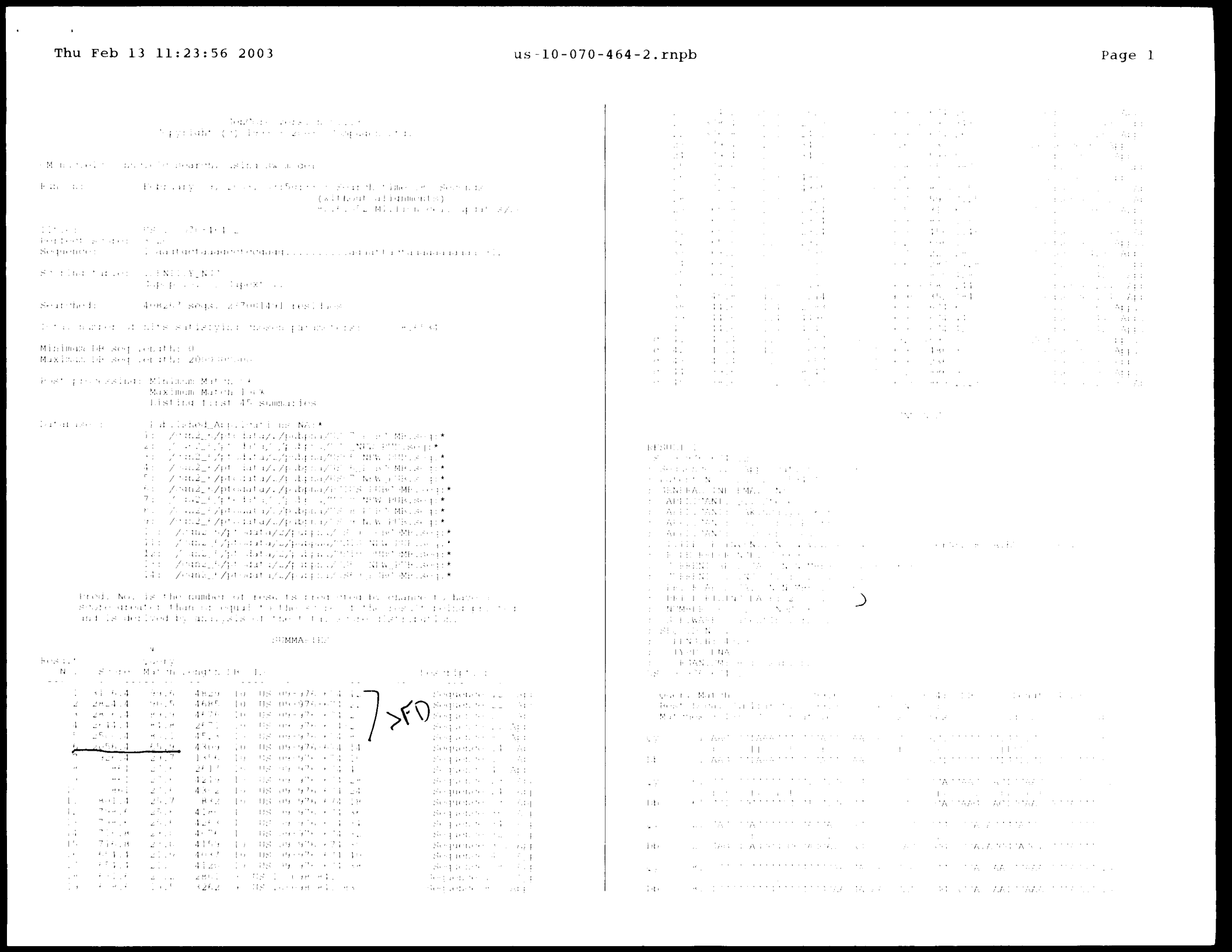


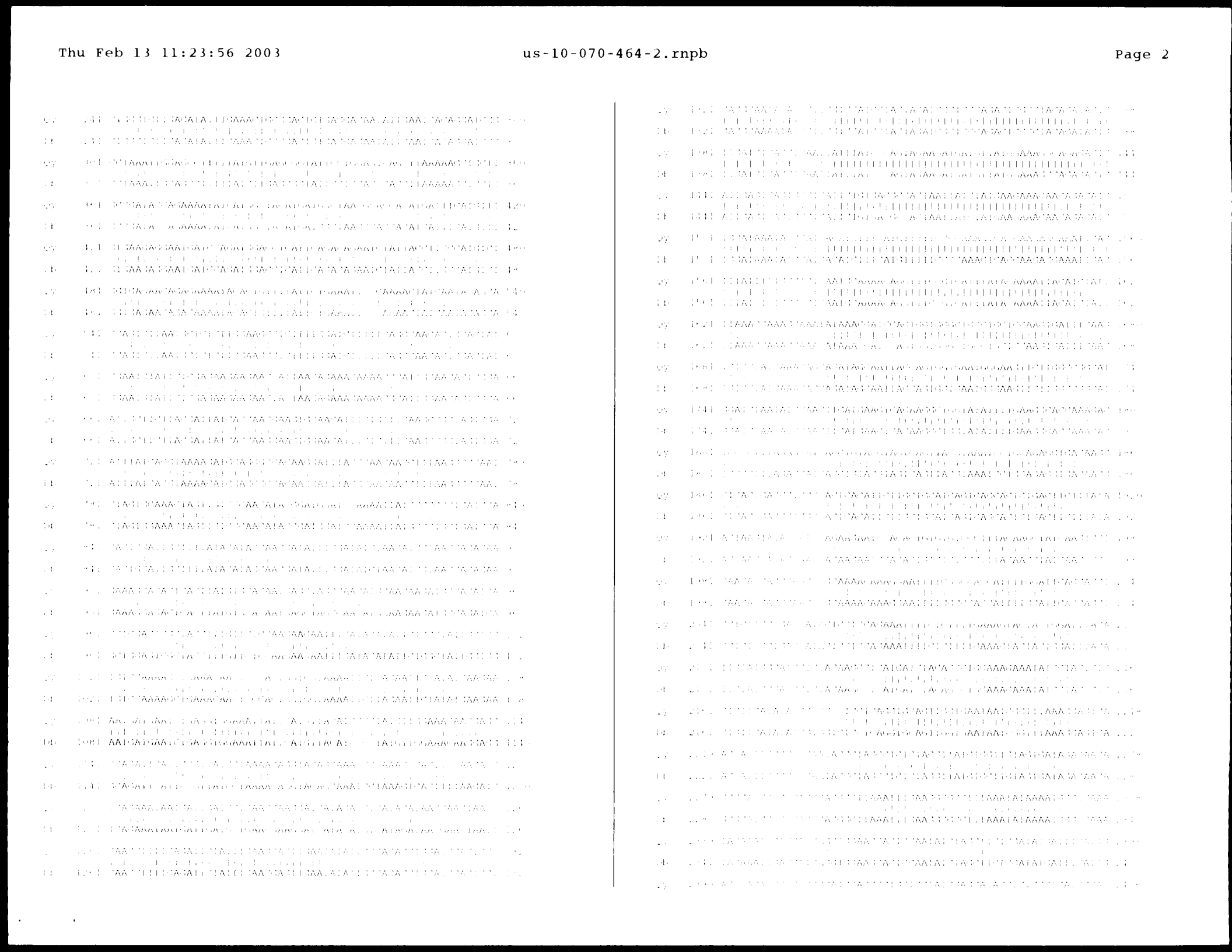


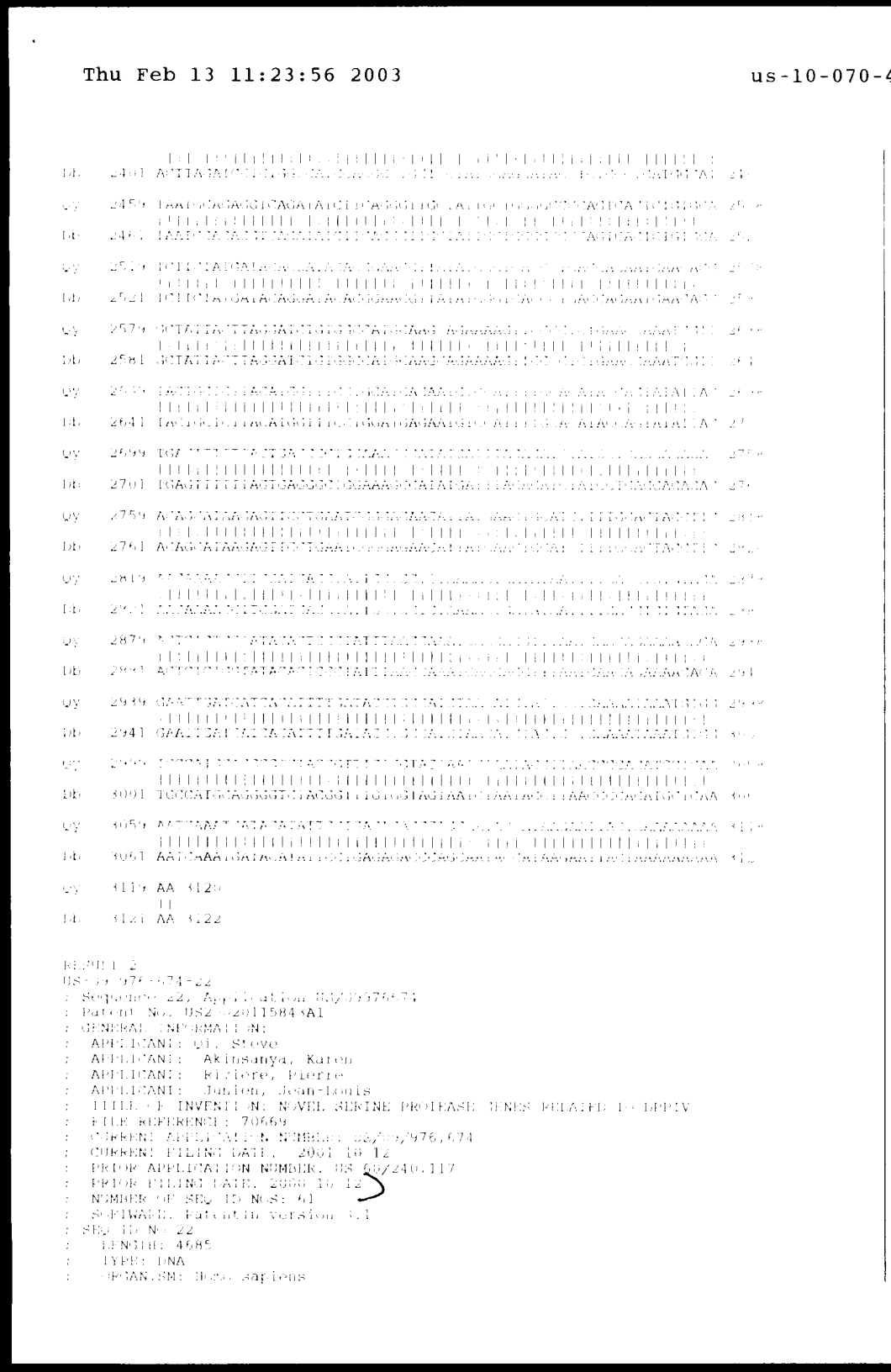




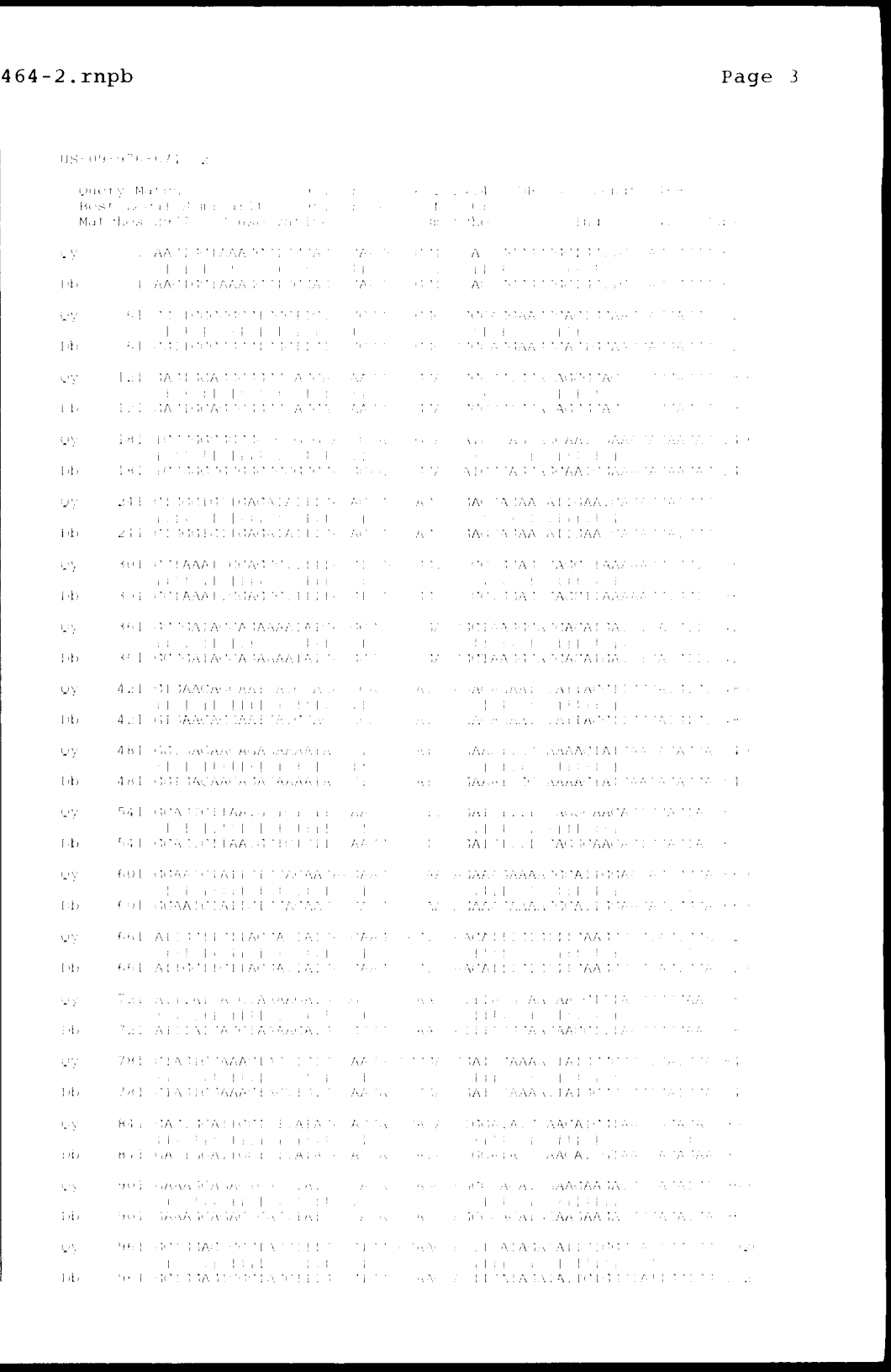


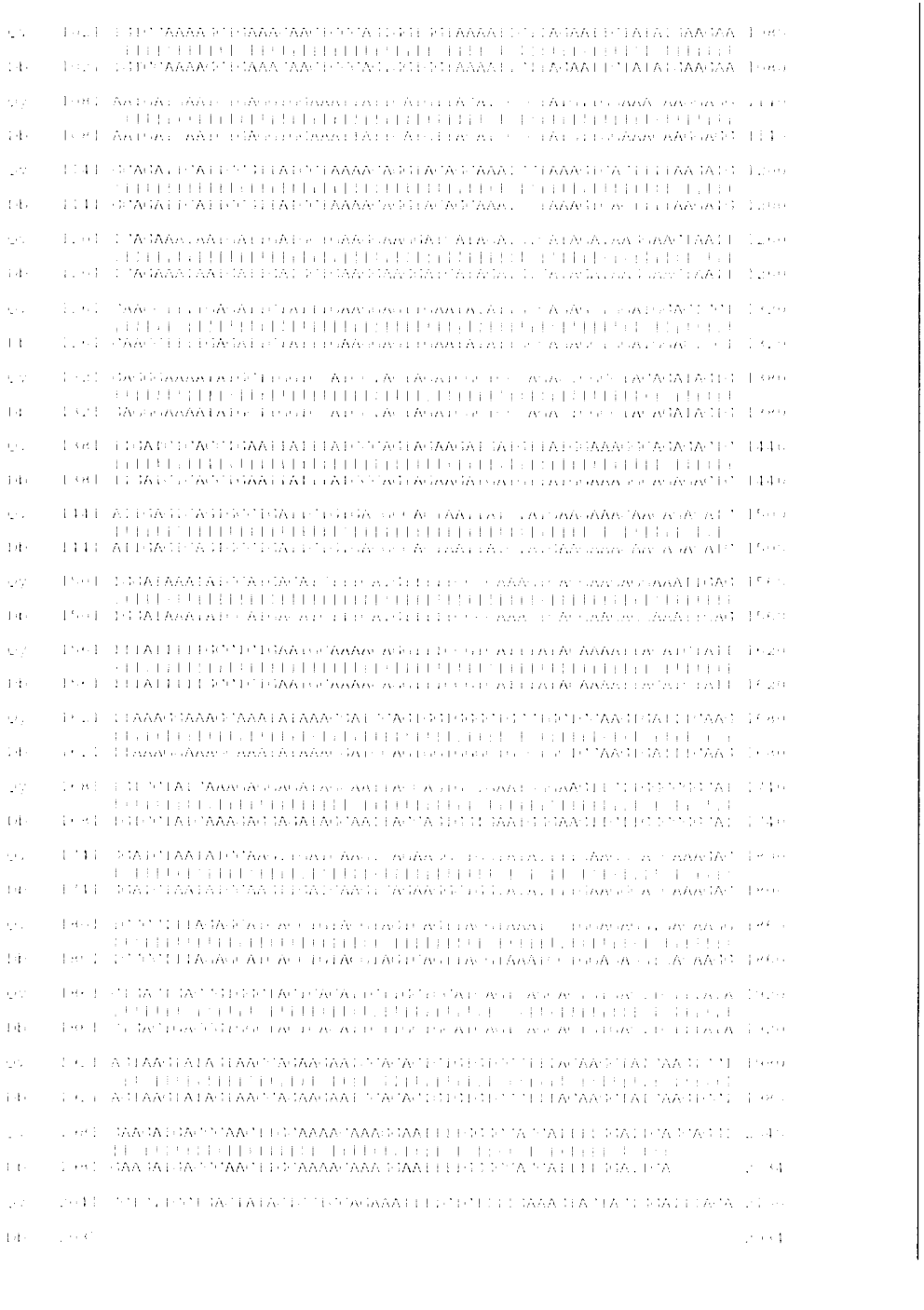






RESULT 2
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; Patent No. US20011584SA1
; GENERAL INFORMATION:
; APPLICANT: Qi, Steve
; APPLICANT: Akinsanya, Karen
; APPLICANT: Richere, Pierre
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: NOVEL SERINE PROTEASE GENES RELATED TO HEPATITIS C
; FILE REFERENCE: 70669
; CURRENT APPLICATION NUMBER: US/09/976,674
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,117
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 22
; LENGTH: 4685
; TYPE: DNA
; ORGANISM: Homo sapiens

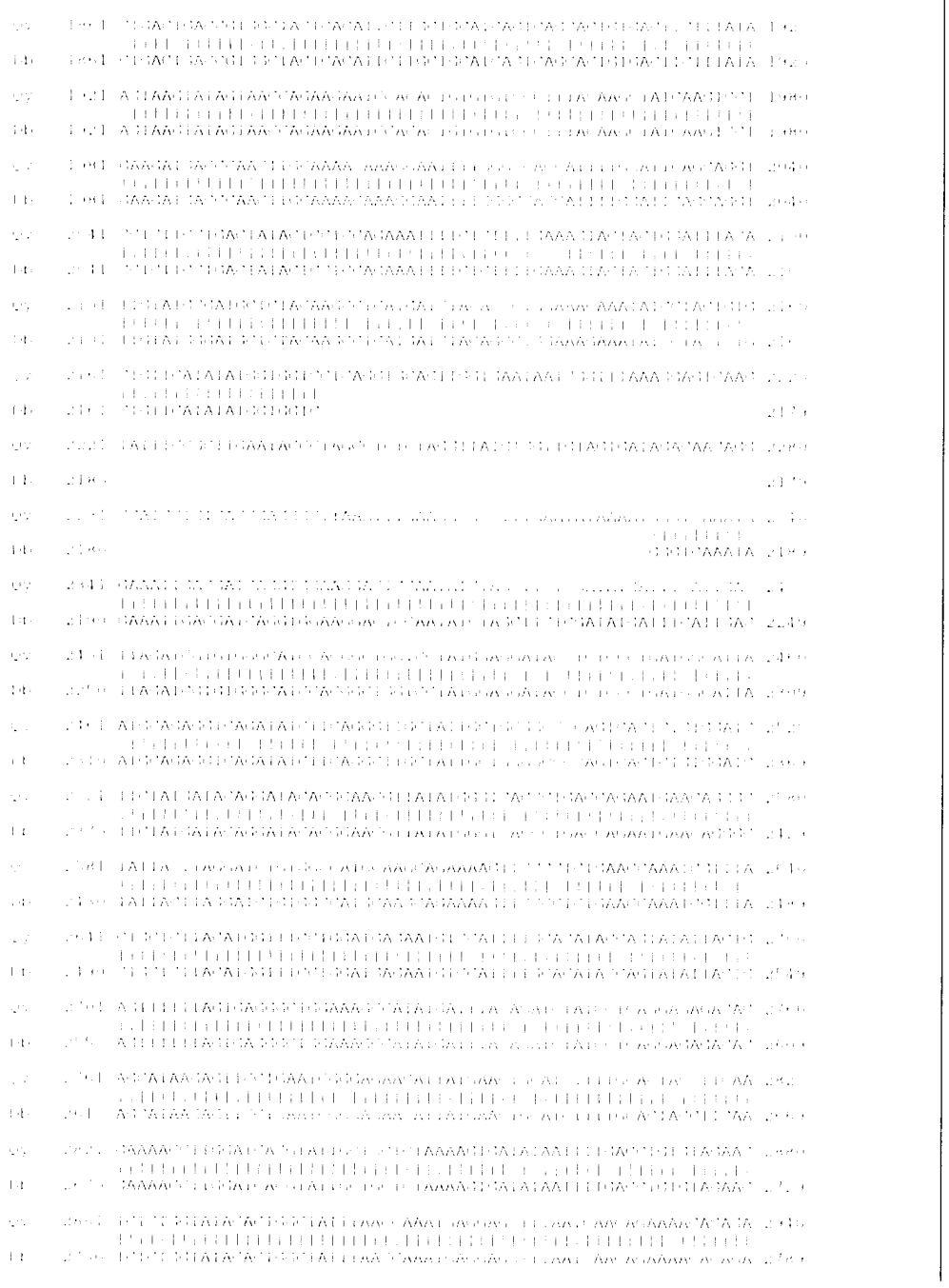




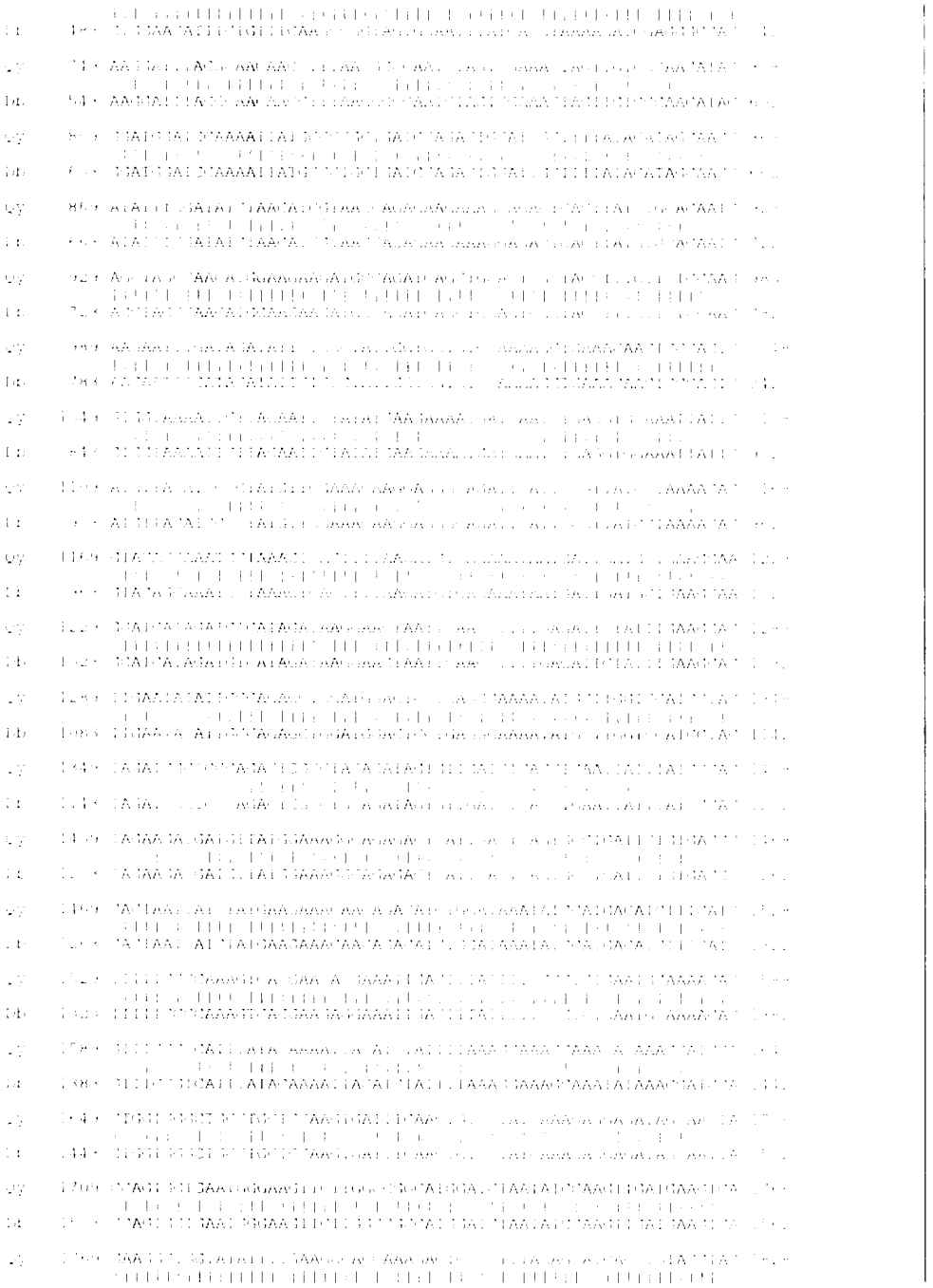
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; Patent No. US6946134

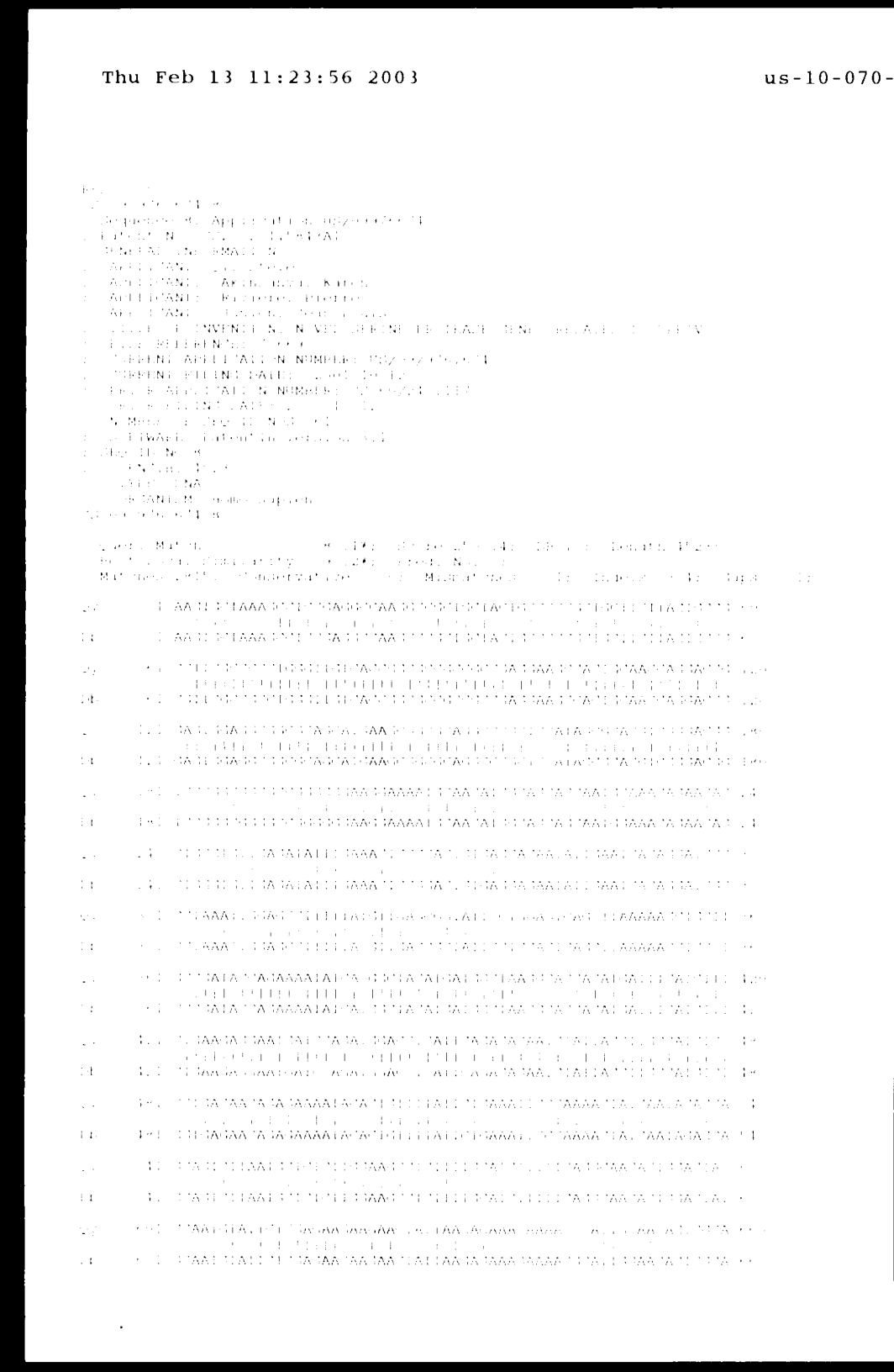
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; GENERAL INFORMATION:
;  APPLICANT: yi, Steve
;  APPLICANT:  Akinsanya, Karen
;  APPLICANT:  Pitziore, Pierre
;  APPLICANT:  Junien, Jean-Louis
;  TITLE OF INVENTION: NOVEL SEKINE PROTEASE, GENES RELATED TO DIPEV
;  FILE REFERENCE: 70669
;  CURRENT APPLICATION NUMBER: US/09/976,674
;  CURRENT FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: US 60/240,117
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;  LENGTH: 4676
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-976-674-20

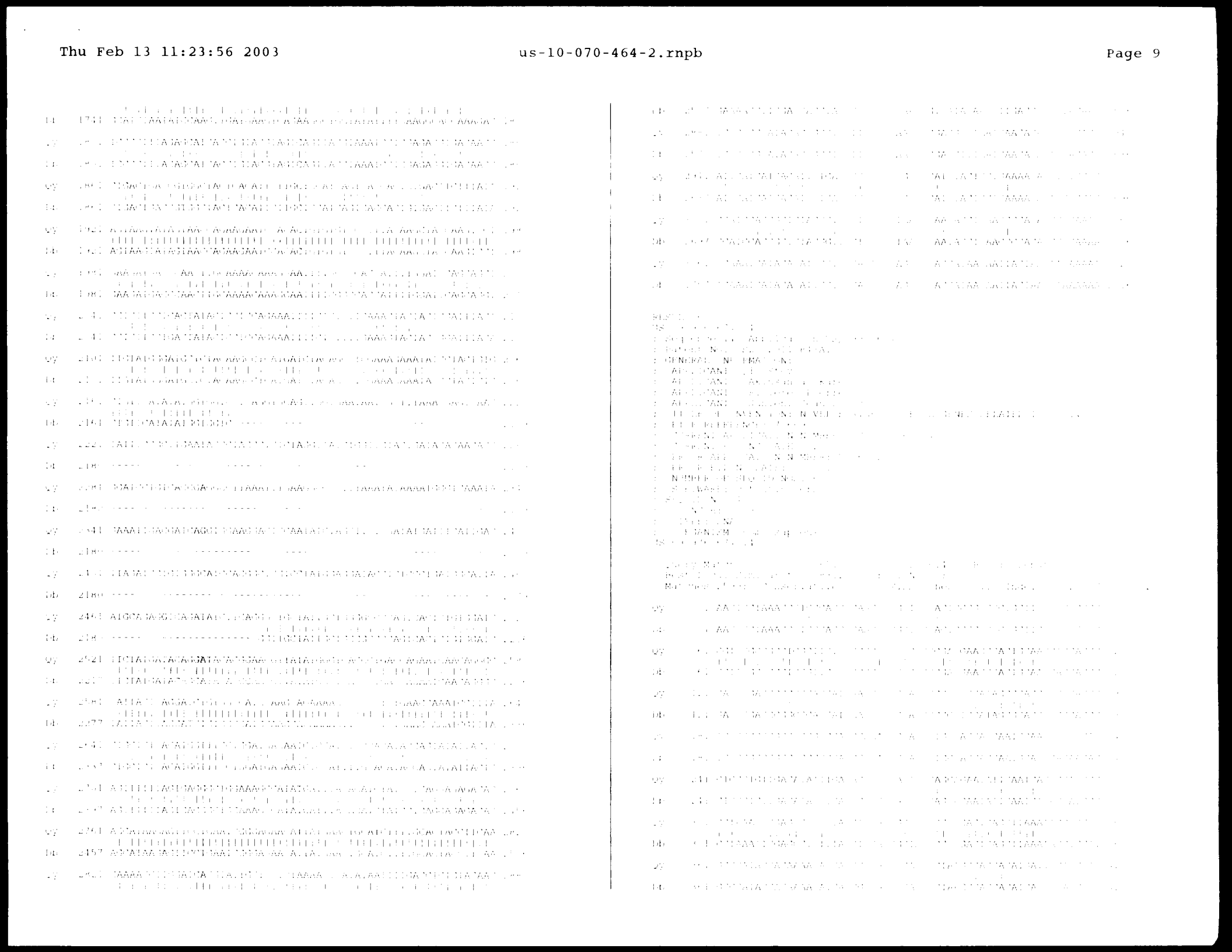
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  Best Local Similarity   95.1%;  Pred. No. --;
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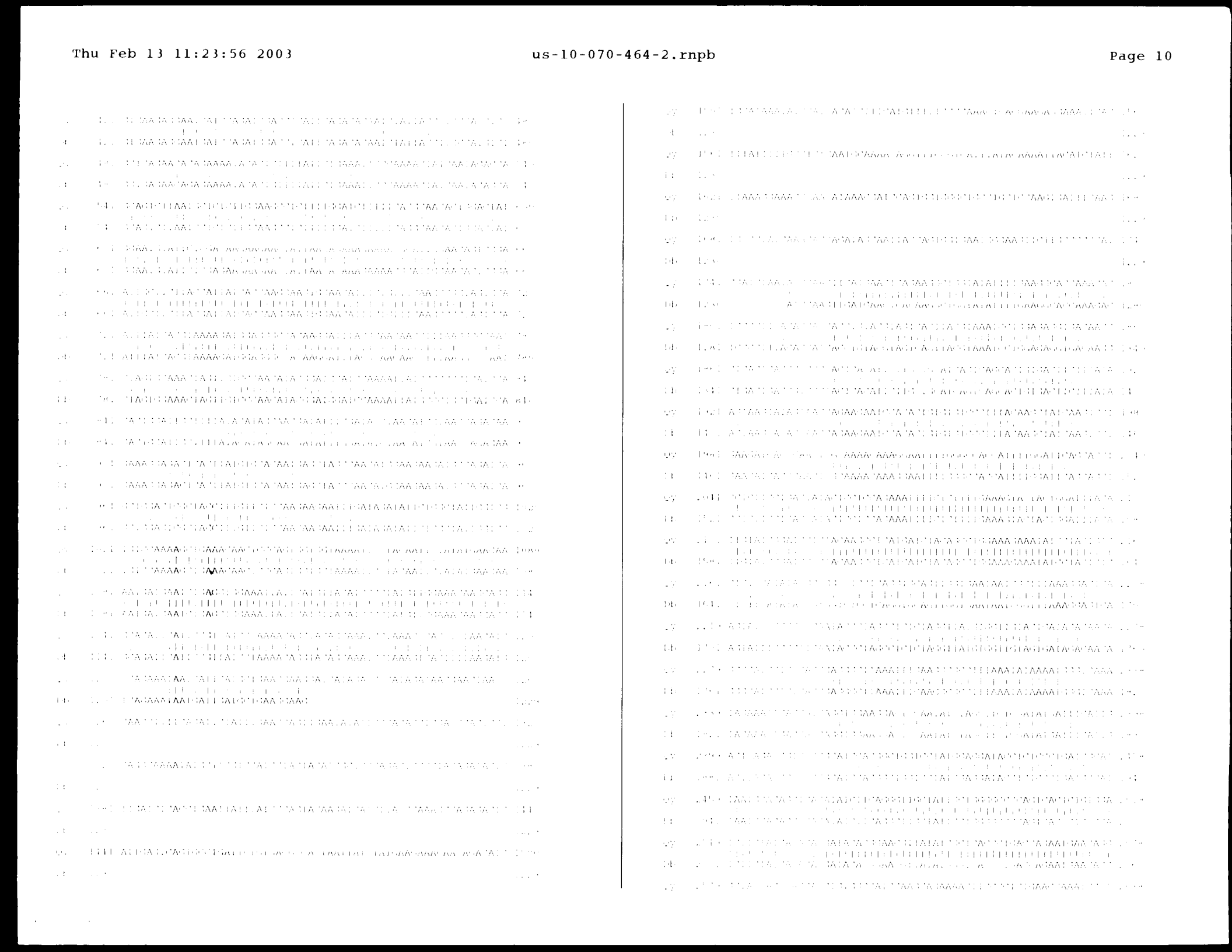


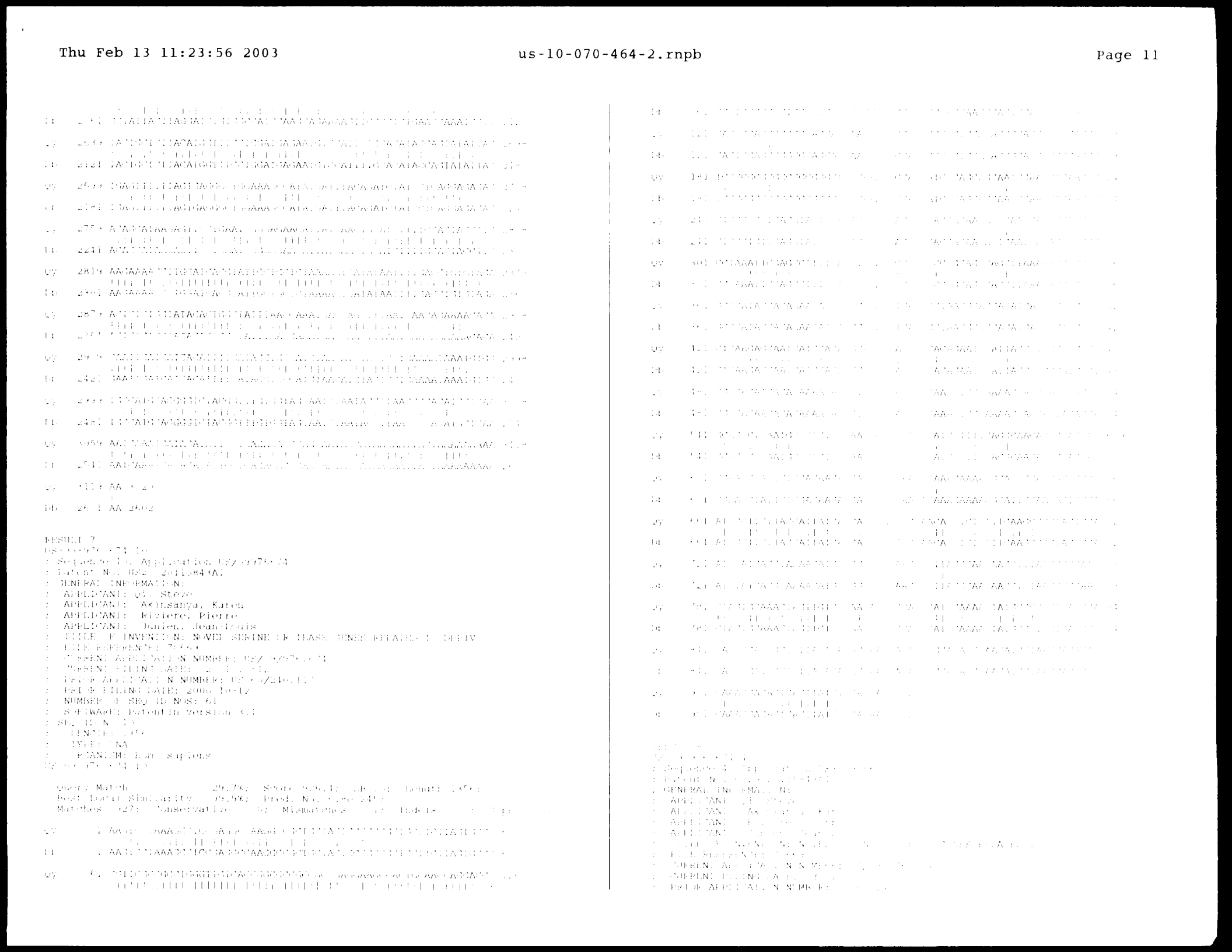
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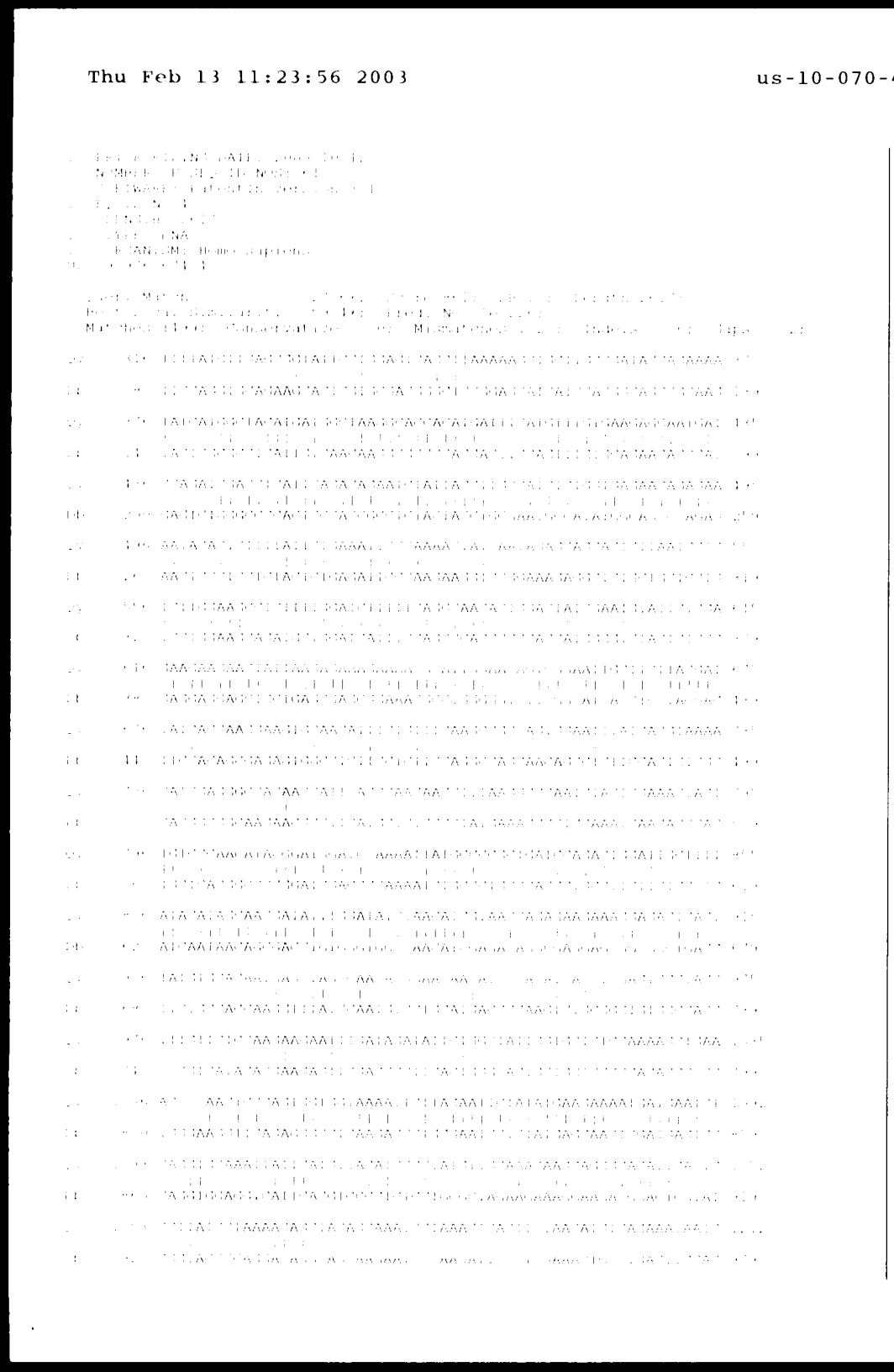


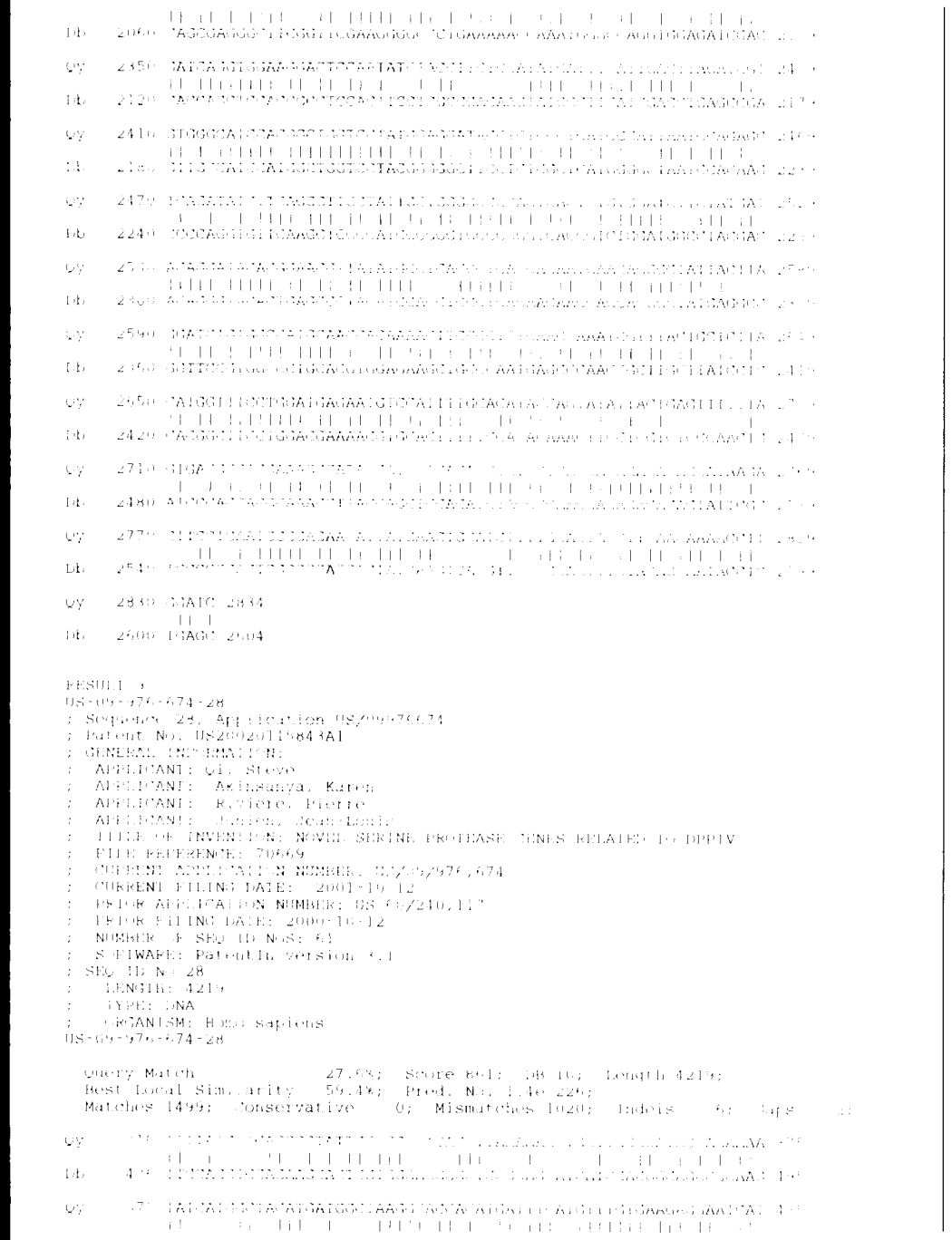












RESULT 1
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; Sequence 28, Application US/09/976674
; Patent No. US20020119843A1
; GENERAL INFORMATION:
; APPLICANT: Qi, Steve
; APPLICANT: Akhsanya, Karen
; APPLICANT: Rajotte, Pierre
; APPLICANT: Junien, Jean-Louis
; TITLE OF INVENTION: NOVEL SERINE PROTEASE GENES RELATED TO DPPIV
; FILE REFERENCE: 70669
; CURRENT APPLICATION NUMBER: US/09/976,674
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,117
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 63
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US-09-976-674-28

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